

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 11:39:55 ; Search time 11007.4 Seconds
(without alignments)
9336.759 Million cell updates/sec

Title: US-10-062-879-1

Perfect score: 2121
Sequence: 1 gatttgcgtgactaactcca.....gtcgtatctaagccggaattc 2121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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1:  gb_ba:*
2:  gb_hcg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_stcs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	2121	100.0	2121	6	AR371346	AR371346 Sequence	
2	2036.2	96.0	2722	9	AF120491	AF120491 Homo sapi	
3	2025	95.5	2041	9	AF187963	AF187963 Homo sapi	
4	1997	94.2	2064	6	AR371347	AR371347 Sequence	
5	1963.2	92.6	1968	9	AF048713	AF048713 Homo sapi	
6	1962	92.5	2072	6	A85166	A85166 Sequence 3	
7	1962	92.5	2072	6	AR204885	AR204885 Sequence	
8	1960	92.4	1968	6	AX956786	AX956786 Sequence	
9	1959.6	92.4	1968	9	AF205857	AF205857 Homo sapi	
10	1901	89.6	1984	9	AF187964	AF187964 Homo sapi	
11	1839.2	86.7	1911	6	AF048712	AF048712 Homo sapi	
12	1838	86.7	2104	9	A85164	A85164 Sequence 1	
13	1838	86.7	2104	6	AR204884	AR204884 Sequence	
14	1836	86.6	1911	9	AF205856	AF205856 Homo sapi	
15	1830	86.3	2104	6	A85168	A85168 Sequence 5	
16	1830	86.3	2104	6	AR204886	AR204886 Sequence	
17	1816.4	85.6	2057	4	AF454388	AF454388 Mustela p	
18	1780.8	84.0	1968	4	AF198445	AF198445 Oryctolag	
19	1718.4	81.0	1968	10	AB003587	AB003587 Rattus no	

ALIGNMENTS

20	1716.8	80.9	1968	10	AF334791	AF334791 Rattus no
21	1699.2	80.1	1958	10	AF107781	AF107781 Mus muscu
22	1631	76.9	1728	10	RNU42975	U42975 Rattus norv
23	1621	76.4	1966	10	RNU75448	U75448 Rattus norv
24	1576.8	74.3	1911	10	AF107782	AF107782 Mus muscu
25	1494.8	70.5	4262	10	RATKV43R	148619 Rattus norv
26	1433.8	67.6	1665	4	AF493549	AF493549 Oryctolag
27	1394.6	65.8	1977	5	AF209722	AF209722 Gallus ga
28	1178.2	55.5	1754	9	AF166009S1	AF166009 Homo sapi
29	1178.2	55.5	149322	2	AC016039	AC016039 Homo sapi
30	1178.2	55.5	169559	9	AL512665	AL512665 Human DNA
31	1178.2	55.5	186666	2	AL592143	AL592143 Homo sapi
32	1138.6	53.7	2840	5	XLU89265	U89265 Xenopus lae
33	1107.8	52.2	1114	6	C0728922	C0728922 Sequence
34	1000	47.1	223192	2	AC127011	AC127011 Rattus no
35	1000	47.1	228013	2	AC105582	AC105582 Rattus no
36	992.4	46.8	1907	4	AF508735	AF508735 Oryctolag
37	982.2	46.3	3066	5	BC045304	BC045304 Danio rer
38	9682	46.3	189669	10	AC123847	AC123847 Mus muscu
39	964.2	45.5	2918	4	AY147192	AY147192 Mustela p
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41	939.2	44.3	2314	5	AF075160	AF075160 Gallus ga
42	935.4	44.1	2351	9	HSAJ10569	AJ010969 Homo sapi
43	935.4	44.1	5333	9	AB028967	AB028967 Homo sapi
44	924.2	43.6	1893	9	AF121104	AF121104 Homo sapi
45	920.2	43.4	4562	10	BC079667	BC079667 Mus muscu

ORIGIN

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Db	1	GATTGTGAACTAACTCCAAGCTGTGTGCTTAGCGTCCGCGCGGCTGCCTGCCCAAGA	60	
QY	61	GCTGAGTCACCATGCGCGCCGGAGTGCCTGCGCTTGTGCTTTGCTCCGGGCTGCGGCC	120	
Db	61	GCTGAGTCACCATGCGCGCCGGAGTGCCTGCGCTTGTGCTTTGCTCCGGGCTGCGGCC	120	
QY	121	ATCGGGTGGATGCGCGGTGGGCCAACTGCCCCCATGCCCCCTGGCCCCGGCCGACAAAGAACAG	180	
Db	121	ATCGGGTGGATGCGCGGTGGGCCAACTGCCCCCATGCCCCCTGGCCCCGGCCGACAAAGAACAG	180	
QY	181	CGGCAGAGTAGCGTGATTGTCCTCAACGTAGTGGCGGAGGTTCCAGACTTGAGAGACC	240	
Db	181	CGGCAGAGTAGCGTGATTGTCCTCAACGTAGTGGCGGAGGTTCCAGACTTGAGAGACC	240	
QY	241	ACGCTGAGCGCTACCCCGGACACCTCTGCTGGGACGACGAGAGAGAGTTCTTCTTCAAC	300	

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Db 301 GAGGACACCAAGAGTACTTCTCGACCGGAGCCCGAGGTGTTCCGTGCTGCTCAAC 360
QY 361 TTCTAACCGCAGGGGAAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCTTACGACGAC 420
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QY 421 GAGCTGGACCTTCTACCGGCATCTCCCGGAGATCATCGGGGAGCTGCTGCTACGAGAGTAC 480
Db 421 GAGCTGGACCTTCTACCGGCATCTCCCGGAGATCATCGGGGAGCTGCTGCTACGAGAGTAC 480
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Db 481 AAGGACCCGAGAGGAGAAACGCCGAGCGGCTCATGACGACAAACGACTCGGAGAAACAC 540
QY 541 CAGGAGTCCATGCCCCCTGCTCAGCTTCCGCCAGACCATGTGGCGGGCTTCGAGAACCCC 600
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QY 1501 CATCACTGCTGCACTGCTGGAAAAAACCACTGGTGTCTTATCTTGTGATGATGCC 1560
Db 1501 CATCACTGCTGCACTGCTGGAAAAAACCACTGGTGTCTTATCTTGTGATGATGCC 1560
QY 1561 CTGTTATCTGTACGAACCTCCACCATCAAGAACCAAGATTATGATGAGAGATGTTT 1620
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Db 1921 ATCCCACTCCCGCAGCGCTTAACCCAGAGGGGAAAAGTGGGCCACCCCTGCGAGCCCA 1980
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Db 1981 GGGCCCAACAGAACTTCTTCCATTAACAGCAATGTTGTCAAGTCTCTGTCTTGA 2040
QY 2041 AATCCCGCGGCAATGGCGCGGAGCATGCGAGCGGCGCAATTCGCTTATAGTG 2100
Db 2041 AATCCCGCGGCAATGGCGCGGAGCATGCGAGCGGCGCAATTCGCTTATAGTG 2100
QY 2101 AGTGTATTAAAGCCGAATTC 2121
Db 2101 AGTGTATTAAAGCCGAATTC 2121

RESULT 2
AF120491 2722 bp mRNA linear PRI 17-APR-2000
LOCUS AF120491
DEFINITION Homo sapiens Shal-related potassium channel Kv4.3 (KCND3) mRNA,
VERSION AF120491
KEYWORDS AF120491.1 GI:5059059
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2722)
AUTHORS Isbrandt,D., Leicher,T., Waldschütz,R., Zhu,X., Luhmann,U.,
TITLE Gene structures and expression profiles of three human KCND (Kv4)
JOURNAL potassium channels mediating A-type currents I(TO) and I(SA)
Genomics 64 (2), 144-154 (2000)
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MEDLINE 20195625
PUBMED 10729221
REFERENCE 2 (bases 1 to 2722)
AUTHORS Zhu,X.R., Walschuetz,R., Isbrandt,D., Sauter,K. and Pongs,O.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1999) ZMNH, Institut fuer Neurale
Signalverarbeitung, Martinistrasse 52, Hamburg 20246, Germany
FEATURES
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489..2456
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ORIGIN

Query Match 96.0%; Score 2036.2; DB 9; Length 2722;
Best Local Similarity 97.5%; Pred. No. 1.2e-306;
Matches 2068; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GATTGCTGAACCTCACTCAAGCTGTGTGCTTACGCTCCGCGGCTGCCGCCCAAGA 60
Db 417 GGTTCGCTGAACCTCACTCAAGCTGTGTGCTTACGCTCCGCGGCTGCCGCCCAAGA 476
QY 61 GCTGAGTCAACATGCGCGCGAGTTCGCGCTGCTGCTTTTGGCCCGGCTGCCGCC 120
Db 477 GCTGAGTCAACATGCGCGCGAGTTCGCGCTGCTGCTTTTGGCCCGGCTGCCGCC 536
QY 121 ATCGGCTGATGCGCGTGCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 537 ATCGGCTGATGCGCGTGCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596
QY 181 CGGACAGATGAGCTGATTTCTTCACTGAGTGGCGGAGTTCCAGACTGAGAGACC 240
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QY 241 ACGCTGAGCGCTACCCCGACACCTGCTGGCAGACAGAGAGAGATTCTTCTTCAAC 300
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QY 301 GAGGACACCAAGAGTACTTTCTTCACTGAGCGGACCCCGAGTGTTCGCTGGTGTCTCAAC 360
Db 717 GAGGACACCAAGAGTACTTTCTTCACTGAGCGGACCCCGAGTGTTCGCTGGTGTCTCAAC 776
QY 361 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCTTACGAGAC 420
Db 777 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCTTACGAGAC 836
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Db 837 GAGCTGGCTTTCTACGCGATCTCCCGGAGATCATCGGGGACTGTGCTACGAGAGTAC 896

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QY 601 CACACGACGCTGGCCCTGTGCTTCTACTACGTAGTGGCTTCTTCAATCGCTGTCCG 660
Db 1017 CACACGACGCTGGCCCTGTGCTTCTACTACGTAGTGGCTTCTTCAATCGCTGTCCG 1076
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QY 721 CCGTGGGGGAGCGCTACTCGTGGGCTTCTTCTGCTGAGACAGCGGCTGCTCATGATC 780
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QY 781 TTCACGCTGAGTACCTCTGCGGCTCTTCCGCGCTCCAGCGGCTACCGCTTCAATCCG 840
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QY 1441 ACGGGACCCCAAGAGAGAGACATGGGCAAGACCACTCATCTGAGAGCCAGCAT 1500
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Db 1917 CATCACTGTGCTGCTGCTGCAAAAAACCACTGGTGTGCTTATCTTGTGATGATCCC 1976

QY	1561	CTGTTATCTGTACGAACTCTCCACATCAAGAACCAGATTATTGATGACAGATGTTT	1620
Db	1977	CTGTTATCTGTACGAACTCTCCACATCAAGAACCAGATTATTGATGACAGATGTTT	2036
QY	1621	GAGCAGAACTGCATGGAGATTTCATGTAGAACCTAACCCATCCACAGAAGTCCCTCACTG	1680
Db	2037	GAGCAGAACTGCATGGAGATTTCATGTAGAACCTAACCCATCCACAGAAGTCCCTCACTG	2096
QY	1681	TCCAGCCACCCAGGCTCTCACTACCACTGTGCTCCGTCGTAGTAAGAACCAACACAC	1740
Db	2097	TCCAGCCACCCAGGCTCTCACTACCACTGTGCTCCGTCGTAGTAAGAACCAACACAC	2156
QY	1741	CTGCCCAATTCTTAACCTGCCAGCTACTCGCTCGCGCAGCATGCAAGAAGCTCAGCAGATC	1800
Db	2157	CTGCCCAATTCTTAACCTGCCAGCTACTCGCTCGCGCAGCATGCAAGAAGCTCAGCAGATC	2216
QY	1801	CACATCCAGGGCAGTGAGCAGCCCTCCCTCACAAACAGTCGCTCCAGCCTTAATTGAAA	1860
Db	2217	CACATCCAGGGCAGTGAGCAGCCCTCCCTCACAAACAGTCGCTCCAGCCTTAATTGAAA	2276
QY	1861	GCAGACGACGGA CTGAGACCAAACTGCAAAACATCCAGATCACCA CAGCCATCATCAGC	1920
Db	2277	GCAGACGACGGA CTGAGACCAAACTGCAAAACATCCAGATCACCA CAGCCATCATCAGC	2336
QY	1921	ATCCCACTCCCCCAGCGCTAACCCCGAGAGGGGAAAGTCGGCCACCCCTGCCAGCCCA	1980
Db	2337	ATCCCACTCCCCCAGCGCTAACCCCGAGAGGGGAAAGTCGGCCACCCCTGCCAGCCCA	2396
QY	1981	GGCCCCAACAGCAATTCCTCCATTAACGACAATGTTGTCAAGGTCTGTGCTTGTAA	2040
Db	2397	GGCCCCAACAGCAATTCCTCCATTAACGACAATGTTGTCAAGGTCTGTGCTTGTAA	2456
QY	2041	AAATCCCGCGGCATGCGCGCCGAGAGCATGCGAGCTGGGCCCAATTGCCCCCTATAGTG	2100
Db	2457	AACCACTGGACAGAGGGCCAGAGTGGGTAGTGGGGAATGAAGGGGAGCTGGCAITGTTGGTG	2516
QY	2101	AGTCGTATTAAAGCCGAATTC 2121	
Db	2517	GGTGGTCACTGAGACCACTCC 2537	

RESULT 3	
AF187963	
LOCUS	
DEFINITION	AF187963 2041 bp mRNA linear PRI 04-OCT-1999
ACCESSION	Homo sapiens voltage gated potassium channel Kv4.3 long splice variant (Kv4.3) mRNA, complete cds.
VERSION	AF187963
KEYWORDS	AF187963.1 GI:6007794
SOURCE	.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 2041)
JOURNAL	Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.
MEDLINE	Cloning and expression of the human kv4.3 potassium channel J. Neurophysiol. 81 (4), 1974-1977 (1999)
PUBMED	99218223
REFERENCE	10200233
AUTHORS	2 (bases 1 to 2041)
TITLE	Dilks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.
JOURNAL	Direct Submission
FEATURES	Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN 8000, Room 1119A, Princeton, NJ 08543-8000, USA
source	Location/Qualifiers
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gene	/cfeature_type="heart; brain"
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CDS	/gene="Kv4.3"
	73..2040

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|||||
Db 721 CCGTGGGGGAGGCTACTCGGTGGCTTCTTCTGCTGACACGGCGTGCATGATC 780
Qy 781 TTACCGGTGAGTACCTCTGCGGCTCTTGGGGCTCCAGCCGCTACCGCTTCATCCG 840
Db 781 TTACCGGTGAGTACCTCTGCGGCTCTTGGGGCTCCAGCCGCTACCGCTTCATCCG 840
Qy 841 AGCGTATGAGCATCATGACGTGGTGGCCATCATGCCCTACTCATCGGTCTGTCATG 900
Db 841 AGCGTATGAGCATCATGACGTGGTGGCCATCATGCCCTACTCATCGGTCTGTCATG 900
Qy 901 ACCAACAAGAGAGAGTGTCCGGCGCTTCGTACGCTCCGGGTCTTCCGCTTCAGG 960
Db 901 ACCAACAAGAGAGAGTGTCCGGCGCTTCGTACGCTCCGGGTCTTCCGCTTCAGG 960
Qy 961 ATCTTCAAGTTTCCCGCACTCCAGGGGCTGGGATCTCGGCTACACACTGAAGAGC 1020
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Db 1021 TGTGCTCCGAAGCTGGGCTTCTCTCTCTCCCTACCATGGCCATCATCTTGGC 1080
Qy 1081 ACTGTGATGTTTATGCGGAGAGGGCTCTCGGCCAGCAAGTTCAACAACATCCCTGCC 1140
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Qy 1141 TCGTTTGTGTAACCATGTGTCAACCATGACCACTGGGATACGGAACATGTGCTTAAG 1200
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Db 1381 AGTTCGAATGCATACCTGACAGAGCGCAACGGGCTCTCAACGAGGCGCTGAGCTG 1440
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Qy 1501 CATCACTGCTGCACTGCTGAAAACCACTGGGTGTCTATCTTGTGATGATGCC 1560
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Qy 1621 GAGCAGACTGATGAGAGATTGACAGAACTAACCATCCACAAGAGTCCCTCACTG 1680
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Qy 1741 CTGCCAATTCTAACCCTGCAAGTACTGCGCTGGGAGCATGAGAGCTCAGACGATC 1800
Db 1741 CTGCCAATTCTAACCCTGCAAGTACTGCGCTGGGAGCATGAGAGCTCAGACGATC 1800
Qy 1801 CACATTCAGGGAGTGAGAGGCTCTCCCTCAACCAAGTGGCTTAAATTGAAA 1860
Db 1801 CACATTCAGGGAGTGAGAGGCTCTCCCTCAACCAAGTGGCTTAAATTGAAA 1860

Db 1801 CACATTCAGGGAGTGAGAGGCTCTCCCTCAACCAAGTGGCTTAAATTGAAA 1860
Qy 1861 GCAGACGAGCGACTGAGACCAAACTGCAAAAACATCCAGATCAACACAGCATCATGAGC 1920
Db 1861 GCAGACGAGCGACTGAGACCAAACTGCAAAAACATCCAGATCAACACAGCATCATGAGC 1920
Qy 1921 ATCCCACTCCCCAGGCTTAACCCAGAGGGGAAAGTGGCCACCCCTGCAGCCCA 1980
Db 1921 ATCCCACTCCCCAGGCTTAACCCAGAGGGGAAAGTGGCCACCCCTGCAGCCCA 1980
Qy 1981 GGGCCCAACAGACATTTCTTCCATTAACAGCAATGTTGTCAAGTCTTGTGTGTA 2040
Db 1981 GGGCCCAACAGACATTTCTTCCATTAACAGCAATGTTGTCAAGTCTTGTGTGTA 2040
Qy 2041 A 2041
Db 2041 A 2041

RESULT 4
AR371347 2064 bp DNA linear PAT 12-SEP-2003
LOCUS AR371347
DEFINITION Sequence 3 from patent US 6395477.
ACCESSION AR371347
VERSION AR371347.1 GI:34608279
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2064)
AUTHORS Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.
TITLE Human potassium channel polynucleotide and polypeptides and uses thereof
JOURNAL Patent: US 6395477-A 3 28-MAY-2002;
FEATURES location/Qualifiers
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Qy 121 ATCGGTGATGCGCGGTGGCCAACTGCCCCATGCCCTGGCCCCGCGCAAGAAC 180
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Qy 241 ACGCTGAGCGCTACCCGGACACCTGCTGGGCGAGCAGAGAGAGTCTTCTTCAAC 300
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Qy 301 GAGGACCAAGAGAGTACTTCTTGAACCGGAGACCCGAGGTGTTCCGCTGCTCAAC 360
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Dp	421	GAGCTGGCCCTTCTACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGGATAC	480
Qy	481	AAGGACCGCAAGAGGGAGAACCGCCGAGCGGCTCATTGA CGACAAAGACTCGGAGAACAC	540
Dp	481	AAAGACCGCAAGAGGGAGAACCGCCGAGCGGCTCATTGA CGACAAAGACTCGGAGAACAC	540
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Dp	541	CAGAGTCCATGCCCTCGCTCAGCTTCCGCGACAGCCATGTCGGCGGCTTTCAGAACCCC	600
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Dp	601	CACACGACGACGCTGGCCCTGCTCTTCTA CTA CGTACGTAGGCTTCTTCATCGCTGCTCG	660
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Dp	661	GTCATCAACCAACGTGTGTGAGACGCTGCCGTGCCGACCGTCCCGGGCAGCAAGGACCTG	720
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Dp	781	TTCAACGTGAGTACCTCTCGCGGCTCTTCGCGGCTCCAGCGCTAACCGCTTCATCCGC	840
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Dp	1021	TGTGCTTCGAACTGGGCTTCTTCTCTCTCCCTCACCATGGCCATCATATCTTTGCC	1080
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Dp	1081	ACTGTGATGTTTATGCCGAGAGGGCTCCGCGCAGCAAGTTCA CAAGCATCCCTGCC	1140
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Dp	1141	TCGTTTGTGTACACCATTTGTCA CCA TGA CCA CACTGGATACGAGACATGGTGCCTTAAG	1200
Qy	1201	ACGATTGCAAGGAAAGATCTTCGGGCTCCATCTGCTCTTGA TGGGCTCTGATTCG	1260
Dp	1201	ACGATTGCAAGGAAAGATCTTCGGGCTCCATCTGCTCTTGA TGGGCTCTGATTCG	1260
Qy	1261	CTGCCAGTCCCTGTGATTTGTTCCA ACTTTAGCCGGA TTTACCA CCA GAATCAGAGAGCT	1320
Dp	1261	CTGCCAGTCCCTGTGATTTGTTCCA ACTTTAGCCGGA TTTACCA CCA GAATCAGAGAGCT	1320
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Dp	1321	GATTAACGACAGGCA CA AAGAAAGGCGCCTTGCCAGAGTCCGTCGTGGCCAAA CAGGC	1380
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Db	1534	-----	-----AACCAAGATTATTGATGAGCAGATGTTT	1563
QY	1621	GAGCAGAACTGTCATGGAGAGATTCAATGCAAGAACTACCAATCCATCCACAAGAACTCCCTCACTG		1680
Db	1564	GAGCAGAACTGTCATGGAGAGATTCAATGCAAGAACTACCAATCCATCCACAAGAACTCCCTCACTG		1623
QY	1681	TCCAGGACACCCAGGCGCTCACTAACCACTGCTGTCCTCCGTCGTAGTAAAGAACCAACACAC		1740
Db	1624	TCCAGGACACCCAGGCGCTCACTAACCACTGCTGTCCTCCGTCGTAGTAAAGAACCAACACAC		1683
QY	1741	CTGCCCAATTCTTAACCTGCGACGCTACTGCTGCGCGAGCATGCAAGAGCTCAGACGATC		1800
Db	1684	CTGCCCAATTCTTAACCTGCGACGCTACTGCTGCGCGAGCATGCAAGAGCTCAGACGATC		1743
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QY	1861	GCAGAGACGGACTGAGACCAAACTGCAAAACATCCAGATCAACAAGCCATCATCAGC		1920
Db	1804	GCAGAGACGGACTGAGACCAAACTGCAAAACATCCAGATCAACAAGCCATCATCAGC		1863
QY	1921	ATCCCACTCCCGCAGCGCTAAACCCACAGAGGGGGAAGTCGGCCACCCCTGCGACGCCA		1980
Db	1864	ATCCCACTCCCGCAGCGCTAAACCCACAGAGGGGGAAGTCGGCCACCCCTGCGACGCCA		1923
QY	1981	GGCCCCAACAAGAACATTTCTTCCATATACAGCAATGTTGTCAAGTCTCTGTCTTGTAA		2040
Db	1924	GGCCCCAACAAGAACATTTCTTCCATATACAGCAATGTTGTCAAGTCTCTGTCTTGTAA		1983
QY	2041	AAATCCCGCGGCATGGCGCGCGCGAGAGCATGCGAGTGGGCCCAATTGCGCCTATAGTG		2100
Db	1984	AAATCCCGCGGCATGGCGCGCGCGAGAGCATGCGAGTGGGCCCAATTGCGCCTATAGTG		2043
QY	2101	AGTCGTATTAAAGCCGAATTC	2121	
Db	2044	AGTCGTATTAAAGCCGAATTC	2064	

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RESULT 5
AF048713
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1968 bp mRNA linear PRI 06-MAR-1998
Homo sapiens Kv4.3 potassium channel long splice variant (Kv4.3)
mRNA, complete cds.
AF048713
AF048713.1 GI:2935435
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1968)
Kong, W. and Tomaselli, G.F.
Direct Submission
Submitted (17-FEB-1998) Medicine, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA
Location/Qualifiers
1..1968
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/chromosome="1"
/map="1p13"
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PSLSFRQTMRAFENPHTSTLALVYVTFPIAVSVITNVETVPCGTVPGSKELPC
GERYSVAFPCLDTAQVMITGEVYLRFPAPSRYRFTIRSVMSIIDVAMPYIGLVM
TNNEVSGAFYTLRFRVRIFKFSRHSQGLRILGYTLKSCASELGFLESLTMAIIT
FATVMFVAEKSSASKFTSIPASFWYITVMTTIGYDMVLKTIAGKISCSISGV
LVIALPVPVIVSNFSRIYHONORADKRAQKARLARIIVAKTGSSNAYLHKKRGLL
NEALELGTPEEHMGTSLIESQHLHLCKLEKTLGYLVDPLSVRTSTIKNH
EFIDQMFQNMESMOMNYPSTRSPSLSHRGLTTCCSRSRKKTTHLPNSNLPAIR
LRSMQELSTHIGSEQPSLTSSSLNLKADBDGLRPNCKTSQITTAIISIPTPALT
PEGESRPPASPBPNTNIPISITSNVYKSVL"

ORIGIN

Query Match 92.6%; Score 1963.2; DB 9; Length 1968;
Best Local Similarity 99.8%; Pred. No. 2.8e-295;
Matches 1965; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 73 ATGGCGCGGAGTTCGCGCTGCTGCTTTTGCCCGGGCTGCGGCATCGGGTGATG 132
DB 1 ATGGCGCGGAGTTCGCGCTGCTGCTTTTGCCCGGGCTGCGGCATCGGGTGATG 60
QY 133 CCGGTGGCCAACTGCCCCATGCCCCGCGGCCGACAAGAACAGCGGCAAGATGAG 192
DB 61 CCGGTGGCCAACTGCCCCATGCCCCGCGGCCGACAAGAACAGCGGCAAGATGAG 120
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DEFINITION Sequence 3 from Patent WO9842833.
VERSION  AB5166.1   GI:6733868
KEYWORDS
SOURCE   unidentified
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ORGANISM  unidentified.
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REFERENCE Bril, A.M. and Calmels, T.P.
AUTHORS   KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE     Patent: WO 9842833-A 3 01-OCT-1998;
          BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)
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ORIGIN
Query Match      92.5%; Score 1962; DB 6; Length 2072;
Best Local Similarity 99.7%; Pred. No. 4.2e-295;
Matches 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      133  CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGCGCAAGAAAGCGCGAGATGAG 192
Db      61  CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGCGCAAGAAAGCGCGAGATGAG 120

Qy      193  CTGATTTCTCTCAAGTGAAGTGGGCGGAGTTTCCAGACCTGAGAGACACGCTGAGCGC 252
Db      121  CTGATTTCTCTCAAGTGAAGTGGGCGGAGTTTCCAGACCTGAGAGACACGCTGAGCGC 180

Qy      253  TACCCGAGACCCCTGCTGGGCAAGCAGAGAGAGTTCCTTCAACGAGGACACCAAG 312
Db      181  TACCCGAGACCCCTGCTGGGCAAGCAGAGAGAGTTCCTTCAACGAGGACACCAAG 240

Qy      313  GAGTACTTCTTGAACCGGGGACCCCGAGGTGTTCCGCTGCGTCTCAACTTACCGCAGC 372
Db      241  GAGTACTTCTTGAACCGGGGACCCCGAGGTGTTCCGCTGCGTCTCAACTTACCGCAGC 300

Qy      373  GGGAGCTGCACTACCCGCGCTAAGAGTGCATCTGCTTACGAGCAGAGCTGGCTTC 432
Db      301  GGGAGCTGCACTACCCGCGCTAAGAGTGCATCTGCTTACGAGCAGAGCTGGCTTC 360

Qy      433  TACGGCATCTCCCGAGATCATCGGGGACTGTGCTACGAGAGTACAAGGACCGCAAG 492
Db      361  TACGGCATCTCCCGAGATCATCGGGGACTGTGCTACGAGAGTACAAGGACCGCAAG 420

Qy      493  AGGAGAGACGCGGAGGCTCATGGAACAACAAGCTCGAGAGAACACAGAGTCCATG 552
Db      421  AGGAGAGACGCGGAGGCTCATGGAACAACAAGCTCGAGAGAACACAGAGTCCATG 480

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Qy      793  TACCTCTGCGGCTCTTTCGGGCTCCACGCCGCTACCCGTTATCCGACAGGTCATGAGC 852
Db      721  TACCTCTGCGGCTCTTTCGGGCTCCACGCCGCTACCCGTTATCCGACAGGTCATGAGC 780

Qy      853  ATCATCGACGTGTGGCCATCATGCCCTACTACATCGGTCTGTGATGACCAACAGAG 912
Db      781  ATCATCGACGTGTGGCCATCATGCCCTACTACATCGGTCTGTGATGACCAACAGAG 840

Qy      913  GACGTGTCCGGCGCTTCGTCACGCTTCGGGCTTCCGGCTTTAGAGATCTTCAAGTTT 972
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Qy      1153  ACCATTGTACCATGACCACTGGGATACGAGACATGTGTCTTAAGACATGTCAGGG 1212
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Db      1141  AAGATCTTCGGCTCCATCTGCTCTTGAAGTGGGCTCTGATTCCTGCAAGTCCCT 1200

Qy      1273  GTGATTTGTTCCAACTTTAGCCGAGTTTACCAACGAATCAGAGAGCTGATTAACGCA 1332
Db      1201  GTGATTTGTTCCAACTTTAGCCGAGTTTACCAACGAATCAGAGAGCTGATTAACGCA 1260

Qy      1333  GCACAAAAGAGGCGGCTTTGCGAGATCCGTGTGGCCAAAACAGGCAAGTTGCAATGCA 1392
Db      1261  GCACAAAAGAGGCGGCTTTGCGAGATCCGTGTGGCCAAAACAGGCAAGTTGCAATGCA 1320

Qy      1393  TACCTGACAGCAAGCGCAAGGCTCCTCAACGAGGCGCTGAGCTGACGGGACCCCA 1452
Db      1321  TACCTGACAGCAAGCGCAAGGCTCCTCAACGAGGCGCTGAGCTGACGGGACCCCA 1380

Qy      1453  GAAAGAGACATGAGGCAAGACCACTCACTCATCGAGAGCCAGCATCATCACTGCTG 1512
Db      1381  GAAAGAGACATGAGGCAAGACCACTCACTCATCGAGAGCCAGCATCATCACTGCTG 1440

Qy      1513  CACTGCTGGAAGAAAACCACTGGGTTGCTCTATCTTGTGATGATCCCTGTATCTGTA 1572
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Db      1501  CGAAGCTCCACCATCAAGAACCAAGAGTTTATGATGACAGATGTTGAGCAGAACTGC 1560

Qy      1633  ATGAGAGATTCAATGCAAGAACTAACCATCCACAAGAAATTCCTCACTGTCCAGCCCA 1692
Db      1561  ATGAGAGATTCAATGCAAGAACTAACCATCCACAAGAAATTCCTCACTGTCCAGCCCA 1620

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QY	1813	AGTGAAGCAGCCCTCCCTCACAACCAAGTCGCTCCAGCCTTAAATTGAAAAGCAGACGCGA	1872
Db	1741	AGTGAAGCAGCCCTCCCTCACAACCAAGTCGCTCCAGCCTTAAATTGAAAAGCAGACGCGA	1800
QY	1873	CTGAGACCAAACTGCAAAACATCCAGATCCACCAAGCCATCATCAGCATCCCACTCCC	1932
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QY	1933	CCAGCGCTAAACCCCAAGAGGGGAAAGTCGGCCACCCCTGCAGGCCAGGCCCAACAGC	1992
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QY	1993	AACATTCCTTCCATTAACCAAGCAATGTTGTCAAGGCTCTGTCTTGTAATA	2042
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DEFINITION	Sequence 3 from patent US 6368823.			
ACCESSION	AR204885			
VERSION	AR204885.1	GI:21502325		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2072)			
	Brill,A.Michel,Alain., Calmels,T.Paul.Gerard.,			
	Faivre,J.-F.Simon,Pierre., Javre,J.-L. and Rouanet,S.			
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	Patent: US 6368823-A 3 09-APR-2002;			
TITLE	Location/Qualifiers			
JOURNAL				
FEATURES				
source	1..2072			

ORIGIN

Query Match	92.5%;	Score 1962;	DB 6;	Length 2072;
Best Local Similarity	99.7%;	Pred. No. 4.2e-295;		
Matches 1965; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

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QY	193	CTGATTGTCTCTCAAAGTGAAGTGGCGGAGTTCCAGACTTGAGGACCAAGCTGGAGCGC	252
Db	121	CTGATTGTCTCTCAAAGTGAAGTGGCGGAGTTCCAGACTTGAGGACCAAGCTGGAGCGC	180
QY	253	TACCCCGGACACCTGCTGGGCGAGCAGGAGAAGAGATTCTTTCAACGAGGACACCAAG	312
Db	181	TACCCCGGACACCTGCTGGGCGAGCAGGAGAAGAGATTCTTTCAACGAGGACACCAAG	240
QY	313	GAGTACTTCTTCGACCGGGGACCCCGGAGGTGTTCCGCTGCGTCAACTTCTACCGCAGC	372
Db	241	GAGTACTTCTTCGACCGGGGACCCCGGAGGTGTTCCGCTGCGTCAACTTCTACCGCAGC	300
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QY	433	TACGGCATCTCCCGAGATCATCGGGACTGCTGCTACGAGAGTACAAGACCGCAAG	492
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QY	493	AGGAGAACGCCGAGCGGCTCATATGAGCGACAACGACTCGGAGAAACAACGAGAGTCCATG	552
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QY	553	CCCTCGCTCAGCTTCCGCGAGAACATGTGGCGGGCTTCGAGAAACCCACACGACGACG	612
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QY	733	CGCTACTCGTGTGGCTTCTTCTGCTGTGACACAGCGCGTGCCTCATGATCTTCAACCGTGAG	792
Db	661	CGCTACTCGTGTGGCTTCTTCTGCTGTGACACAGCGCGTGCCTCATGATCTTCAACCGTGAG	720
QY	793	TACCTCTCGGGCTCTTTCGGGGCTCCACGCCCTAACCGCTTCATCCGACGGTCATAGC	852
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QY	853	ATCATGACGTTGTGGCCATCATATGCCCTACTACATCGGTCTGTATGACCAACAACGAG	912
Db	781	ATCATGACGTTGTGGCCATCATATGCCCTACTACATCGGTCTGTATGACCAACAACGAG	840
QY	913	GACGTGTCCGGCGCTTTCGTACAGCTCCGGGTCTTCCGGTCTTCAAGATCTTCAAGTTT	972
Db	841	GACGTGTCCGGCGCTTTCGTACAGCTCCGGGTCTTCCGGTCTTCAAGATCTTCAAGTTT	900
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QY	1633	ATGAGAGTTCAATGACAGAACTACCCATCCACAAGAAAGTCCCTCACTGTCCAGCCACCCA	1692
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QY	1813	AGTGAAGCAGCCCTCCCTCACAACCAAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGA	1872
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QY	1873	CTGAAGACCAAACTGCAAAACATCTCCAGATCAACCAAGCCATCATAGCATCCCCCATCTCC	1932
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QY	1933	CCAGCGCTAACCCCGAGAGGGGGAAGTCGGGCAACCCCTGCGAGCCGACGAGCCCAACACG	1992
Db	1861	CCAGCGCTAACCCCGAGAGGGGGAAGTCGGGCAACCCCTGCGAGCCGACGAGCCCAACACG	1920
QY	1993	AACATTCTTTCATAACGAGCAATGTTGTCAAGGTCCTGTCTTGTAATAA	2042
Db	1921	AACATTCTTTCATAACGAGCAATGTTGTCAAGGTCCTGTCTTGTAATAA	1970

RESULT 8	AX956786	AX956786	1968 bp	DNA	linear	PAT 08-JAN-2004
LOCUS	AX956786	Sequence	4	from Patent WO03097682.		
DEFINITION	AX956786					
ACCESSION	AX956786.1			GI:40785267		
VERSION						

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1	Kaletta, T.J., Dewulf, N.E. and Plaetinck, G.K.	Methods for identifying and developing compounds that interact with

JOURNAL Patent: WO 03097682-A 4 27-NOV-2003;

FEATURES	Location/Qualifiers
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ORIGIN

Query Match	92.4%	Score 1960;	DB 6;	Length 1968;
Best Local Similarity	99.7%	Pred. No. 8.7e-295;		
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133 CCGGTGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCCGACAAGACAGCGGAGGATGAG 192

DB 61 CCGTGGCCACTGCCCCCATGCCCCCTGGCCCCCGCCGACCAAGAACAGCGGCAGATGAG 120

27 252

Db 121 CTGATTGTCTCAACGTCGAGTGGCGGAGGTTCCAGACCTGGAGGACCAACCTGGAGCCG 180

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QY	313	GAGTACTTCTTGACCCGGACCCCGAGGTGTTCCGCTGCTCAACTTCAACGCAAG	372
Db	241	GAGTACTTCTTGACCCGGACCCCGAGGTGTTCCGCTGCTCAACTTCAACGCAAG	300

Db 301 GGAAGCTGCACTACCCGGCTACGAGTGATCTCTGCCCTACGACGACGAGCTGGCCTTC 360

433 TACGGCATCTCCCCGAGATCATCGGGACTGCTGCTACGAGAGTACAAGACCCGAAG 492

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QY 1993 AACATTCTTCCATTAACGAGCAATGTTGCAAGGTCCTGTCTGTAA 2040

Db 1921 AACATTCTTCCATTAACGAGCAATGTTGCAAGGTCCTGTCTGTAA 1968

RESULT 9
AF205857
LOCUS AF205857 1968 bp mRNA linear PRI 29-DEC-1999
DEFINITION Homo sapiens potassium ionic channel Kv4.3 long isoform mRNA,
complete cds.
ACCESSION AF205857
VERSION AF205857.1 GI:6644151
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 Calmeils,T.P.G., Faivre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.
AUTHORS and Bril,A.
TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,
Expression, Electrophysiology, Pharmacology and Phosphorylation by
Protein Kinase C
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1968)
AUTHORS Calmeils,T.P.G., Faivre,J.-F., Javre,J.-L. and Bril,A.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline
Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France
FEATURES Location/Qualifiers

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ORIGIN

Query Match 92.4%; Score 1959.6; DB 9; Length 1968;
Best Local Similarity 99.7%; Pred. No. 1e-294;
Matches 1962; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 241 GAGTACTTCTGACCGGGAGACCGGAGTTCGCTGCGTCAACTTCAACCGCAGC 300

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QY 493 AGGAGAACCGGAGCGGCTGACGAGCAACGACTCGGAGAACCAACGAGAGTCCATG 552

Db 421 AGGAGAACCGGAGCGGCTGACGAGCAACGACTCGGAGAACCAACGAGAGTCCATG 480

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Db 481 CCCTCGCTAGCTTCCGCGGAGACCATGCGGGCTTCGAGAACCCCAACAGACAG 540

QY 613 CTGCGCTGCTTCTTCACTACGAGTGCCTTCTCATCGCTGCTCGGTATCAACCAAC 672

Db 541 CTGCGCTGCTTCTTCTTCACTACGAGTGCCTTCTCATCGCTGCTCGGTATCAACCAAC 600

QY 673 GTGGTGAAGACGCTGCGGAGACGCTTCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 732

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Db 1861 CCAGCGCTAACCCAGAGGGGAAAGTCCGCCACCCCTGCCAGCCAGGCCCAACAG 1920
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RESULT 10
AF187964
LOCUS
DEFINITION
Homo sapiens voltage gated potassium channel Kv4.3 short splice
variant (Kv4.3) mRNA, complete cds.
ACCESSION
AF187964
VERSION
AF187964.1 GI:6007796
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1984)
DiLks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.
Cloning and expression of the human kv4.3 potassium channel
J. Neurophysiol. 81 (4), 1974-1977 (1999)
JOURNAL
99218223
MEDLINE
10200233
PUBMED
2 (bases 1 to 1984)
DiLks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.
Direct Submission
Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN
8000, Room 1119A, Princeton, NJ 08543-8000, USA
JOURNAL
location/Qualifiers
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ORIGIN

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Query Match      89.6%; Score 1901; DB 9; Length 1984;
Best Local Similarity 96.7%; Pred. No. 1.3e-285;
Matches 1974; Conservative 0; Mismatches 10; Indels 57; Gaps 1;

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Db 301 GAGGACACCAAGAGATGCTTCTTCCGAGCCCGGAGCTGCTGCTGCTGCTCAAC 360
QY 361 TTCTACCGACCGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTGCTTACGAGAC 420
Db 361 TTCTACCGACCGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTGCTTACGAGAC 420
QY 421 GAGCTGGCTTCTACGAGCTCTCCGAGATCATCGGGGACTGCTGCTACGAGAGTAC 480
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DEFINITION Homo sapiens Kv4.3 potassium channel short splice variant (Kv4.3)
mRNA, complete cds.

ACCESSION AF048712
 VERSION AF048712.1 GI:2935433
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 1911)
 AUTHORS Kong, W. and Tomasselli, G. F.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA

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ACCESSION	A85164
VERSION	A85164.1
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ORGANISM	unidentified unidentified unclassified.
REFERENCE	1 (bases 1 to 2104)
AUTHORS	Bril,A.M. and Calmels,T.P.
TITLE	KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES
JOURNAL	Patent: WO 9842833-A 1 01-OCT-1998; BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)
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VERSION           AR204884.1  GI:21502324
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REFERENCE          1 (bases 1 to 2104)
AUTHORS            Bril,A.Michel,Alain., Calmels,T.Paul, Gerard.,
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TITLE             Kv potassium channel polypeptides and polynucleotides
JOURNAL            Patent: US 6368823-A 1 09-APR-2002;
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Best Local Similarity 96.4%; Pred. No. 7.7e-276;

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VERSION AF205856.1 GI:6644149
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AUTHORS Calmels,T.P.G., Faltvre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.
and Bril,A.
TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,
Expression, Electrophysiology, Pharmacology and Phosphorylation by
Protein Kinase C
JOURNAL 2 (bases 1 to 1911)
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TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline
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VERSION A85168.1 GI:6733869
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AUTHORS Brill A.M. and Calmels T.P.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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7	798.2	37.6	3424	US-09-336-643A-9	Sequence 9, Appli
8	261	12.3	3260	US-09-949-016-2456	Sequence 2456, Ap
9	240	11.3	3004	US-09-949-016-2293	Sequence 2293, Ap
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19	202.2	9.5	2118	US-09-016-434-1304	Sequence 1304, Ap
20	196	9.2	1599	US-08-288-405A-9	Sequence 9, Appli
21	185.4	8.7	1542	US-09-949-016-4417	Sequence 4417, Ap
22	183.8	8.7	2127	US-08-464-340A-1	Sequence 1, Appli
23	183.8	8.7	2127	PCT-US94-08449A-1	Sequence 1, Appli
24	162.6	7.7	2022	US-09-719-919A-18	Sequence 18, Appl
25	159.8	7.5	4234	US-09-949-016-325	Sequence 325, App
26	159.8	7.5	4237	US-09-949-016-2146	Sequence 2146, Ap
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29	159	7.5	2084	4	US-09-949-016-3989	Sequence 3989, Ap
30	159	7.5	2266	4	US-09-181-339-11	Sequence 11, Appl
31	159	7.5	2293	3	US-09-336-643A-5	Sequence 5, Appli
32	159	7.5	19161	4	US-09-949-016-15731	Sequence 15731, A
33	154.2	7.3	3102	3	US-09-336-643A-17	Sequence 17, Appl
34	150.4	7.1	2494	4	US-09-181-339-6	Sequence 6, Appli
35	146.8	6.9	1805	1	US-07-955-916-6	Sequence 6, Appli
36	146	6.9	1638	4	US-09-833-466-2	Sequence 2, Appli
37	146	6.9	2103	4	US-09-833-466-1	Sequence 1, Appli
38	145.6	6.9	248	4	US-09-016-434-790	Sequence 790, App
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ALIGNMENTS

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; Sequence 1, Application US/09178109									
; Patent No. 6395477									
; GENERAL INFORMATION:									
; APPLICANT: Cocke, Mark I.									
; APPLICANT: Dilke, Daniel W.									
; APPLICANT: Sokol, Patricia T.									
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and									
; FILE REFERENCE: ahp-98089									
; CURRENT APPLICATION NUMBER: US/09/178,109									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 1									
; LENGTH: 2121									
; TYPE: DNA									
; ORGANISM: human									
US-09-178-109-1									
Query Match									
Best Local Similarity 100.0%; Score 2121; DB 3; Length 2121;									
Matches 2121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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; Sequence 3, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang, Ling-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3
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Query Match 94.2%; Score 1997; DB 3; Length 2064;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;
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RESULT 3
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; Sequence 3, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Ancoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142, 791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402871.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-3

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Query Match	92.5%	Score 1962;	DB 3;	Length 2072;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1965; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

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QY	1453	GAAAGAGAGCACAATGGGCAAGACCACT	CACTCATTCGAGAGCCAGCATCATCACTGCTG	1512
Db	1381	GAAAGAGAGCACAATGGGCAAGACCACT	CACTCATTCGAGAGCCAGCATCATCACTGCTG	1440
QY	1513	CACCTGCTGAAAAAAACCACTGGGTGT	GTCTATCTTGTGTGATGATCCCTGTATCTGTA	1572
Db	1441	CACCTGCTGAAAAAAACCACTGGGTGT	GTCTATCTTGTGTGATGATCCCTGTATCTGTA	1500
QY	1573	CGAACCTCCACCATCAAGAACCAAGATTT	ATTGATGAGCAGATGTTTGTGACGAAGACTGC	1632
Db	1501	CGAACCTCCACCATCAAGAACCAAGATTT	ATTGATGAGCAGATGTTTGTGACGAAGACTGC	1560
QY	1633	ATGAGAGTTCAATGACGAACCTAACCAT	CCACAAGAGTCCCTCACTGTCCAGCCACCCA	1692
Db	1561	ATGAGAGTTCAATGACGAACCTAACCAT	CCACAAGAGTCCCTCACTGTCCAGCCACCCA	1620
QY	1693	GGCCTCACTACCACTGTGCTGTCCGCTGT	AGTAAAGACCAACACACTGTGCCAAATTCT	1752
Db	1621	GGCCTCACTACCACTGTGCTGTCCGCTGT	AGTAAAGACCAACACACTGTGCCAAATTCT	1680

QY	1753	AACCTGCCAGCTACTCGCTTGGCGGAGCATGCAGAAGCTCAGCAGCATCCACATCCAGGGC	1812
Db	1681	AACCTGCCAGCTACTCGCTTGGCGGAGCATGCAGAAGCTCAGCAGCATCCACATCCAGGGC	1740
QY	1813	AGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCAGCCTTAATTGAAAGCAGACGCGGA	1872
Db	1741	AGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCAGCCTTAATTGAAAGCAGACGCGGA	1800
QY	1873	CTGAGACCAAACTGCAAAACATCCAGATACCAACAGCATCATCAGCATCCCACTCCC	1932
Db	1801	CTGAGACCAAACTGCAAAACATCCAGATACCAACAGCATCATCAGCATCCCACTCCC	1860
QY	1933	CCAGCGCTAACCCAGAGGGGGAAGTCGGCCACCCCTGCCAGCCGAGCCCAACAG	1992
Db	1861	CCAGCGCTAACCCAGAGGGGGAAGTCGGCCACCCCTGCCAGCCGAGCCCAACAG	1920
QY	1993	AACATTCCTTCATTAACGACGAATGTTGTCAAGGTCTCTGTCTTGTAAAA	2042
Db	1921	AACATTCCTTCATTAACGACGAATGTTGTCAAGGTCTCTCTGTGTAAAA	1970

RESULT 4

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US-09-142-791A-1
; Sequence 1, Application us/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Rai
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-1

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Query Match	86.7%;	Score 1838;	DB 3;	Length 2104;
Best Local Similarity	96.4%;	Pred. No. 0;		
Matches 1914; Conservative	0;	Mismatches 15;	Indels 57;	Gaps 1;

[illegible]

Db	241	GAGTACTTCTTCGACCGGGGACCCCGAGGTTGTCGCGTGCTCTCACTTCTACCGCACG	300
QY	373	GGGAAGCTGCACTACCCGGCGCTACGAGTGCATCTCTGCTTACGACGACGACTGGCTTC	432
Db	301	GGGAAGCTGCACTACCGCGCGCTACGAGTGCATCTCTGCTTACGACGACGAGCTGGCTTC	360
QY	433	TACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAAGACCGCAAG	492
Db	361	TACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAAGACCGCAAG	420
QY	493	AGGAGAAACCGCGAGCGGCTCATGACGACAAACGACTCGGAGAACAAACGAGTTCATG	552
Db	421	AGGAGAAACCGCGAGCGGCTCATGACGACAAACGACTCGGAGAACAAACGAGTTCATG	480
QY	553	CCCTCGCTCAGCTTCGCGCAGACCATGTGGCGGCTTTGAGAAACCCCGACACGACAG	612
Db	481	CCCTCGCTCAGCTTCGCGCAGACCATGTGGCGGCTTTGAGAAACCCCGACACGACAG	540
QY	613	CTGCGCCTGCTCTTCTACTACGTCGACTGCGCTTCTTCATCGCTGCTCGCTCATCAAC	672
Db	541	CTGCGCCTGCTCTTCTACTACGTCGACTGCGCTTCTTCATCGCTGCTCGCTCATCAAC	600
QY	673	GTGTGTGAGACGCTGCGGTGCGGACCGTCCCGGACAGCAAGAGCTGCGTGGGGAG	732
Db	601	GTGTGTGAGACGCTGCGGTGCGGACCGTCCCGGACAGCAAGAGCTGCGTGGGGAG	660
QY	733	CGCTACTCGGTGGCTTCTCTGCTGTGACACGCGGTGCTCATGATCTTCAACCGTGAG	792
Db	661	CGCTACTCGGTGGCTTCTCTGCTGTGACACGCGGTGCTCATGATCTTCAACCGTGAG	720
QY	793	TACCTCTGCGGCTCTTCGCGGCTCCGACCGCTAACCGCTTCATCCGACGGTCATGAGC	852
Db	721	TACCTCTGCGGCTCTTCGCGGCTCCGACCGCTAACCGCTTCATCCGACGGTCATGAGC	780
QY	853	ATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGCTGTGTCATGACCAACAGAG	912
Db	781	ATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGCTGTGTCATGACCAACAGAG	840
QY	913	GACGTGTCCGGCGCTTCTGTCACAGCTCCGGGCTTTCGGGCTTTCAGAGATTTCAAGTTT	972
Db	841	GACGTGTCCGGCGCTTCTGTCACAGCTCCGGGCTTTCGGGCTTTCAGAGATTTCAAGTTT	900
QY	973	TCCCGCCACTCCGACGGGCTCGGGGATCCGGGCTACACACTGAAGAGCTGCGCTCCGAA	1032
Db	901	TCCCGCCACTCCGACGGGCTCGGGGATCCGGGCTACACACTGAAGAGCTGCGCTCCGAA	960
QY	1033	CTGGGCTTCTCTCTCTCTCCCTCACCAATGAGCCATCATCTTGGCACTGTGATGTTT	1092
Db	961	CTGGGCTTCTCTCTCTCTCCCTCACCAATGAGCCATCATCTTGGCACTGTGATGTTT	1020
QY	1093	TATGCGGAGAAAGGCTCTCGCGCAGCAAGTTCAACAAGATCCCTGCTGTTTGGTAC	1152
Db	1021	TATGCGGAGAAAGGCTCTCGCGCAGCAAGTTCAACAAGATCCCTGCTGTTTGGTAC	1080
QY	1153	ACCATTTGTACCATGACACACATGGGATACGGAGACATGCTGCTTAAGACGATTGACAGG	1212
Db	1081	ACCATTTGTACCATGACACACATGGGATACGGAGACATGCTGCTTAAGACGATTGACAGG	1140
QY	1213	AAGATCTTGGGCTCCATCTGCTCTTGAATGAGCGTCTCGTGTCAATGGCCCTGACGTCCT	1272
Db	1141	AAGATCTTGGGCTCCATCTGCTCTTGAATGAGCGTCTCGTGTCAATGGCCCTGACGTCCT	1200
QY	1273	GTGATTTGTTTCAACTTTAGCCGGATTTAACACAGAAATCAGAGAGCTGATTAACGACAG	1332
Db	1201	GTGATTTGTTTCAACTTTAGCCGGATTTAACACAGAAATCAGAGAGCTGATTAACGACAG	1260
QY	1333	GCACAAAGAAAGGCGCGCTTGCACAGATCCGCTGCGCAAAAACAGGACGTTGCAATGCA	1392
Db	1261	GCACAAAGAAAGGCGCGCTTGCACAGATCCGCTGCGCAAAAACAGGACGTTGCAATGCA	1320
QY	1393	TACCTGCACAGACGCAACGCGGCTCTCAACGAGGCGCTGAGCTGACGGGCAACCCCA	1452
Db	1321	TACCTGCACAGACGCAACGCGGCTCTCAACGAGGCGCTGAGCTGACGGGCAACCCCA	1380

QY 1453 GAAGAGAGACATGGGCAAGACCACTCTACTCATCGAGAGCCAGCATCATCTGCTG 1512
DB 1381 GAAGAGAGACATGGGCAAGACCACTCTACTCATCGAGAGCCAGCATCATCTGCTG 1440
QY 1513 CACTGCTGGAAAAAACCACTGGGTGTCTATCTTGTGATGATCCCTGTATCTGTA 1572
DB 1441 CACTGCTGGAAAAAACCACT----- 1461
QY 1573 CGAACCTCCACCATCAAGAACCAAGATTATTGATGAGCAGATGTTTGAGCAAGACTGC 1632
DB 1462 -----AACCAAGATTATTGATGAGCAGATGTTTGAGCAAGACTGC 1503
QY 1633 ATGGAGAGTTCAATGAGAACTAACCCATCCACAGAAAGTCCCTCACTGTCCAGCCACCA 1692
DB 1504 ATGGAGAGTTCAATGAGAACTAACCCATCCACAGAAAGTCCCTCACTGTCCAGCCACCA 1563
QY 1693 GGCCTCACTAACCACTGCTGCTCCGCTGTAGTAAGAAAGACACACACCTGCCCATTCT 1752
DB 1564 GGCCTCACTAACCACTGCTGCTCCGCTGTAGTAAGAAAGACACACACCTGCCCATTCT 1623
QY 1753 AACCTGCCAGCTACTGCTGCTGCGAGCATGCAAGAGCTCAGCAGCATCCCAATCCAGGCG 1812
DB 1624 AACCTGCCAGCTACTGCTGCTGCGAGCATGCAAGAGCTCAGCAGCATCCCAATCCAGGCG 1683
QY 1813 AGTGAAGAGCCTCTCCCTCAACAACAGTGCCTCCAGCCTTAATTGAAAGCAGACGAGGA 1872
DB 1684 AGTGAAGAGCCTCTCCCTCAACAACAGTGCCTCCAGCCTTAATTGAAAGCAGACGAGGA 1743
QY 1873 CTGAAGACCAAACTGCAAAACATCCCAAGATCAACAGCCATCATCAGCATCCCACTCC 1932
DB 1744 CTGAAGACCAAACTGCAAAACATCCCAAGATCAACAGCCATCATCAGCATCCCACTCC 1803
QY 1933 CCAGCGCTAACCCCAAGAGGGGAAAGTCCGACCCCTGCGAGCCAGCCCAACAG 1992
DB 1804 CCAGCGCTAACCCCAAGAGGGGAAAGTCCGACCCCTGCGAGCCAGCCCAACAG 1863
QY 1993 AACCTTCCTTCCATAACCAAGCAATGTTGTCAAGGTCTGTCTTGTAAAAATCCGCGCG 2052
DB 1864 AACCTTCCTTCCATAACCAAGCAATGTTGTCAAGGTCTGTCTTGTAAAAATCCGCGCG 1923
QY 2053 CATGGC 2058
DB 1924 GAGGCG 1929

RESULT 5

US-09-142-791A-5
; Sequence 5, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2104
; TYPE: DNA

! ORGANISM: HOMO SAPIENS
US-09-142-791A-5

Query Match 86.3%; Score 1830; DB 3; Length 2104;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 20; Indels 57; Gaps 1;

QY 73 ATGGCGGCGGAGTTGGCGGCTGCTGCTTTTCCCGGGCTGCGGCATCGGGTGATG 132
DB 1 ATGGCGGCGGAGTTGGCAAGCTTGCTGCTTTTCCCGGGCTGCGGCATCGGGTGATG 60
QY 133 CCGGTGGCAACTGCCCCCAATGCCCTTGGCCCCCGGCGCAAGAACAGCGGCAAGTAG 192
DB 61 CCGGTGGCAACTGCCCCCAATGCCCTTGGCCCCCGGCGCAAGAACAGCGGCAAGTAG 120
QY 193 CTGATTGCTCTCAACGTGAGTGGGCGGAGTTCCAGACTGTGAGACACGCTGAGCGC 252
DB 121 CTGATTGCTCTCAACGTGAGTGGGCGGAGTTCCAGACTGTGAGACACGCTGAGCGC 180
QY 253 TACCCGAGACCTGCTGCGGAGAGAGAGAGAGTTCTTCTTCAACGAGACACCAAG 312
DB 181 TACCCGAGACCTGCTGCGGAGAGAGAGAGTTCTTCTTCAACGAGACACCAAG 240
QY 313 GAGTACTTCTTCAACGAGAGACCCCGAGGTTCCTGCTGCTCAACTTCAACCGCAG 372
DB 241 GAGTACTTCTTCAACGAGAGACCCCGAGGTTCCTGCTGCTCAACTTCAACCGCAG 300
QY 373 GGGAGCTGCACTACCCGCGCTACAGTGCATCTGCTTACGACGAGCTGCGCTTC 432
DB 301 GGGAGCTGCACTACCCGCGCTACAGTGCATCTGCTTACGACGAGCTGCGCTTC 360
QY 433 TACGGCATCTCCCGAGATCATCGGGAGCTGCTTACGAGAGTACAAAGACCGCAAG 492
DB 361 TACGGCATCTCCCGAGATCATCGGGAGCTGCTTACGAGAGTACAAAGACCGCAAG 420
QY 493 AGGAGAAAGCCGAGCGGCTCATGAGCAACAGACTGGAAGAACACAGAGTCCATG 552
DB 421 AGGAGAAAGCCGAGCGGCTCATGAGCAACAGACTGGAAGAACACAGAGTCCATG 480
QY 553 CCTCGCTCAGCTTCCGCAACCATGTGGCGGGCTTGGAGAACCCCAACACAGCAG 612
DB 481 CCTCGCTCAGCTTCCGCAACCATGTGGCGGGCTTGGAGAACCCCAACACAGCAG 540
QY 613 CTGGCCCTGATCTTCTACTCATGATGCTGCTTCTCATGCTGTCTGATCACCAAC 672
DB 541 CTGGCCCTGATCTTCTACTCATGATGCTGCTTCTCATGCTGTCTGATCACCAAC 600
QY 673 GTGGTGAGACGCTGCGGCTGCGGCAACGCTCCCGGCGAGAGAGCTGCGGGGAG 732
DB 601 GTGGTGAGACGCTGCGGCTGCGGCAACGCTCCCGGCGAGAGAGCTGCGGGGAG 660
QY 733 CGCTACTGCGGCTTCTTCTGCTGCGGCAACGCGGCTGATGATCTTCAACGTTGAG 792
DB 661 CGCTACTGCGGCTTCTTCTGCTGCGGCAACGCGGCTGATGATCTTCAACGTTGAG 720
QY 793 TACCTCTGCGGCTTCTTCTGCGGCTCCAGCCGCTTACCGCTTACGCGGCTATGAGC 852
DB 721 TACCTCTGCGGCTTCTTCTGCGGCTCCAGCCGCTTACCGCTTACGCGGCTATGAGC 780
QY 853 ATCATGAGCTGTGGCCATATGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 912
DB 781 ATCATGAGCTGTGGCCATATGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 913 GAGGTGTCCGCGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
DB 841 GAGGTGTCCGCGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 973 TCCCGGCACTCCAGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1032
DB 901 TCCCGGCACTCCAGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 960
QY 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1092

Db	961	CTGGGCTTTCTCTCTCTCTCCCTCA	CCATGGCCATCATCTTTGGCACTGTGATGTTT	1020
QY	1093	TATGCCGAGAAAGGCTCTCTCGGCGACA	GCAAGTTTCAAAACATCCCTGCTGTGGTATC	1152
Db	1021	TATGCCGAGAAAGGCTCTCTCGGCGACA	GCAAGTTTCAAAACATCCCTGCTGTGGTATC	1080
QY	1153	ACCATTTGTCAACATGACACACTGGGATA	CGGAGACATGCTGCTTAAGACATTGGAGGG	1212
Db	1081	ACCATTTGTCAACATGACACACTGGGATA	CGGAGACATGCTGCTTAAGACATTGGAGGG	1140
QY	1213	AAGATCTTCGCGCTCCATCTGTCTCTGA	TGTGGCGTCTGTGTCATTGCCCTGCCAGTCCCT	1272
Db	1141	AAGATCTTCGCGCTCCATCTGTCTCTGA	TGTGGCGTCTGTGTCATTGCCCTGCCAGTCCCT	1200
QY	1273	GTCGATTTGTTTCCAACCTTTAGCCGGA	ATTACCAACAGAAATCAGAGAGCTGATTAACGCAAG	1332
Db	1201	GTCGATTTGTTTCCAACCTTTAGCCGGA	ATTACCAACAGAAATCAGAGAGCTGATTAACGCAAG	1260
QY	1333	GCACAAAAAGAGGCGCGCGCTTGCCAGA	ATCCGTGTGGCCAAAACAGGCACTTCGAATGCA	1392
Db	1261	GCACAAAAAGAGGCGCGCGCTTGCCAGA	ATCCGTGTGGCCAAAACAGGCACTTCGAATGCA	1320
QY	1393	TACCTGCACAGCAAGCGCAACGGGCTCT	CAACGAGCGCTGGAGCTGACGGGCAACCCCA	1452
Db	1321	TACCTGCACAGCAAGCGCAACGGGCTCT	CAACGAGCGCTGGAGCTGACGGGCAACCCCA	1380
QY	1453	GAAAGAGAGACATGGGCGAAGACCACTCA	CTCATCGAGAGCCAGCATCATCACTGCTG	1512
Db	1381	GAAAGAGAGACATGGGCGAAGACCACTCA	CTCATCGAGAGCCAGCATCATCACTGCTG	1440
QY	1513	CATGCGCTGGA AAAAACCACTGGGTGTCT	ATCTGTGTGATGATCCCTGTTATCTGTA	1572
Db	1441	CATGCGCTGGA AAAAACCACTGGGTGTCT	ATCTGTGTGATGATCCCTGTTATCTGTA	1461
QY	1573	CGAAGCTCCACCATCAAGAACCAAGAGTT	TATGTATGAGACAGATGTTTGAAGACAGACTGC	1632
Db	1462	CGAAGCTCCACCATCAAGAACCAAGAGTT	TATGTATGAGACAGATGTTTGAAGACAGACTGC	1503
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Db	1504	ATGAGAGAGTTTCAATGACGAAGTCTCCAT	CCATCCACAAGAAAGTCCCTCACTGTCCAGCCACA	1563
QY	1693	GGCCTCACTACCACTGCTGCTCCGCTCGT	AGTAAGAAGACCAACCTGCGCCCAATTCT	1752
Db	1564	GGCCTCACTACCACTGCTGCTCCGCTCGT	AGTAAGAAGACCAACCTGCGCCCAATTCT	1623
QY	1753	AACTTGCCAGCTACTCGCTGCGGACGATG	CAAGAGCTCAGACAGATCCACATCCAGGGGC	1812
Db	1624	AACTTGCCAGCTACTCGCTGCGGACGATG	CAAGAGCTCAGACAGATCCACATCCAGGGGC	1683
QY	1813	AGTGAGCAGCCCTCCCTCACAACCAAGTGC	CTCCAGCTTAATTGAAAACAGACAGACGGA	1872
Db	1684	AGTGAGCAGCCCTCCCTCACAACCAAGTGC	CTCCAGCTTAATTGAAAACAGACAGACGGA	1743
QY	1873	CTGAGACCAAACTGCAAAAACATCCAGAT	TACCAACAGCCATCATCAGCATCCCACTCCC	1932
Db	1744	CTGAGACCAAACTGCAAAAACATCCAGAT	TACCAACAGCCATCATCAGCATCCCACTCCC	1803
QY	1933	CCAGCGCTAACCCCAAGAGGGGGAAGTCCG	CCACCCCTGACGACCCCAAGCCCAACACG	1992
Db	1804	CCAGCGCTAACCCCAAGAGGGGGAAGTCCG	CCACCCCTGACGACCCCAAGCCCAACACG	1863
QY	1993	AACATTTCTTTCCATTAACCAAGCAATGTT	GTGCAAGGTCTCTGTCTTTGTAATAATCCCGCGGC	2052
Db	1864	AACATTTCTTTCCATTAACCAAGCAATGTT	GTGCAAGGTCTCTGTCTTTGTAATAATCCCGCGGC	1923
QY	2053	CATGGC 2058		
Db	1924	GAGGAC 1929		

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/ Sequence 957, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CU001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 957
/ LENGTH: 5333
/ TYPE: DNA
/ ORGANISM: Human
/
US-09-949-016-957

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Query Match	44.1%	Score 935.4	DB 4	Length 5333
Best Local Similarity	-70.7%	Pred. No. 3.6e-192		
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				Gaps 5
QY	66	AGTACCATGCGCCCGAGTGTGGCGCTGGCTGCTTTTGTCCCGGCGTGGCCATCGG	125	
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QY	126	GTGGATGCGCGTGGCCAACTGCCCATGCCCCCTGGCCCC--GGCGACAAGAACAGCG	182	
DB	1019	GTGGATGCTGTGGCTCGGGGCTTATGCCGCTCCCGGAGCAGAGAGAGAAAGGAC	1078	
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DB	1079	CCAGATGCTCTCATTTGTGCTGAATGTGAGTGGACCCGCTTCCAGAGCTGGCAGACAC	1138	
QY	243	GCTGAGCGCTACCCCGACACCCGCTGGCGACGACGAGAGAGATCTTCTTCAACGA	302	
DB	1139	CCTGAACGTTACCCAGACACTCTACTGGCGAGTCTGAGAGGAGACTTTTCTTACACCC	1198	
QY	303	GGACACCAAGAGTACTTCTTGCACCGGGAACCCCGAGGTCTCCGCTGCTCAACTT	362	
DB	1199	AGAACTCAGCAGTATTTCTTGAACGTGACCCAGACATCTTCCGCCACATCTGAAATT	1258	
QY	363	CTACCGCAGCGGGAGCTGCATACCCGCGCTACGATGCATCTCTGCTACGACGACA	422	
DB	1259	CTACCGCACTGGGAAGCTCCACTATCTTGCCACGAGTGATCTCTGCTTACATGAAGA	1318	
QY	423	GCTGGCTTCTACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAA	482	
DB	1319	ACTGGCTTCTTTGGCTTCATCCCGAAATCATCGCGACTGCTGTATAGAGGTACAA	1378	
QY	483	GGACCGCAAGAGGAGAACGCCGAGCGGCTCATGACGACACGACTCGAGAACAAACA	542	
DB	1379	GGATCGCAGCGGAGAGAACGCCGAGCGCTGCAAGACGACCGGATACCGACACCGCTGG	1438	
QY	543	GGAG---TCCATGCCCCGTGCTCACTTCCGCCAGACCATGTGGCGGGCTTGGAGAACCC	599	
DB	1439	GGAGAGCGCTTGGCCACCATGACTGCAAGGACAGAGAGGTGTGGAGGGCTTGGAGAACCC	1498	
QY	600	CCACACGACGACGCTGGCCCTGTCTTACTACGTGACTGAGCTTCTTCATCGCTGTCTC	659	
DB	1499	CCACACGACGACGATGGCCCTGTGTCTTACTATATTCACCGGGTTTTCATTTGCGCTCTC	1558	
QY	660	GCTCATCACCAAGTGTGGAGACGAGTGGCGGTGGGACAGGTCGCCGG--CAGCAAGGA	716	
DB	1559	TGTCAATCGCAATGTGTGGAAACAGTGCCTGCGGATCAAGCCACGCTCACATTAAAGA	1618	
QY	717	GCTGCGTGGCGGAGCGCTACTCGGTGCTTCTTCTGCTGAGACGCGCTGCTGAT	776	


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Db 1619 ACTGCCCTGTGGAGACGGGTATGCTGTGCGCTTCTTCTGTGGACA CGGCGTGCAT 1678
Qy 777 GATCTTACCGTGAAGTACCTCTGCGGCTCTTGGCGGCTCCAGCGCTACCGCTCAT 836
Db 1679 GATCTTACCGTGAAGTATTTGCTTCCGCTGGCTGCGAGCGGCTAGTGTACCGTTTGT 1738
Qy 837 CCGAGCGCTGATGAGATCATGAGTGTGGGCAATCATGCGCTACTACATCGGCTGTGT 896
Db 1739 GCGTAGTGTATGATGATCATGAGTGTGGGCAATCATGCGCTTATATCATTTGGGCTGT 1798
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Db 2219 AGCAGACAAAGAGAGGAGCAAAAGAGAGTGTGCGAGATCCGCGAGCGCAAAAG 2278
Qy 1377 AGCAGATTCGATGATGATCTGTGCAAGAGCGGCAAGCGGCTCTCAAGAGCGCTGGA 1436
Db 2279 CGAAGCGGCAATGCTTACATGAGAGAGAGAGAGATGTTTACTCATGATATGAGTGA 2338
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Db 2396 GCACCAACCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2431
Qy 1557 TCCCTGTATCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1616
Db 2432 -----GAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2458
Qy 1617 GTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676
Db 2459 CTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2518
Qy 1677 ACTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
Db 2519 ACTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2578
Qy 1737 ACACCTGCGCAATTTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1796
Db 2579 TCGCATCCCAATGCGCAATGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2638
Qy 1797 GATCAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
Db 2639 GATCAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2698
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Qy 1857 GAAAGCAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
Db 2699 CAAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2758
Qy 1917 CAGCATCCCACTTCCCGGCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1965
Db 2759 AAGCATCCCACTTCCCGGCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807

RESULT 7
US-09-336-643A-9
; Sequence 9, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Ruter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-09-336-643A-9

Query Match 37.6%; Score 798.2; DB 3; Length 3424;
Best Local Similarity 72.8%; Pred. No. 1.2e-162;
Matches 1079; Conservative 1; Mismatches 379; Indels 24; Gaps 3;
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QY 485 ACCGAGAGGAGAAACCGGAGCGGCTCATGAGCAACAGACTCGAGAAACCAACGAG 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 ACCGAAAGAGAGAAATGCGAGCGCTGCGAGAGATGAGAGGAGAGAGAGCGCGGG 728
QY 545 AGTCCATGCCCTGCGC-----TCAGCTTCCGCCAGACCATGTGGCGGCTTCGAGA 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 ACGGCCAGCGCTGCGAGAGGAGCTCCCTGCGGAGCGGCTCTGGCGGCTTCGAGA 788
QY 596 ACCCCACACACGAGCAGCGCTGGCCCTGCTCTTACTAGTGTGCTTCTTCATCGCTG 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 789 ATCCACACACGAGCAGCGAGCGCTGCTTCTTACTATGTGACCGGCTTCTTCATCGCG 848
QY 656 TCTCGGTTCATCAACCAACGTGTGAGACGGTCCGTGGGCGACGGTCCCGGGAG----- 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 849 TGTGGTTCATCGCCCAATGTGTGTGAGACCATCCATGCGGCTCTGACAGCGATCTT 908
QY 711 -CAAGAGCTGCCGTGCGGGAGCGCTACTGCGGTGCGCTTCTTCTGCTGAGACCGCGT 769
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 CAAGGAGAGCAGCGCTGTGGCGAAGCTTCCACAGGCTTTTCTGCAATGAGACAGCGCT 968
QY 770 GCGTCATGATCTTACCGGTGAGTACTCTGCGGCTCTTCTGCGGCTCCAGCGGCTTACC 829
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 969 GTGTACTCATATTCACAGGTGAATACCTCTGCGGCTGTTTTCGCGCCCGCGGCTTGGCC 1028
QY 830 GCTTCATCCGCGAGCGTCATGAGCATTCAGAGTGTGTGGCCATATGCGCTTACTATCG 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1029 GCTTCTGCGGAGTGTCAATGAGCCTCATGAGTGTGTGGCCATCTGCGCTTACTATCG 1088
QY 890 GTCTGTGATGACCAACAGAGAGGTGTCCGGCGGCTTCTGCAAGCTCCGGGTCTTCC 949
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1089 GCGTTTGTGTGCGCAAGACAGCATGTCTGTGGCGCTTGTGACCGCTGCGTGTCTCC 1148
QY 950 GCGTCTTCAGATCTTCAAGTTTTCGCCCACTCCAGGCGCTGCGGATCTGCGGTACA 1009
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1149 GGGTGTTCGATCTTCAAGTTCTTCAAGGCACTCACAGGCGCTGAGGATCTGGGCTACA 1208
QY 1010 CACTGAAGAGTGTGCTCCGAATGCGGCTTCTTCTTCTCCCTCAACCATGCGCATCA 1069
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1209 CACTCAAGAGTGTGCTTGAAGTGGGCTTCTCTCTTTTCCCTAACCATGCGCATCA 1268
QY 1070 TCATCTTGGCACTGTGATGTTTATGCGGAGAGGCGTCTCGGCGAGCAAGTTCAAA 1129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1269 TCATCTTGGCACTGTGATGTTTATGCTGAGAGGCGCAAAACAGCAACTTTACAA 1328
QY 1130 GCATCCCTGCTGCTTGTGTGTACACCATTTGATGACCATGACCACTGGGATACGAGACA 1189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1329 GCATCCCTGCGGCTTGTGTGTATACCATTTGATGACCATGACCACTGGGATACGAGACA 1388
QY 1190 TGGTGCCTAAGCATTTGAGAGGAGATCTTGGGCTCATCTGCTCTTGAAGTGGCTCC 1249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1389 TGGTGCCTAAGCATTTGAGAGGAGATTTTGGGCTCATCTGCTCTTGAAGTGGCTCC 1448
QY 1250 TGGTCAATGCTGCTGCGAGTCCGTGATTTTTCAACTTTAGCGGATTTACACACAGA 1309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1449 TGGTCAATGCTGCTGCTGCGAGTCCGTGATTTTTCAACTTTAGCGGATTTACACACAGA 1508
QY 1310 ATCAGAGAGCTGATTAACGAGGAGCAAAAGAGGCGGCTTGGCAGAGATCCGCTGG 1369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1509 ACCAGCGGCTGAGCAAGCGCGAGACAGCAAGAGTGGCTTGGCAAGATCCGATGG 1568
QY 1370 CCAAAACAGGAGTTCGATGATGCTGACAGCAAGCGGAGCGGCTCTTCAACGAGG 1429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1569 CAAAGAGTGTATCCACCAATGCTTCTCTGAGTACAGCAAGATGGGCGGCTTGA----- 1623
QY 1430 CGCTGAGCTGAGCGGCGACCCCAAGAGAGAGACATGGGCAAGACCACTCATCATCG 1489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1624 ----GGACAGCGGAGTGGCGAGAGAACAGGCTTTTGTGTAGAGAACCGTTCTGCTTGG 1679
QY 1490 AGAGCAGCATCATCACTGCTGCACTGCGTGAAGAAAAACAC 1532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1680 AACAGCAATACCACTTGTGCTGCACTGTCTTAGAGAGAACAC 1722
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RESULT 8
US-09-949-016-2456
; Sequence 2456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2456
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2456

Query Match      12.3%; Score 261; DB 4; Length 3260;
Best Local Similarity 61.5%; Pred. No. 8.3e-47;
Matches 488; Conservative 0; Mismatches 245; Indels 60; Gaps 2;

QY 1173 ACTGGATACGAGACATGCTGCTTAAGCATTCAGAGGAGATCTTGGCTCATCTG 1232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 ACTCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 61
QY 1233 CTCCTGATGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TTCGTGATGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 121
QY 1293 CCGGATTTACCAACGAGATCAGAGCTGATTAACGAGGAGCAAAAGAGCGCGCT 1352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 TCGCATCTACCAACGAGATCAGAGCTGATTAACGAGGAGCAAAAGAGCTAGACT 181
QY 1353 TGGCAGATCCGTGTGCGCAAAACGAGCTGATGATGATGATGATGATGATGATGATG 1412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GGCAGGATCCGGGAGCGCAAAAGCGGAGCGCAATGCTTACATGACAGAACGAA 241
QY 1413 CGGCTCTCAACGAGCGCTGAGCTGACGGGACCCAGAGAGAGACATGGGCAA 1472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 TGGTTTACTCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 298
QY 1473 GACCACTCATCTATCGAGAGCGAGCATATCACCCTGCTGCACTGCTGAAAAAACAC 1532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 ATCCGCTCCAGCTTGTGAACCCAGACCAACCACTGCTTCACTGCGTGAACCAACAC 358
QY 1533 TGGTGTCTATCTTGTGATGATCCCTGTTATCTGTAGCAAACTCCACATCAAGAA 1592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 -----GAA 361
QY 1593 CCAGAGTTTATGATGAGCAGATGTTTGAAGAGAACTGATGAGAGATTCATAGCAGAA 1652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TCACGAGTTTGTGAGCAGAACAGTCTTTGAAGAAAGCTGCAAGAGTTGCAACGTAA 421
QY 1653 CTACCATCCACAGAGTCCCTTCACTGTGCAAGCCAGCGCTCACTACCACTGCTG 1712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 TCGTCTTCAAGTCAAGTCTTCACTGTCTTCAACAAAGAGTCAACAGCACTGCTG 481
QY 1713 CTCGCTGTAGTAAAGAGACACACACCTGCCCCAATTCTTAACTTGCAGCTACTGCGCT 1772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 TTCAGACGACACAAAGAACTTTTGTGATCCCAATGCAATGTATATCAGGAAGCATCA 541
QY 1773 GCGCAGATGAGAGCTGAGCAGATCCATCCAGGGCAGTGAAGAGCGCTCCCTCAC 1832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 AGGTGATATACAAAGACTCAGACGATTCAGATCAGATGTGTGAGAGAACACCTCTGTC 601
```

OY		1833	AACCACTGCCTCCAGCCTTAATTGAAAAGACAAGCACCGACTGAAGACCATACTGCCAAATC	18922
Dd		602	TAACAGCCGATCCAGTTTAAATGGCAAATGGAGAAGTGGTGTTAAACTTAACTGTGAACA	661
OY		1893	ATCCGAGATCACCAAGCCCATCATGACATCCCCAAGTCCCCAGCGCTAACCCAGAGGG	19522
Dd		662	ACCTTAGTGTACTACAGCAATATAAAGCATCCCAACCTCCAGTAAACACACCGAAGG	721
OY		1953	GGAAGTCGGCCA	1965
Dd		722	AGACGATAGGCCA	734

RESULT 9

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US-09-949-016-2293
; Sequence 2293, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2293
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2293

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Query Match	11.3%	Score 240;	DB 4;	Length 3004;
Best Local Similarity	53.4%	Pred. No. 2.7e-42;		
Matches 712; Conservative	0;	Mismatches 575;	Indels 47;	Gaps 8

QY	13	CAAGCTGTGTGCTTAGCGTCGCCCGCGCTGCCCGCCCAAGAGCTGGAGTCAACCATGGCG	78
Db	72	CGAGCTGCCGCCCGACATGACCGTGTGCCCCGGGGACACCTGTGTGAG--CCGGAGGTG	129
QY	79	GCCGGAATTGCGCGCTGGCTGCTTTTGGCCCGGCTGCGGCATCGGGTGAGATGCGGTG	138
Db	130	GCCGATGATGAGGGGGCCCCCGCTCAAGCGGGCTGTGGCGGGCGGCGCTGCCACCGCTAC	189
QY	139	GCCAACTGCCCCCATGCCCCCTTGGCCCCCGCCGACAAAGAACAAAGCGGACAGATGAGTGA	198
Db	190	GAGCGCGTCCGCCCTCACTGCCCGGCGCGGGCGAGCAGACTGTGCGGGAGCGCGTG	249
QY	199	GTCCTCAACGTGATGGGCGGAGTTCCAGACTGAGAGCACCAGCTGGAGCGCTAACCGG	258
Db	250	GTCATCAACATCTCCGGGCTGCGCTTCGAGACGACGTGAAGACCTTTGGCAGTTCCCC	309
QY	259	GACACCCCTGCTGGGCGAGCAGCGAGAAAGAGTTCC--TTCTTCAACGAGGACACCAAGAG	315
Db	310	GAGACGCTGTGGGCGACCCCAAGCGGCGCATGAGTACTTCAACCCGCTCCGCAACGAG	369
QY	316	TACTTCTTCGACCGGGAGCCCCGAGGTTCGCGTGCCTGCTCAACTTCAACGCAACGGGG	375
Db	370	TACTTCTTCGACCGCAACCGGCCCAAGCTTCGACGCGCATCTCTACTACTATCACTGTCGGG	429
QY	376	AAGC--TGCACTACCCGCGCTACGAGTGCACTCTTCGCTACGACGACGAGCTGGCTTC	432
Db	430	GGCCGCACTCGCCGCGCGGTCAACGTGCCCATCGACATTTTCTTCGAGGAGATCCGCTTC	489
QY	433	TACGGCATCTCCCGGAGATCATCGGGGACTGTCTCTACGAGGAGTCAAGACCTCGAAG	492

Db	490	TACCAGCTGGGCGAGGAGGCCATGGAAGATTCCGCGAGGACGAGGGCTTCTCGCGGAG	549
QY	493	AGGGAACCGCCGAGCGGCTCATGTGACGACAAGCACTCGGAGAAACAACAGAGTCCATG	552
Db	550	GAGAGCGGCGCTTGCCCCGCGCGACTTCCAGCGCCAGGTG---TGGCTCTCTTGAG	606
QY	553	CCCTGCTCAGCTTCCGCCAGACCATGTGGCGGCTTTCAGAAACCCACACAGACG	612
Db	607	TACCCGAGAGCTCCGGGCGGCTCCGGGCAATCGCCATCGTGTGCTGTCATCTTC	666
QY	613	CTGGCCCTGCTTCTACTACGTAAGTGGCTT-----CTTCATGCTGTCTCGTATC	666
Db	667	ATCTCATTTGTATCTTCTGCTCGGAGACGCTGCGGAGTTCCGGACGAGAAAGACTAC	726
QY	667	ACCAACGTGTGGAGACGGTGCCTGCGCACGGTCCCGGCGAGCAAGAGCTGCGCTGC	726
Db	727	CCCGCTTCGACGTGCGAGACTATTGCAAGCACCGGCAACAGCAGCTCGGGGTCCCGC	786
QY	727	GGGGAG-----CGTACTCGGTGGCTTTCTTCTGCTGGAACACGGCGTGTGCTATGTC	780
Db	787	GCAGGAGCTCCAGCTTCTCCGATCCCTTCTTCTGTTGGAGACGCTGTGCATCATCTGG	846
QY	781	TTTACCGTGAAGTACCTCTCGGGCTCTTCGGGCTCCGAGCCGCTAACCGCTTCATCCGC	840
Db	847	TTCTCCTTGAACTGTGTGTCGGTCTTCTGCTTGTCTCTGACAAAGCACCTTCTCGGA	906
QY	841	AGCGTATGAGCATCATCGACGTGTGGCCATCATGCCCTACTACATCGCTGTGTCATG	900
Db	907	AACATCATGAACCTGATGACATTGTGGCCATCATTTCTTAATTATACCTCTGGGTACC	966
QY	901	ACCAA-----CAACGAGACGTGTCCGGCGCTTCTGTCACGCTCCGGTTC	945
Db	967	GAGCTGGCCGAACGACAGGGCAATGACAGAGGCGATGCTCTGACCATCCTGAGGGTTC	1026
QY	946	TTCCGC-----GTCTTCAGATCTCAAGTTTTCGCCCACTCCCAAGGCGCTCGG	996
Db	1027	ATCCGCTGTGAAGGCTCTTCCGATCTTCAAGCTGTCCGGCCACTCCAAAGGGCTGAG	1086
QY	997	ATCTGGGCTACACACTGAAGAGCTGTGCTCCGAAGTGGGCTTTCTTCTTCTCCCTC	1056
Db	1087	ATCCTCGGGCAACGCTGAAGGCTCCATGCGGAGCTGGGATGTCTATCTTCTTCTC	1146
QY	1057	ACCATGGCCATCATCATCTTTGCCACTGTGATGTTTATGCCGAGAAGGGCTCTCGCC	1116
Db	1147	TTTATTGGGGTATCCTTTCTTCTCAGCGGGTCTACTTGTCCGAGCAGACCACTCACT	1206
QY	1117	AGCAAGTTCACAAGCATCCCTGCTGTTTGTGTAACCAATGTGTCAACATGACCACTG	1176
Db	1207	TCAGGTTTCAGCAGCATCCCGATGCTTCTGTGGGCACTGTAAACATGACAAAGTG	1266
QY	1177	GGATACGGAGACATGTGTCTAAGACGATTTGAGGGAAGATCTTGGCTCCATCTGCTCC	1236
Db	1267	GGTACGGCGATATGACACCAAGTACCAATAGGGGCAAGATTTGGGATCTCTCTGTGCC	1326
QY	1237	TTGAGTGGCGTCTGTGATTTGCCCTGACAGTCCCTGTGATTTGTTTCCAATTAGCCGG	1296
Db	1327	ATCGCCGCTGTCTTGACCATCGCATTTGCCAGTTCCTCGTGAATGTTTCCAATTCAATTAC	1386
QY	1297	ATTTACCAACAGAA 1310	
Db	1387	TTCTACACCGGGA 1400	

RESULT 10

US-09-949-016-12066
 ; Sequence 12066, Application US/09949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12066
 LENGTH: 7055
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-12066

Query Match 11.3%; Score 240; DB 4; Length 7055;
 Best Local Similarity 53.4%; Pred. No. 3.4e-42;
 Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

QY 19 CAAGCTGCTGCTAGCGTCCGCGCGCTCCGCGGAGAGCTGAGTCAACATGGCG 78
 Db 2072 CGAGCTGCCCGCCGACATGACCGTGTGTCGCGGAGCACCTGCTGAG--CCGAGGTG 2129
 QY 79 GCGGAGTGTGCGGCTGCTGCTTTTGGCGGGCTGCGGCCATCGGTGATGCGGTG 138
 Db 2130 GCGGAGTGTGAGGGGCGGCGGCTTCAAGGCGCTGTGCGGCGGCTGCGACCGCTAC 2189
 QY 139 GCCAATGCCCATGCCCCGCGCGCGCGGCGGAGAGAGAGAGAGAGATGAGTGTAT 198
 Db 2190 GAGCGGCTGCGCGCTCACTGCGCGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 2249
 QY 199 GTCTCAACGAGTGTGCGGAGAGTTCAGACTGAGAGAGAGAGAGAGAGAGAGAGAG 258
 Db 2250 GTCTCAACATGCTCGGCGCTGCGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 2309
 QY 259 GACACCTGTGCGGAG 315
 Db 2310 GAGAGCTGTGCGGAG 2369
 QY 316 TACTTCTTGAAGCGGAG 375
 Db 2370 TACTTCTTGAAGCGGAG 2429
 QY 376 AAGC---TGACTAAGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
 Db 2430 GCGGCGATCCGCGCGCGCGCTCAAGTGCATGACATTTTCTTCGAGAGAGAGAGAG 2489
 QY 433 TAGGCGATCTCCCGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
 Db 2490 TACAGCTGTGCGGAG 2549
 QY 493 AGGAGAGAGCGGAG 552
 Db 2550 GAGGAGCGGCGCTTGCCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2606
 QY 553 CCCTGCTAGCTTCCGCGAG 612
 Db 2607 TACCCGAG 2666
 QY 613 CTGCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 666
 Db 2667 ATCTCATTTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2726
 QY 667 ACCAAGCTGTGAG 726
 Db 2727 CCGGCTGAG 2786
 QY 727 GGGAG-----CGTACTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
 Db 2787 GAGAGAGCTTCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2846
 QY 781 TTACCGGTGAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840

Db 2847 TTCTCTTGAAGCTGTGCTGCGGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2906
 QY 841 AGCGTATGAGATCATGAG 900
 Db 2907 AACATCATGAG 2966
 QY 901 ACCAA-----CAAG 945
 Db 2967 GAGTGGCGGAG 3026
 QY 946 TTCCGC-----GTCTTCAAGATCTTCAAGTCTTCCCGGAGAGAGAGAGAGAGAGAG 996
 Db 3027 ATCCGCTGTGAG 3086
 QY 997 ATCTGGCTACAG 1056
 Db 3087 ATCTGGCGGAG 3146
 QY 1057 ACCATGGCATCATCTTTTCCCACTGTGATGTTTATGCGAGAGAGAGAGAGAGAGAG 1116
 Db 3147 TTTATTTGGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3206
 QY 1117 AGCAATTCAG 1176
 Db 3207 TCAGTTTCAAG 3266
 QY 1177 GATACGAG 1236
 Db 3267 GGTACGCGGATATGACAG 3326
 QY 1237 TTGAGTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1296
 Db 3327 ATGCGCGGTGCTTGTACATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3386
 QY 1297 ATTACACAG 1310
 Db 3387 TTCTACACAG 3400

RESULT 11

US-09-949-016-14035
 Sequence 14035, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14035
 LENGTH: 7056
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-14035

Query Match 11.3%; Score 240; DB 4; Length 7056;
 Best Local Similarity 53.4%; Pred. No. 3.4e-42;
 Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

QY 19 CAAGTGTGTGCTAGCGTCCGCGCGCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
 Db 2072 CGAGCTGCCCGCCGACATGACGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 2129
 QY 79 GCGGAGTGTGCGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 138

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Db 2130 GCCGATGGTGGAGGGGCCCCCGCTCAAGCGGCTGTGGCGCGCGCGCTGCCAACCGCTAC 2189
Qy 139 GCCAACTGCCCCCATGCCCCCTGGCCCCCGCGCAAGAACAGCGGAGATGAGTGAATT 198
Db 2190 GAGCGCTGCGCCCTCACTGCGCGCGCGGAGACAGAGACTGTGCGGAGACGCGTG 2249
Qy 199 GTCTCAACGTAGTGGCGGAGTTCAGACTGAGAGACCAAGCTGAGGCGTACC 258
Db 2250 GTCATCAACATCTCCGGGCTGCGCTTGAAGACGAGCTGAAGACCTTTGCGAGTTCC 2309
Qy 259 GACACCTGCTGGGAGACGAGAGAGAGTTC--TTCTTCAACGAGACACCAAGAG 315
Db 2310 GAGACGCTGCTGGGAGACCCCAAGCGGCGATGAGTACTTGAACCGGCTCCGCAACGAG 2369
Qy 316 TACTTCTTGAACCGGAGACCCGAGAGTTCCTGCTGCTCAACTTCTACCGCACGCGG 375
Db 2370 TACTTCTTGAACCGGAGACCCGCGGCTTGAACCGCTCTCTACTATCATGATCCGCGG 2429
Qy 376 AAGC---TGCATACCCCGCTACGAGTGCATCTTGCCTACGACGAGCTGGCTTC 432
Db 2430 GGGCGCATCGCCCGCGCGGTCAACGTGCCCATGACATTTTCTCCGAGAGATCCGCTTC 2489
Qy 433 TACGGCATCTCCCGAGATCATCGGAGACTGCTGCTACGAGAGTACAAAGACCGAAG 492
Db 2490 TACCAGCTGGCGGAGAGAGCCATGAGAAATTCCGCGAGAGAGAGGCTTCTGCGGAG 2549
Qy 493 AGGAGAACCGCGAGCGGCTCATGAGACCAACGACTCGGAGAACCAAGAGTCCATG 552
Db 2550 GAGAGAGCGGCGCTTCCCGCGCGGCTTCCAGCGCCAGGTG--TGGCTGCTTCCAG 2606
Qy 553 CCTCGCTAGCTTCCGCGAGACCATGTGGCGCTTCCAGAACCCCGACACGAGACG 612
Db 2607 TACCCGAGAGCTCGGCGCGCGCGCATCGGCGCATGCTGCTGCTGCTGCTGCTGCT 2666
Qy 613 CTGGCCCTGCTCTTCTACTAGCTGAGTGTGCTT-----CTTCATCGCTGTCTGCTATC 666
Db 2667 ATCTCCATTTGTCTTCTGCTGAGAGCGTCCGAGTTCGCGGACGAGAAAGACTATC 2726
Qy 667 ACCAAGTGTGAGACGCTGCGGTGCGGACGCTCCCGGAGACGAGAGAGCTGCGTGC 726
Db 2727 CCGGCTCGAGCTCGAGAGACTTTCAGAGACGCGGAGACGAGCTGCGGCTCCGCG 2786
Qy 727 GGGGAG-----CGTACTCGGTGGCTTCTTGTGCTGAGACGCGGCTGCTGATGATC 780
Db 2787 GCAGAGAGCTTCAGCTTCTCCGATCCCTTCTTGTGTGAGAGCGTGTGATCATCTG 2846
Qy 781 TTCACCGTGAAGTACCTCTGCGGCTCTTGGCGGCTCCAGCGCTACCGCTTATCCGC 840
Db 2847 TTCTCTTCAACTGCTGTGCGGCTTCTGCTGTCTTACGAAAGCACTTCTGCGGA 2906
Qy 841 AGCGTATGAGCATCATGACGCTGTGCGCATCATGCGCTACTACATCGGTCTGTATG 900
Db 2907 AACATCATGAACCTGATCGACATTTGTGCGCATCTCTTATTTTATCACTGCGGTACC 2966
Qy 901 ACCAA-----CAACGAGAGCTGTCCGCGCTTCTGTCACGCTCCGCGTCC 945
Db 2967 GAGCTGGCCGAGACGAGGAGCATGACAGAGGCGCATGTCTGCGCATCTGAGGAGTCC 3026
Qy 946 TTCCGC-----GTCTTCAAGATCTTCAAGTTTCCCGGCACTCCAGGCGCTGCGG 996
Db 3027 ATCCGCTGTGAAGGCTTCCGATCTTCAAGCTGTGCGGCACTCAAGGCGCTGAG 3086
Qy 997 ATCTGGGCTACACATGAAGAGCTGTGCTCCGAACTGGGCTTCTTCTCTCTCCCTC 1056
Db 3087 ATCTCGGCGAAGCGTGAAGGCTTCATGCGGAGCTGGGATTTGCTCATCTTCTCTCC 3146
Qy 1057 ACCATGGCATCATCTTTGCACTGTGATGTTTATGCGGAGAGGCTCTCGGCG 1116
Db 3147 TTTATTTGGGCTCATCTTTTCTCAGCGGCTTACTTTGCGAGGAGACGACCCCACT 3206
Qy 1117 AGCAAGTTCAAGCATCCCTGCTGTTTGTACACCATTTGTACCATGACACACTG 1176
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Db 3207 TCAGTTTACGACGATCCCGGATGCTTGTGTGGGAGTGTAAACCATGACAAAGT 3266
Qy 1177 GATACGAGACATGTGCTTAAGACGATTGCAAGGAGATCTTGGCTCATCTGCTCC 1236
Db 3267 GGTACCGGATATGACCCAGTACGATGAGGGGCAAGATTGGGATCTCTGTGCG 3326
Qy 1237 TTGAGTGGCTCTGTGATGTCCTGCGCATGCTGATGTTTCCACTTAGCGCG 1296
Db 3327 ATGCGGCTGTCTGACCATGCAATGCGATGTCAGTTCCTGATGTTTCAACTTAC 3386
Qy 1297 ATTACCAACAGAA 1310
Db 3387 TTCTACCAACGCGGA 3400

RESULT 12
US-09-949-016-324
; Sequence 324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-324

Query Match 11.2%; Score 236.8; DB 4; Length 3004;
Best Local Similarity 53.2%; Pred. No. 1.3e-41;
Matches 710; Conservative 0; Mismatches 577; Indels 47; Gaps 8;

Qy 19 CAACTGTGTGCTTACGCTTCCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 78
Db 68 CGAGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 125
Qy 79 GCGGAGTTTGGCGGCTGCTGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 138
Db 126 GCGGATGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185
Qy 139 GCCAAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
Db 186 GAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245
Qy 199 GTCTCAACGTAGTGGGCGGAGTTCAGACTGAGAGACCAAGCTGAGCGCTACCCG 258
Db 246 GTCATCAACATCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 305
Qy 259 GACACCTGCTGGGAGACGAGAGAGAGTTC--TTCTTCAACGAGAGACCAAGAG 315
Db 306 GAGACGCTGCTGGGAGACCCCAAGCGGCGGAGTACTTGCAGCCGCTCCGCAAG 365
Qy 316 TACTTCTTGAACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCACTTCTACCGACGCGG 375
Db 366 TACTTCTTGAACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCACTTCTACCGACGCGG 425
Qy 376 AAGC---TGCATACCCCGCTACGAGTGCATCTGCTTACGAGACGAGCTGCGCTTC 432
Db 426 GGGCGCATCGCGCGCGGCTTCAACGAGTGCATGCAATTTTCTCGAGAGATCCGCTTC 485
Qy 433 TACGGCATCTCCCGAGATCATCGGGAAGTGTGCTGCTACGAGAGTACAAAGACCGGAG 492
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Db 486 TACAGCTGGCGAGAGGAGCCATGAGAACTTCGCGAGAGAGAGGAGGCTTCGCGGAG 545
Qy 493 AGGAGAACCGGAGCGGCTCATGACGACAAAGACTCGAGAAACAGAGAGTCCATG 552
Db 546 GAGAGAGGCGGCTTGGCCCGCGGAGCTTCAGCGGCGAGGTG---TGGCTGCTTTCAG 602
Qy 553 CCCTCGCTAGCTTCCGCGAGACCAATGTGGGGGCTTCGAGAACCCCAACAGAGAG 612
Db 603 TACCCGAGAGCTCCGGCGGCGGCGGAGATCGCATCGTGTGCTGCTGATCCTC 662
Qy 613 CTGCGCTGTCTTCTACTAGTGAAGTGGCTT-----CTTACGCTGTCTGCTGCTATC 666
Db 663 ATCTCATGTGATCTTCTGCTGAGAGAGCTGCGGAGTTCGCGAGAGAGAGACTAC 722
Qy 667 ACCAAGCTGTGAGAGAGCGGTCCGCGGAGAGCTCCGCGGAGAGAGAGAGTCCGCTG 726
Db 723 CCCGCTCGAGCTCGAGAGACTCATTCGAGAGAGCGGAGAGAGAGAGAGTGGGCTCCG 782
Qy 727 GGGAG-----CGCTACTCGGTGGCTTCTCTGCTGAGACAGCGGCTGCTGATGATC 780
Db 783 GCAGAGAGCTCCAGCTTCTCGATCCCTTCTGCTGAGAGAGAGCTGCTGATCATCTG 842
Qy 781 TTCAAGCTGAGTACCTCTGCGGCTTTCGCGGCTCCGAGCGGCTACCGCTTATCCG 840
Db 843 TTCTCTTCTGAGTCTGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
Qy 841 AGCTGATGAGTATCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 903 AACATCATGAACTGATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
Qy 901 ACCAA-----CAACGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Db 963 GAGTGGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
Qy 946 TTCCG-----GTCTTCAAGATCTTCAAGTTTCCCGGAGCTCCGAGGCTGCTG 996
Db 1023 ATCCGCTGTAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082
Qy 997 ATCTGCGCTACAGTCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056
Db 1083 ATCTGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1142
Qy 1057 ACCATGCGCATCATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1116
Db 1143 TTTATTTGGGCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1202
Qy 1117 AGCAAGTTCACAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1176
Db 1203 TCAGGTTTACAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262
Qy 1177 GATACGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1236
Db 1263 GGTACGCGATATGACACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAG 1322
Qy 1237 TTGATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1296
Db 1323 ATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382
Qy 1297 ATTACACAGANA 1310
Db 1383 TTCTACACCGGA 1396

RESULT 13
US-09-949-016-1604
; Sequence 1604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1604
; LENGTH: 1802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1604

Query Match 10.2%; Score 216; DB 4; Length 1802;
Best Local Similarity 53.7%; Pred. No. 3.6e-37;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy 294 CTTCAACGAGACCAAGAGTACTTCTTTCGACCGGAGCCCGAGAGTTCGCTGCTGCT 353
Db 207 CTACGACCGCGGAGAGGAGTCTTCTTTCGACCGGAGCCCGAGAGTTCGCTGCTGCT 266
Qy 354 GCTCACTTCAACGAGAGGAGTCTTCTTTCGACCGGAGCCCGAGAGTTCGCTGCTGCT 413
Db 267 CATCGAGTGTACTTCTTTCGAGAGGAGTCTTCTTTCGACCGGAGCCCGAGAGTTCGCT 326
Qy 414 GCAGAGAGCTGCTTCTTTCGAGAGTCTTCTTTCGAGAGTCTTCTTTCGAGAGTCTTCT 470
Db 327 CAAGAGAGAGTCTTCTTTCGAGAGTCTTCTTTCGAGAGTCTTCTTTCGAGAGTCTTCT 386
Qy 471 -----CGAGAGTCAAGAGAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 521
Db 387 CCACCTGAG 446
Qy 522 CAACGAGTGGAG 581
Db 447 GCAGAGAGTGGAG 506
Qy 582 GCGGCTTTCGAG 641
Db 507 GAAGTCTGAG 566
Qy 642 CTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
Db 567 CTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
Qy 702 CCGGAG 761
Db 627 GCTGAG 677
Qy 762 CAGGAG 821
Db 678 GACGAG 737
Qy 822 CCGTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 881
Db 738 CAAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
Qy 882 CTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
Db 798 CTACGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 857
Qy 921 CCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 980
Db 858 GCAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 917
Qy 981 CTCCAG 1040
Db 918 CTCTGAG 977
Qy 1041 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1100

Db 978 GCTGCTCAGTACCTGGCAGTGGGATATCTTCTCTGTCCTGCGGCTACACCATGGA 1037
Qy 1101 GAAGGCTCTCTGGCCAGCAAGTTTCAACAAGCATCCCTGCTGTTTGTAGACCATTTGT 1160
Db 1038 GCAGAGCCATCCAGAGACCCTGTTTAAAGCATCCCGAGCTCTTGTGTGGCCATCAT 1097
Qy 1161 CACCATGACCACTGGGATACGAGACATGTGTGCTTAAGCGATTGCAAGGAGATCTT 1220
Db 1098 CACCATGACCACTGGGATACGAGACATGTGTGCTTAAGCGATTGCAAGGAGATCTT 1157
Qy 1221 CGGCTCCATCTGCTCTGAGTGGCGCTCTGTGATTTGCCCTGCCAGTCCCTGTGATTTG 1280
Db 1158 CGCGGCATCAGCTTCTGTGTGTGATCATGCGCATGCGCTGCCCATCCCATCATCAT 1217
Qy 1281 TTCCAACTTTAGCCGATTTTACCAACGAGATC 1312
Db 1218 CAACCACTTTGTCAAGTACTACCAACAGCAGC 1249

RESULT 14

US-08-464-340A-3
; Sequence 3, Application US/08464340A
; Patent No. 5710019
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,340A
; FILING DATE: June 5,1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
; US-08-464-340A-3

Query Match 10.2%; Score 216; DB 1; Length 2483;
Best Local Similarity 53.7%; Pred. No. 3.9e-37;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy 294 CTTCAACGAGACACCAAGAGTACTTTGACCGGAGCCCGAGGTGTTCCGCTGCGT 353
Db 891 CTACGACCCCGGCAAGCGGAGTTTCTTGTGACGGAGCCCGGAGCCTTCAAGTGTG 950
Qy 354 GCTCAACTTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTCATCTGCTTA 413

Db 951 CATCGAGGTACTATTTCGGGGAGGTCACATGAAGAGGCAATCTGCCCATCTGCTT 1010
Qy 414 CGACGACGAGTGGCTTCTTACGCAATCTCTCCGAGATCATCGGGAGCTGCTA--- 470
Db 1011 CAAGAACGAGATGACTTCTGAAAGGTGGAACCTCAAGTTCCTGAGCACTGTTCAGAG 1070
Qy 471 -----CGAGAGTACAAAGACCGCAAGAGGAGAAACCGGAGCGCTCATGACGA 521
Db 1071 CCACTGACCGAAGAGCGGAGAGTGGAGAGATCGGGCGCGGCTGCACTCATCTT 1130
Qy 522 CAACGATCGGAGAACCAACGAGAGTTCATGCTGCTGCTCAGCTTCCGCAACCATGTG 581
Db 1131 GGAACGACCTGGCGGTGAGACGCGGCGGAGGCGGCTGGCGGCTGCGAGAGTGGCTG 1190
Qy 582 GCGGCGCTTCGAGAACCCCAACCAACGACGCTGCGCTGCTTCTTACTACTGATGAG 641
Db 1191 GAAGTTCCTGAGAGAGCCGAGTCTGCTGCTGCGCGGCGGAGTGGCGGAGCTCTCTT 1250
Qy 642 CTTCTTCAATGCTGCTCTGCTCATCAACGATGTGAGACGCGTGGCGGACCGT 701
Db 1251 CCGTCTCATCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310
Qy 702 CCGGCGACAAAGAGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 761
Db 1311 GCTGACGCGGAGG--GCAACGCGTGGAGACACCGACGCTGAG-----AAGTGA 1361
Qy 762 CACGCGCTGCTCATGATCTTCAACGAGATACCTCTGCGGCTCTTCCGCGCTCCAG 821
Db 1362 GACGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
Qy 822 CCGCTACGCTTCAATCCGAGCGTCAAGAGCATCATGAGTGTGAGTGTGAGTGTGAGTGT 881
Db 1422 CAAGCTGACCTTCCGCTGCTGCTTCAAGAACATGTGAGTGTGAGTGTGAGTGTGAGTGT 1481
Qy 882 CTACATGCTGCTGCTCATGACCAACAGAG-----ACGTGTC 920
Db 1482 CTACGTGAGCTCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1541
Qy 921 CGGCGCTTCTGTCAGCTCGGCTCTCCGCTCTTCCGCTTCAAGTGTTCGCGCA 980
Db 1542 GCAGGCGGTGAGGCGGCTGGGATCATGCGCATGCGGCGCATCTTCAAGTGTGCGCA 1601
Qy 981 CTCACGAGGCTCGGATCTGCGCTACACACTGAAGAGCTGTGCTCGGATGCGGCTT 1040
Db 1602 CTCCTCGGCTGAGACCTTCACTATGCTTCAAGCGAGCTTCAAGGAGCTGGGCT 1661
Qy 1041 TCTTCTCTTCTCCTCAGCATGCGCATCATCTTGTGCACTGTGATTTATGCGCA 1100
Db 1662 GCTGCTCATGTACTGCGAGTGGATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
Qy 1101 GAAGGCTCTCGGCGAGCAAGTTCAACAAGCATCCCTGCTGCTTGTGTAACCATGT 1160
Db 1722 GCAGAGCCATCCAGACCTGTTTAAAGAACATCCCCCACTTCTGTGTGGCCATCAT 1781
Qy 1161 CACCATGACCACTGGAGATACGAGACATGTGCTTAAGAGATGTCAGGGAAGATCTT 1220
Db 1782 CACCATGACCACTGGAGATACGAGACATGTGCTTAAGAGATGTCAGGGAAGATCTT 1841
Qy 1221 CGGCTCATCTGCTCTTGTGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280
Db 1842 CGGCGCATTCAGCTTCTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901
Qy 1281 TTCCAACTTTAGCCGATTTTACCAACGAGATC 1312
Db 1902 CAACCACTTTGTCAAGTACTACCAACAGCAGC 1933

RESULT 15

PCT-US94-08449A-3
; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.

TITLE OF INVENTION: Potassium Channel Protein 1 and 2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
FILING DATE: SUBMITTED HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-08449A-3

Query Match 10.2%; Score 216; DB 5; Length 2483;
Best Local Similarity 53.7%; Pred. No. 3.9e-37;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

QY 294 CTTCAACGAGACACCAAGAGTACTTCTTCGACCGGAGACCCCGAGGTGTCCTCGCT 353
DB 891 CTACGACCCCGGAGCGGAGTCTTACTTGACAGGAGACCCGAGCCTTCAAGTGT 950
QY 354 GCTCACTTCTACCGACGCGGAACTGCACTACCCGCTACAGAGTGCATCTCTGCTTA 413
DB 951 CATCGAGGTGTAATTTCTCGGAGGTTCACATGAAGAGGCACTGCTCCATCTGCTT 1010
QY 414 CGACGACGAGCTGCTTCTACCGGATCTCTCCGAGATCATCGGGAGCTGCTGCTA--- 470
DB 1011 CAAGAACGAGATGACTTCTGGAAGTGCACCTCAAGTTCCTGAGACGACTGTGCAAGAG 1070
QY 471 -----CGAGAGTACAAGACCGCAAGAGGAGAGAACCGCAGCGGCTCATGAGCA 521
DB 1071 CCACGTAGCGAGAGCGGAGAGCTGAGAGATCGCGCGCGCTGAGCTCATCT 1130
QY 522 CAACGACTCGGAGAAACAACAGAGTCCATGCTCTGCTCAGCTTCCGCGCAGACCATGTG 581
DB 1131 GGACGACCTGGGCTGAGCGGCGGAGGCTGCTGCGCGCTGCGCAGAGTGTCTGTG 1190
QY 582 GCGGCTTCGAGAACCCCAACAACAGACGCTGCGCTGCTTCTTACTACGTGACTGG 641
DB 1191 GAAGTTCCTGAGAGCGGAGTCTGCTGCGCGCGGCTGTGGCGGAGCTCTCTT 1250
QY 642 CTTCTTCATCGCTGCTCGCTCATCAACAACGTGTGAGAGCGGTCCGCTGCGGAGCGGT 701
DB 1251 CTTGCTCATCTCTGCTCTCTGCTGCTGCTCATGTGACATCACTCCCGAAGTGCAGGT 1310
QY 702 CCGGCGAGCAGAGAGCTGCGGTGCGGAGGAGCTACTCGGTGCTTCTTCTGCTGGA 761
DB 1311 GCTGAGCGCGAGG-GCAACCGCGGTGAGACCCGACGCTGAG-----AACGTGGA 1361

QY 762 CACGCGTGCCTCATGATCTTACCGGTGAGTACTCTCGGCTCTTCCGCGCTCCAG 821
DB 1362 GACGGGTGATTTGGCTGGTTCACCTGAGTACTGCTGCGCTCTTCTGTCACCCAA 1421
QY 822 CCGCTACCGCTTCATCCGACGCTCATGAGCATCATGACGTGTGGCATCATGCCCTA 881
DB 1422 CAAGCTGACCTTGGCGCTGCTTCATGATGAGACGTGTGCGCATCTCCCTT 1481
QY 882 CTACATCGGTGTGTATGACCAACAGAG-----ACGTGTC 920
DB 1482 CTACGTAGAGCTTACAGCTTACAGCAGCTGTGGTCCCGCATGATGAGTCAACCAAGTGA 1541
QY 921 CGGCGCTTCGTACAGCTTCGCGGTCTTCCGCTTTCAGATCTTCAAGTTTCCGCCA 980
DB 1542 GCAGGCGGTGACAGCGCTGCGGATCATGCGCATCGCGCGCATTTCAAGTGGCCGCA 1601
QY 981 CTCCAGGCGCTGCGGATCTGCGCTACACATGAGAGCTGTGCCGAAGTGGCTT 1040
DB 1602 CTCTGCGGCTGACAGACCTTACCTATGCTTCAAGCGAGCTTCAAGGAAGTGGGCT 1661
QY 1041 TCTTCTTCTCTCCCTACCATGCGCATCATCTTTCACATGTGATGTTTATGCCGA 1100
DB 1662 GCTGCTCATGTAAGTGTGAGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
QY 1101 GAAGGCTCTTCGCGGACGAGTTCACAGATCTCCCTGCTGTTTGTGTAACCATTTGT 1160
DB 1722 GCAGAGCATTCAGAGACCTGTTAAGACATCCCAAGTCTTCTGTTGGGCTCAT 1781
QY 1161 CACCATGACCACTGGGATACGAGATGAGTCTTAAGAGATTTGAGAGATCTT 1220
DB 1782 CACCATGACCACTGGGATACGAGATGAGTCTTAAGAGATTTGAGAGATCTT 1280
QY 1221 CGGCTTCATCTGCTCTTGAAGGCTGCTGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCT 1280
DB 1842 CGCGGCTATGAGCTTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901
QY 1281 TTCCACTTTAGCCGATTTACCAACGATC 1312
DB 1902 CAACAACTTTGCTGAGTACTACCAACGAGC 1933

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Job time : 365.767 secs

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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 07:58:39 ; Search time 2500.09 Seconds
(without alignments)
5022.120 Million cell updates/sec

Title: US-10-062-879-1

Perfect score: 2121
Sequence: 1 gatttgctgaactaactcca.....gtcgtattaaagccgaattc 2121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn190s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2121	100.0	2121	6	ABN84400	Abn84400 Human Kv4
2	1997	94.2	2064	6	ABN84401	Abn84401 Human Kv4
3	1962	92.5	2072	2	AAV61572	Aav61572 Human Kv
4	1960	92.4	1968	12	ADFP91397	Adfp91397 Wild-type
5	1838	86.7	2104	2	AAV61571	Aav61571 Human Kv
6	1830	86.3	2104	2	AAV61573	Aav61573 Human Kv
7	935.4	44.1	2351	4	AAH21247	Aah21247 Human Kv4
8	935.4	44.1	2351	11	ADM10922	Adm10922 Human O64
9	935.4	44.1	2351	12	ADJ11252	Adj11252 Human ova
10	935.4	44.1	2351	12	ADM43513	Adm43513 Human ova
11	935.4	44.1	5333	11	ADM10923	Adm10923 Human O64
12	935.4	44.1	5333	11	ADM10921	Adm10921 Human O64
13	935.4	44.1	5333	12	ADJ11253	Adj11253 Human ova
14	935.4	44.1	5333	12	ADJ11251	Adj11251 Human ova
15	935.4	44.1	5333	12	ADM43512	Adm43512 Human ova
16	935.4	44.1	5333	12	ADM43514	Adm43514 Human ova
17	935.4	44.1	5333	12	ADP21361	Adp21361 Gene KCND
18	800.2	37.7	2711	4	AAH21246	Aah21246 Human Kv4
19	798.2	37.6	3424	2	AAZ11901	Aaz11901 Human pot
20	795.4	37.5	2578	4	AAH99538	Aah99538 Human pro

21	739.8	34.9	1716	4	ABL29811	Ab129811 Drosoph11
22	679	32.0	5404	11	ADM10924	Adm10924 Human O64
23	679	32.0	5404	12	ADJ11254	Adj11254 Human ova
24	679	32.0	5404	12	ADM43515	Adm43515 Human ova
25	637.8	30.1	2033	4	AAH21248	Aah21248 Human KCN
26	634.2	29.9	1121	12	ACH91582	Ach91582 Human gen
27	540	25.5	8075	4	ABL29810	Ab129810 Drosoph11
28	435	20.5	1737	12	ADFP1396	Adfp1396 Worm Kv4.
29	357	16.8	1083	4	AAH21264	Aah21264 Human Kv4
30	354.4	16.7	1597	11	ADM10925	Adm10925 Human O64
31	354.4	16.7	1597	12	ADJ11255	Adj11255 Human ova
32	354.4	16.7	1597	12	ADM43516	Adm43516 Human ova
33	338	15.9	612	4	AA128128	Aa128128 Probe #18
34	338	15.9	612	4	ABA76453	Abat76453 Human foe
35	338	15.9	612	4	AA157133	Aa157133 Probe #25
36	338	15.9	612	4	ABA40984	Abat40984 Probe #19
37	338	15.9	612	4	AAK51097	Aak51097 Human bon
38	338	15.9	612	4	AAK25090	Aak25090 Human bra
39	338	15.9	612	4	ABS50654	Abs50654 Human liv
40	338	15.9	612	6	ABS24615	Abs24615 Human gen
41	266	12.5	2882	13	ADS16307	Ads16307 Rabbit vo
42	259.2	12.2	3254	11	ADM10920	Adm10920 Human O64
43	259.2	12.2	3254	12	ADJ11250	Adj11250 Human ova
44	259.2	12.2	3254	12	ADM43511	Adm43511 Human ova
45	240	11.3	3004	13	ABD33130	Abd33130 Human can

ALIGNMENTS

RESULT 1	
ABN84400	
ID	ABN84400 standard; cDNA; 2121 BP.
XX	
AC	ABN84400;
XX	
DT	01-OCT-2002 (first entry)
XX	
DE	Human Kv4.3 potassium channel (long form) cDNA.
XX	
KW	Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KW	neotrophic; neuroprotective; cardiact; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "Kv4.3"
XX	
XX	US6395477-B1.
XX	
PD	28-MAY-2002.
XX	
PF	23-OCT-1998; 98US-00178109.
XX	
PR	23-OCT-1998; 98US-00178109.
XX	
PA	(AMHP) AMERICAN HOME PROD CORP.
XX	
PI	Cockett MI, Dilks DW, Ling HC, Sokol PT;
XX	
DR	WPI; 2002-556093/59.
XX	
XX	P-PSDB; ABB79584.
PT	New isolated polynucleotide encoding human Kv4.3 potassium channel
PT	polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT	acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT	diseases.
XX	
PS	Claim 5; Col 15-18; 19pp; English.
XX	
CC	The present sequence is that of cDNA encoding the long isoform of novel

human potassium channel Kv4.3. To obtain the cDNA, oligonucleotides based on the published rat sequence were used to screen a whole heart cDNA library. A 511 bp fragment was obtained and used as a probe to rescreen the library. The resulting clones lacked the extreme 5' and 3' coding regions, and 5' and 3' RACE was therefore used to amplify these sequences from a human brainstem cDNA library. 2 isoforms of human Kv4.3 were identified. One form is full-length (hKv4.3 long) while the second form has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are useful in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease

Sequence 2121 BP; 457 A; 694 C; 557 G; 413 T; 0 U; 0 Other;

Query Match	100.0%	Score 2121	DB 6	Length 2121
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2121; Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY	I	GATTGGTGAAC	TAACTCCAA	GGTGTGTG	CTAGGCTCCGGGCGGCTG	CCGACCA	AGA	60
Db	1	GATTGGTGAAC	TAACTCCA	AGTGTGTG	CTAGGCTCCGGGCGGCTG	CCGACCA	AGA	60
QY	61	GCTGAGTCA	CCATGCGCGCCG	GAAGTTGCGGCTG	CCCTTTTGCCCGGCTG	CGGC		120
Db	61	GCTGAGTCA	CCATGCGCGCCG	GAAGTTGCGGCTG	CCCTTTTGCCCGGCTG	CGGC		120
QY	121	ATCGGGTGA	TGCTCCGTTG	SCCACTGCCCCATG	CCCCCTGGCCCCCGG	CCGACCA	AGA	180
Db	121	ATCGGGTGA	TGCTCCGTTG	SCCACTGCCCCATG	CCCCCTGGCCCCCGG	CCGACCA	AGA	180
QY	181	CGGCAGATG	AGCTGATTGTC	TCAAGTAGTGGGCG	GAGGTTCCAGAC	CTG	AGA	240
Db	181	CGGCAGATG	AGCTGATTGTC	TCAAGTAGTGGGCG	GAGGTTCCAGAC	CTG	AGA	240
QY	241	ACGCTGAG	CGCTACCCCGA	CACCTGTG	GGCAGACG	GAGAA	GAGTCTTCTTCA	300
Db	241	ACGCTGAG	CGCTACCCCGA	CACCTGTG	GGCAGACG	GAGAA	GAGTCTTCTTCA	300
QY	301	GAGGACCA	CAAGGAGTACTT	CTTGACCGG	GACCCCGAGGTG	TC	CCGTGCTCA	360
Db	301	GAGGACCA	CAAGGAGTACTT	CTTGACCGG	GACCCCGAGGTG	TC	CCGTGCTCA	360
QY	361	TTCTACCG	CACGGGGAAG	GTGCAC	TACCCGGCTAC	GAGTGA	CTTCTGCTTAC	420
Db	361	TTCTACCG	CACGGGGAAG	GTGCAC	TACCCGGCTAC	GAGTGA	CTTCTGCTTAC	420
QY	421	GAGCTGG	CCCTTCTAC	GCATCCTCCG	GAGTCA	TGCGGA	CTGCTGCTAC	480
Db	421	GAGCTGG	CCCTTCTAC	GCATCCTCCG	GAGTCA	TGCGGA	CTGCTGCTAC	480
QY	481	AAGGACCG	CAAGAGGAGAA	CGCCGAGCG	CTCATG	GACGAC	CAACTCGGAGAAC	540
Db	481	AAGGACCG	CAAGAGGAGAA	CGCCGAGCG	CTCATG	GACGAC	CAACTCGGAGAAC	540
QY	541	CAGGAGTC	CATGCCCTCG	CTCAGCTTCCG	CAGACCA	TGTGCGGG	CCCTTGAGAA	600
Db	541	CAGGAGTC	CATGCCCTCG	CTCAGCTTCCG	CAGACCA	TGTGCGGG	CCCTTGAGAA	600
QY	601	CACACCA	GCACGCTGGCC	CTGTCTTCTT	ACTACGTA	CTGCTTCTT	CATGCTGTCTG	660
Db	601	CACACCA	GCACGCTGGCC	CTGTCTTCTT	ACTACGTA	CTGCTTCTT	CATGCTGTCTG	660
QY	661	GTATATCA	CCAA	CGTGTG	GAGACGGTGC	CGGCA	CGGCGCA	720
Db	661	GTATATCA	CCAA	CGTGTG	GAGACGGTGC	CGGCA	CGGCGCA	720
QY	721	CCGTGCGG	GAGCGCTACT	CGGTGCGCTT	CTTCTG	CC	TGACACGCGCGT	780
Db	721	CCGTGCGG	GAGCGCTACT	CGGTGCGCTT	CTTCTG	CC	TGACACGCGCGT	780

QY	781	TTTACCGGTGAGATACCTTCTTGGGGCTCTTGGGGCTCCAGCCCGCTTACCTCCGCTTATCCG	840
Db	781	TTTACCGGTGAGATACCTTCTTGGGGCTCTTGGGGCTCCAGCCCGCTTACCTCCGCTTATCCG	840
QY	841	AGCGTCATGAGCATCATCGACGTCGTGGCCATCATGCCCCCTAATACTACATCCGCTCTGTGATG	900
Db	841	AGCGTCATGAGCATCATCGACGTCGTGGCCATCATGCCCCCTAATACTACATCCGCTCTGTGATG	900
QY	901	ACCAACAACGAGGACGTCGTCCGGCGCTTGTACAGCTCCGGGTCTTCCGGCTCTTCAAG	960
Db	901	ACCAACAACGAGGACGTCGTCCGGCGCTTGTACAGCTCCGGGTCTTCCGGCTCTTCAAG	960
QY	961	ATCTTCAAGTTTCCCGCCACTCCAGGGCCTGGGGATCCTGGGCTACACACTGAAGAGC	1020
Db	961	ATCTTCAAGTTTCCCGCCACTCCAGGGCCTGGGGATCCTGGGCTACACACTGAAGAGC	1020
QY	1021	TGTGCTCCGAACTGGGCTTCTTCTCTTCTCCCTCACCATGGCCATCATCTTTGGC	1080
Db	1021	TGTGCTCCGAACTGGGCTTCTTCTCTTCTCCCTCACCATGGCCATCATCTTTGGC	1080
QY	1081	ACTGTGATGTTTATATGCCGAGAAAGGGCTCTCGGCCAGCAAGTTTACAAGATCCCTGCC	1140
Db	1081	ACTGTGATGTTTATATGCCGAGAAAGGGCTCTCGGCCAGCAAGTTTACAAGATCCCTGCC	1140
QY	1141	TGCTTTTGGTACACCAATGTGTACCATGACACACACTGGGATACGGAGACATGGTGCTTAAG	1200
Db	1141	TGCTTTTGGTACACCAATGTGTACCATGACACACACTGGGATACGGAGACATGGTGCTTAAG	1200
QY	1201	ACGATTGCAGGGAAGATCTTGGCTCCATCTGCTCTTGAATGGGCTCTGGTCAATTGCC	1260
Db	1201	ACGATTGCAGGGAAGATCTTGGCTCCATCTGCTCTTGAATGGGCTCTGGTCAATTGCC	1260
QY	1261	CTGCCAGTCCCTGTGATGTTTTCCTTCCACTTTAGCCGGATTTACCAACGAAATCAGAGACT	1320
Db	1261	CTGCCAGTCCCTGTGATGTTTTCCTTCCACTTTAGCCGGATTTACCAACGAAATCAGAGACT	1320
QY	1321	GATTAACGCAAGGGCACAAGAAGAGGCCCGCTTGGCAGGATCCGTGTGCCAACAACAGGC	1380
Db	1321	GATTAACGCAAGGGCACAAGAAGAGGCCCGCTTGGCAGGATCCGTGTGCCAACAACAGGC	1380
QY	1381	AGTTCCGAATGCATACCTTCACACAGCAAGGCCAACCGGCTCCTCAACGAGCGCTGAGCTG	1440
Db	1381	AGTTCCGAATGCATACCTTCACACAGCAAGGCCAACCGGCTCCTCAACGAGCGCTGAGCTG	1440
QY	1441	ACGGGCACCCCAGAGAAGAGGACATGGGCAAGACCACTCACTCATTCGAGAGCCAGCAT	1500
Db	1441	ACGGGCACCCCAGAGAAGAGGACATGGGCAAGACCACTCACTCATTCGAGAGCCAGCAT	1500
QY	1501	CATCACTGCTGCATCTGCTTGAAAAAACCACTGGGTTGTCCTATCTTTGTGATGATCCC	1560
Db	1501	CATCACTGCTGCATCTGCTTGAAAAAACCACTGGGTTGTCCTATCTTTGTGATGATCCC	1560
QY	1561	CTGTTATCTGTACGAACCTCCACCATCAAGAACACAGAGTTTATTGATGAGCAGATGTT	1620
Db	1561	CTGTTATCTGTACGAACCTCCACCATCAAGAACACAGAGTTTATTGATGAGCAGATGTT	1620
QY	1621	GAGCAGAACTGCATGAGAGATTCAATGCAAGACTAACCATTCACAAAGAAAGTCCCTCACTG	1680
Db	1621	GAGCAGAACTGCATGAGAGATTCAATGCAAGACTAACCATTCACAAAGAAAGTCCCTCACTG	1680
QY	1681	TCCAGGCCACCCAGGCTCACTACCACTGTCGTCCCGTGTAGTAAGAAACCAACACAC	1740
Db	1681	TCCAGGCCACCCAGGCTCACTACCACTGTCGTCCCGTGTAGTAAGAAACCAACACAC	1740
QY	1741	CTGCCCAATTTCTAACCTGCACGCTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGATC	1800
Db	1741	CTGCCCAATTTCTAACCTGCACGCTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGATC	1800
QY	1801	CACATCAGGGCAGTGAACAGCCCTCCCTACAAACAGTCGCTCCAGCCTTAATTGGAA	1860
Db	1801	CACATCAGGGCAGTGAACAGCCCTCCCTACAAACAGTCGCTCCAGCCTTAATTGGAA	1860

[illegible]

RESULT 2

ID	ABN84401	standard; cDNA; 2064 BP.
XX	ABN84401	
AC	ABN84401;	
XX		
DT	01-OCT-2002	(first entry)
XX		
DE	Human Kv4.3 potassium channel (short form) cDNA.	
XX		
KM	Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;	
KM	neurotropic; neuroprotective; cardiac; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	73..1983
FT		/+tag= a
FT		/product= "Kv4.3"
XX		
PN	US6395477-B1.	
XX		
PD	28-MAY-2002.	
XX		
PF	23-OCT-1998;	98US-00178109.
XX		
PR	23-OCT-1998;	98US-00178109.
XX		
PA	(AMHP) AMERICAN HOME PROD CORP.	
XX		
PI	Cockett MI, Dilks DW, Ling HC, Sokol PT;	
XX		
DR	WPI; 2002-556093/59.	
XX	P-PSDB; ABB79585.	
PT		
PT	New isolated polynucleotide encoding human Kv4.3 potassium channel	
XX	polypeptide, useful as probe in a diagnostic method for detecting nucleic	
PT	acid encoding human Kv4.3, and for treating Alzheimer's and heart	
PT	diseases.	
PS		
XX	Claim 7; Col 21-22; 19pp; English.	
XX		
CC	The present sequence is that of cDNA encoding the short isoform of novel	
CC	human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been	
CC	identified. One form is full-length (hKv4.3 long) while the second form	
CC	has a deletion of 19 amino acids in the carboxy domain after the	
CC	predicted sixth transmembrane domain (hKv4.3 short). Human heart	
CC	primarily expresses hKv4.3 long, whereas human brain contains both forms.	
CC	To obtain the present hKv4.3 short cDNA, PCR amplification was performed	
CC	using primers that flanked the 57 bp insert in hKv4.3 long. The invention	
CC	provides Kv4.3 polypeptides, polynucleotides, and methods for producing	
CC	these polynucleotides. The Kv4.3 polypeptides and polynucleotides are	

CC useful in the diagnosis, treatment and screening of human diseases
CC relating to an excess or deficiency of hKv4.3 activity, including
CC Alzheimer's disease and heart disease

Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;

Query Match	Score	1997; DB 6; Length	2064;
	94.28;		

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      27.58; 1.00; 0.00;
      2064; 0; 57; 1;

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Qy	1	GATTGCTGAACTAACTCCAAAGCTGCTGCTTAAGCGTCCGGCGGCTGCTCGGCCCAAGA	60
Db	1	GATTGCTGAACTAACTCCAAAGCTGCTGCTTAAGCGTCCGGCGGCTGCTCGGCCCAAGA	60
Qy	61	GCCTGAGTCACCAATGCGCGCGCGAGTTGCGGCTGGCTGCTTTTGCCCGGGCTGCGGCC	120
Db	61	GCTGGAATCACCAATGCGCGCGCGAGTTGCGGCTGGCTGCTTTTGCCCGGGCTGCGGCC	120
Qy	121	ATCGGGTGGATGCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCCCAAGAACAG	180
Db	121	ATCGGGTGGATGCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCCCAAGAACAG	180
Qy	181	CGGCAGGATGAGCTGATTGTCTCAACGTGAGTGGGCGGAGGTTCCAGACTTGAGAGACC	240
Db	181	CGGCAGGATGAGCTGATTGTCTCAACGTGAGTGGGCGGAGGTTCCAGACTTGAGAGACC	240
Qy	241	ACGCTGGAGCGCTACCCGGACACCTGCTGGGACAGCAGGAGAGAGATTCTTCTTCAAC	300
Db	241	ACGCTGGAGCGCTACCCGGACACCTGCTGGGACAGCAGGAGAGAGATTCTTCTTCAAC	300
Qy	301	GAGGACACCAAGAGTACTTCTTGCACCGGAGCCCCGAGGTGTTCCGCTGCGTCAAC	360
Db	301	GAGGACACCAAGAGTACTTCTTGCACCGGAGCCCCGAGGTGTTCCGCTGCGTCAAC	360
Qy	361	TTCTACCGCACCGGGAAGCTGCATCAACCCGCTACGAGTGCACTCTGCTCTACGACGAC	420
Db	361	TTCTACCGCACCGGGAAGCTGCATCAACCCGCTACGAGTGCACTCTGCTCTACGACGAC	420
Qy	421	GAGCTGGCTTCTACCGGATCTCTCCCGGAGATCATCGGGGACTGCTGCTACGAGAGTAC	480
Db	421	GAGCTGGCTTCTACCGGATCTCTCCCGGAGATCATCGGGGACTGCTGCTACGAGAGTAC	480
Qy	481	AAGGACCGCAAGAGGAGAACGCCGAGCGGCTCATGGACGACACGACTCGGAGAACAC	540
Db	481	AAGGACCGCAAGAGGAGAACGCCGAGCGGCTCATGGACGACACGACTCGGAGAACAC	540
Qy	541	CAGGAGTCCATGCTCTGCTCAGCTTCCGCCAGACCAATGTGCGGGCTTCGAGAACCCC	600
Db	541	CAGGAGTCCATGCTCTGCTCAGCTTCCGCCAGACCAATGTGCGGGCTTCGAGAACCCC	600
Qy	601	CACACCAAGCAGCTGGCCCTGTCTTCTACTACGTGACTGGCTTCTTCAATGCTGTCTCG	660
Db	601	CACACCAAGCAGCTGGCCCTGTCTTCTACTACGTGACTGGCTTCTTCAATGCTGTCTCG	660
Qy	661	GTTCATCACCAACGTGTGGAGACCGTGGCCGTGCGGCAACGCTCCCGGGGCAAGAGCTG	720
Db	661	GTTCATCACCAACGTGTGGAGACCGTGGCCGTGCGGCAACGCTCCCGGGGCAAGAGCTG	720
Qy	721	CCGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGAGACAGGCGTGGCTCATGATC	780
Db	721	CCGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGAGACAGGCGTGGCTCATGATC	780
Qy	781	TTCACCGTGAAGTACTCTGCGGCTTCTTGGCGGCTCCAGCCGCTTCAATCCGC	840
Db	781	TTCACCGTGAAGTACTCTGCGGCTTCTTGGCGGCTCCAGCCGCTTCAATCCGC	840
Qy	841	AGCGTCAATGAGCATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGTCTGTCATG	900
Db	841	AGCGTCAATGAGCATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGTCTGTCATG	900
Qy	901	ACCAACAACGAGGACGTGTCCGGCGCTTCTGTACGCTCCGGGTCTTCCGCTTTCAGG	960
Db	901	ACCAACAACGAGGACGTGTCCGGCGCTTCTGTACGCTCCGGGTCTTCCGCTTTCAGG	960

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QY 961 ATCTCAAGTTTCCCGCCACTCCCAAGGCGCTGCGATCCTGGGCTACACACTGAAGC 1020
DB 961 ATCTCAAGTTTCCCGCCACTCCCAAGGCGCTGCGATCCTGGGCTACACACTGAAGC 1020
QY 1021 TGTGCTCCGAACCTGGGCTTTCTTCTCTCTCTCCCTCACCATGGCCATCATCTTTGCC 1080
DB 1021 TGTGCTCCGAACCTGGGCTTTCTTCTCTCTCTCCCTCACCATGGCCATCATCTTTGCC 1080
QY 1081 ACTGTGATGTTTATGCGGAGAAAGGCTCTCGGCGAGCAAGTTCCACAGCATCCCTGCC 1140
DB 1081 ACTGTGATGTTTATGCGGAGAAAGGCTCTCGGCGAGCAAGTTCCACAGCATCCCTGCC 1140
QY 1141 TCGTTTGGTACACCAATGTGACCAATGACCACTGGGATTAACACCAATCAGAGCT 1200
DB 1141 TCGTTTGGTACACCAATGTGACCAATGACCACTGGGATTAACACCAATCAGAGCT 1200
QY 1201 ACGATTGCGGGAAGATCTTGGGCTCCATCTGCTCTTGTAGTGCGCTCTGTCATTGCC 1260
DB 1201 ACGATTGCGGGAAGATCTTGGGCTCCATCTGCTCTTGTAGTGCGCTCTGTCATTGCC 1260
QY 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACACCAATCAGAGCT 1320
DB 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACACCAATCAGAGCT 1320
QY 1321 GATTAACGAGGCGCACAAAAGAGGCGGCTTGGCCAGATCCGTGGCCAAACAGGC 1380
DB 1321 GATTAACGAGGCGCACAAAAGAGGCGGCTTGGCCAGATCCGTGGCCAAACAGGC 1380
QY 1381 AGTTCGAATGATACCTGACAGCAAGGCGCAACGCGCTCCTCAACGAGCGCGTGAAGCTG 1440
DB 1381 AGTTCGAATGATACCTGACAGCAAGGCGCAACGCGCTCCTCAACGAGCGCGTGAAGCTG 1440
QY 1441 ACGGGCAACCCGAGAAAGAGAGACATGCGGCAAGACCACTCACTCATCGAGAGCCAGCAT 1500
DB 1441 ACGGGCAACCCGAGAAAGAGAGACATGCGGCAAGACCACTCACTCATCGAGAGCCAGCAT 1500
QY 1501 CATCACCTGCTGACCTGCGCTGGAAGAAACCACTGGGTTGTCCTATCTGTGATGATCCC 1560
DB 1501 CATCACCTGCTGACCTGCGCTGGAAGAAACCACTGGGTTGTCCTATCTGTGATGATCCC 1560
QY 1561 CTGTATCTGTACGAACCTCCACATCAAGACCAAGATTATGATGAGCAGATGTTT 1620
DB 1561 CTGTATCTGTACGAACCTCCACATCAAGACCAAGATTATGATGAGCAGATGTTT 1620
QY 1621 GAGCAGAACTGATGAGAGATTCAATGACAGAACTAACCCATCCACAAGAAAGTCCCTCACTG 1680
DB 1621 GAGCAGAACTGATGAGAGATTCAATGACAGAACTAACCCATCCACAAGAAAGTCCCTCACTG 1680
QY 1681 TCCAGCCACCCAGGCTCTACCTACCACTGCTGCTCCGCTAGTAAGAAAGACACACAC 1740
DB 1681 TCCAGCCACCCAGGCTCTACCTACCACTGCTGCTCCGCTAGTAAGAAAGACACACAC 1740
QY 1741 CTGCCCCAATTCTTAACCTGCGAGCTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGCATC 1800
DB 1741 CTGCCCCAATTCTTAACCTGCGAGCTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGCATC 1800
QY 1801 CACATCCAGGGGAGTAGAGAGCGCTCCCTCCACAAACAGTGGCTCCAGCCTTAATTGAAA 1860
DB 1801 CACATCCAGGGGAGTAGAGAGCGCTCCCTCCACAAACAGTGGCTCCAGCCTTAATTGAAA 1860
QY 1861 GCAGACGAGGAGTGAAGACCAAACTGCAAAACATCCAGATCCACAGACCATCATCAGC 1920
DB 1861 GCAGACGAGGAGTGAAGACCAAACTGCAAAACATCCAGATCCACAGACCATCATCAGC 1920
QY 1921 ATCCCACTTCCCGCAGCGCTAACCCCAAGAGGGGAAAGTGGCCACCCCTGCGAGCCCA 1980
DB 1921 ATCCCACTTCCCGCAGCGCTAACCCCAAGAGGGGAAAGTGGCCACCCCTGCGAGCCCA 1980
QY 1981 GGGCCCAAGCAAGAACTTCTTCATTAACAGCAATGTTGCAAGGTCTGTCTTGTAA 2040
DB 1981 GGGCCCAAGCAAGAACTTCTTCATTAACAGCAATGTTGCAAGGTCTGTCTTGTAA 2040

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QY 2041 AATCCCGCGCCATGCGCGCGGAGCATGCGAGCTGCGGCCCAATTCCCTATAGTG 2100
DB 1984 AATCCCGCGCCATGCGCGCGGAGCATGCGAGCTGCGGCCCAATTCCCTATAGTG 2043
QY 2101 AGTCGTATTAAGCCGAATTC 2121
DB 2044 AGTCGTATTAAGCCGAATTC 2064

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RESULT 3

AAV61572
ID AAV61572 standard; cDNA; 2072 BP.

AAV61572;

11-JAN-1999 (first entry)

Human Kv potassium channel hkv4.3 (longer isoform) cDNA.

Potassium channel; Kv; hkv4.3; human; Alzheimer's disease; arrhythmia;

therapy; diagnosis; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..1965

FT /tag= a

PN W09842833-A2.

PD 01-OCT-1998.

PF 23-MAR-1998; 98WO-EP001901.

PR 27-MAR-1997; 97GB-00006377.

PR 09-DEC-1997; 97EP-00402971.

PR 11-DEC-1997; 97EP-00403007.

PA (SMIX) SMITHKLINE BEECHAM LAB PHARM.

PI Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;

DR WPI; 1998-542277/46.

DR P-PSDB; AAW79590.

XX New potassium channel polypeptides, hkv4.3 - and hkv4.3-encoding.

PT poly:nucleotide(s) useful in the treatment of disorders including cardiac

PT arrhythmias and Alzheimer's disease.

PS Claim 2; Page 26; 47pp; English.

XX This cDNA sequence codes for human Kv potassium channel hkv4.3 (see

CC AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.

CC A 1914 bp fragment corresponding to hkv4.3 full-length cDNA was isolated

CC from human heart cDNA by PCR amplification (see AAV61574-77). Another

CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589)

CC of hkv4.3 having 19 fewer amino acid residues. The invention relates to

CC these hkv4.3 polynucleotides and polypeptides and to methods for

CC producing such polypeptides by recombinant techniques. Also claimed are

CC methods for utilising the hkv4.3 polynucleotides for the treatment of

CC subjects in need of enhanced or reduced activity or expression of hkv4.3

CC polypeptide. These include the treatment of cardiac arrhythmias and

CC Alzheimer's disease. The invention can also be used to identify agonists

CC and antagonists of hkv4.3, and to detect disease associated with

CC inappropriate hkv4.3 expression or activity

XX Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;

SQ

Query Match 92.5%; Score 1962; DB 2; Length 2072;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 ATGGCGGCGGAGTTGCGGCTGCTGCTTTGCCCGGAGCTGCGCCATCGGGTGAATG 132

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Db 1 ATGGCGGAGAGTTGACAGCTGGCTCTTGTGCCCCGGGCTGCGCCATCGGGTGATG 60
Qy 133 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCGGCGGACAAAGAGGAGATGAG 192
Db 61 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCGGCGGACAAAGAGGAGATGAG 120
Qy 193 CTGATTGTCCTCAACGTGAGTGGGGGAGTTCCAGACTGTGAGAGCCACGTTGAGGCG 252
Db 121 CTGATTGTCCTCAACGTGAGTGGGGGAGTTCCAGACTGTGAGAGCCACGTTGAGGCG 180
Qy 253 TACCCGGACACCCCTGTGGGAGACGAGAGAGAGTTCTTCTTCAAGAGACACCAAG 312
Db 181 TACCCGGACACCCCTGTGGGAGACGAGAGAGAGTTCTTCTTCAAGAGACACCAAG 240
Qy 313 GAGTACTTCTTCAACCGGAGACCCCGAGGTGTTCCGCTGCTCAACTTTACCGGACG 372
Db 241 GAGTACTTCTTCAACCGGAGACCCCGAGGTGTTCCGCTGCTCAACTTTACCGGACG 300
Qy 373 GGAAGCTGCACTACCCGGCTACGAGTGCATCTTGCCCTACGAGACGAGCTGGCTTC 432
Db 301 GGAAGCTGCACTACCCGGCTACGAGTGCATCTTGCCCTACGAGACGAGCTGGCTTC 360
Qy 433 TACGGCATCTCCCGGAGATCATCGGGAGTGTGCTTACGAGAGATCAAGAGACCGGAG 492
Db 361 TACGGCATCTCCCGGAGATCATCGGGAGTGTGCTTACGAGAGATCAAGAGACCGGAG 420
Qy 493 AGGAGAACCGGAGCGGCTCATGAGCAGAACGACTCGGAGAACACGAGAGTCCATG 552
Db 421 AGGAGAACCGGAGCGGCTCATGAGCAGAACGACTCGGAGAACACGAGAGTCCATG 480
Qy 553 CCCTCGCTCAGCTTCCCGGAGACCATGTGCGGGCTTCGAGAACCCCGACACGAGCG 612
Db 481 CCCTCGCTCAGCTTCCCGGAGACCATGTGCGGGCTTCGAGAACCCCGACACGAGCG 540
Qy 613 CTGGCCCTGTCTTCTTACTGAGTGAAGTGGCTTCTTCAATGCTGTCTCGGTATCAACA 672
Db 541 CTGGCCCTGTCTTCTTACTGAGTGAAGTGGCTTCTTCAATGCTGTCTCGGTATCAACA 600
Qy 673 GTGTGAGACGGTGCCTGCGGAGACGGTCCGGGAGAGAGCTGCGGTGCGGGAG 732
Db 601 GTGTGAGACGGTGCCTGCGGAGACGGTCCGGGAGAGAGCTGCGGTGCGGGAG 660
Qy 733 CGTACTCGGTGCTTCTTCTGCTGAGACAGCGGTGCTGATGATCTTCAACGTTGAG 792
Db 661 CGTACTCGGTGCTTCTTCTGCTGAGACAGCGGTGCTGATGATCTTCAACGTTGAG 720
Qy 793 TACCTCTGCGGCTTCTTCTGCGGGCTCCAGCGCTTCAATCGGAGGTCAATGAGC 852
Db 721 TACCTCTGCGGCTTCTTCTGCGGGCTCCAGCGCTTCAATCGGAGGTCAATGAGC 780
Qy 853 ATCATGACGAGTGGGACATCATGACCTTACTCATCGGTGTGATGACCAACAGAG 912
Db 781 ATCATGACGAGTGGGACATCATGACCTTACTCATCGGTGTGATGACCAACAGAG 840
Qy 913 GACGTGTCCGGGCTTCTGTCACGCTCCGGGTCTTCCGGTCTTCAAGATCTTCAAGTT 972
Db 841 GACGTGTCCGGGCTTCTGTCACGCTCCGGGTCTTCCGGTCTTCAAGATCTTCAAGTT 900
Qy 973 TCCCGCACTCCAGGGGCTGCGGATCTCGGCTACACACTGAAGAGCTGTCGCGAA 1032
Db 901 TCCCGCACTCCAGGGGCTGCGGATCTCGGCTACACACTGAAGAGCTGTCGCGAA 960
Qy 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092
Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
Qy 1093 TATGCGAGAGGAGCTCTCGGCGAGCAAGTTCACAAAGCATCCCTGCGCTTGTGATG 1152
Db 1021 TATGCGAGAGGAGCTCTCGGCGAGCAAGTTCACAAAGCATCCCTGCGCTTGTGATG 1080
Qy 1153 ACCATTGTACCATGACCACTGGGATACGAGACATGTGCTTAAGAGATTTGAGAGG 1212
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Db 1081 ACCATTGTACCATGACCACTGGGATACGAGACATGTGCTTAAGAGATTTGAGAGG 1140
Qy 1213 AAGATCTTGGGCTCCATCTGCTCTCTTGGAGTGGCTCTGCTGATGTTGCCCTGACATCCCT 1272
Db 1141 AAGATCTTGGGCTCCATCTGCTCTCTTGGAGTGGCTCTGCTGATGTTGCCCTGACATCCCT 1200
Qy 1273 GTGATTGTTTCCAACTTTAGCCCGGATTTACCAACAGATTCAGAGAGCTGATTAACGAGG 1332
Db 1201 GTGATTGTTTCCAACTTTAGCCCGGATTTACCAACAGATTCAGAGAGCTGATTAACGAGG 1260
Qy 1333 GCACAAAAGAGGCGGCTTGGCCAGATCCGTTGGCCAAAACAGGAGTTGAAATGCA 1392
Db 1261 GCACAAAAGAGGCGGCTTGGCCAGATCCGTTGGCCAAAACAGGAGTTGAAATGCA 1320
Qy 1393 TACCTGACAGAGCGGCAACGGGCTCTCAACGAGGCGTGGAGCTGAGGGGACCCCA 1452
Db 1321 TACCTGACAGAGCGGCAACGGGCTCTCAACGAGGCGTGGAGCTGAGGGGACCCCA 1380
Qy 1453 GAAAGAGACATGGGCAAGACCACTCTCATCTGAGAGCCAGCATCATCACTGCTG 1512
Db 1381 GAAAGAGACATGGGCAAGACCACTCTCATCTGAGAGCCAGCATCATCACTGCTG 1440
Qy 1513 CACTGCTGGAAGAAACCACTGGGTTGCTTATCTTGTGATGATGCCCTGTTATCTGTA 1572
Db 1441 CACTGCTGGAAGAAACCACTGGGTTGCTTATCTTGTGATGATGCCCTGTTATCTGTA 1500
Qy 1573 CGAACCTCCACCATCAAGAACCAAGATTTATGATGAGCAGAGTGTGACAGAACTGC 1632
Db 1501 CGAACCTCCACCATCAAGAACCAAGATTTATGATGAGCAGAGTGTGACAGAACTGC 1560
Qy 1633 ATGAGAGTTCAATGCAAACTATCCATCCACAAAGAGTCCCTCACTGTCCAGCCCA 1692
Db 1561 ATGAGAGTTCAATGCAAACTATCCATCCACAAAGAGTCCCTCACTGTCCAGCCCA 1620
Qy 1693 GGCCTCACTACCACTGCTGCTCCGCTGATGAAAGACCAACACCTGCCCAATTCT 1752
Db 1621 GGCCTCACTACCACTGCTGCTCCGCTGATGAAAGACCAACACCTGCCCAATTCT 1680
Qy 1753 AACCTGCCAGTACTCGGCTGCGAGCATGCAAGAGCTCAGCAGATCCATCCAGGGG 1812
Db 1681 AACCTGCCAGTACTCGGCTGCGAGCATGCAAGAGCTCAGCAGATCCATCCAGGGG 1740
Qy 1813 AGTGAGACGCTCCCTTCAACCAAGTGGCTCCAGCTTAAATTGAAAGAGACGAGCGGA 1872
Db 1741 AGTGAGACGCTCCCTTCAACCAAGTGGCTCCAGCTTAAATTGAAAGAGACGAGCGGA 1800
Qy 1873 CTGAGACCAAACTGGAACCAATCCAGATCCACAGACCATCATAGCATCCCACTCCC 1932
Db 1801 CTGAGACCAAACTGGAACCAATCCAGATCCACAGACCATCATAGCATCCCACTCCC 1860
Qy 1933 CCAGGCTTAACCCAGAGGGGGAAGTGGGCCAACCCCTGCGAGGCCAGGCCCAACAG 1992
Db 1861 CCAGGCTTAACCCAGAGGGGGAAGTGGGCCAACCCCTGCGAGGCCAGGCCCAACAG 1920
Qy 1993 AACATTCTTCATTAACAGCAATGTTGCAAGTCTCTGTTGTAATA 2042
Db 1921 AACATTCTTCATTAACAGCAATGTTGCAAGTCTCTGTTGTAATA 1970

RESULT 4
ADF91397
ID ADF91397 standard, cDNA, 1968 BP.
XX
AC ADF91397;
XX
DT 26-FEB-2004 (first entry)
XX
DE
XX wild-type hkv4.3 cDNA #SEQ ID 4.
XX
KW Antiarhythmic; cardiovascular; anticonvulsant; cerebroprotective;
KW tranquiliser; sedative; neuroprotective; nootropic; antiparkinsonian;
KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;
KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;
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KW tachycardia; congestive heart failure; epilepsy; stroke;
KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;
KW Parkinson's disease; gene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1968 /*tag= a
PT /product= "hkv4.3"
XX MO2003097682-A1.
XX PN
XX PD 27-NOV-2003.
XX PF 14-MAY-2003; 2003WO-IB002453.
XX PR 15-MAY-2002; 2002GB-00011123.
PR 15-MAY-2002; 2002US-0378076P.
PR 15-MAY-2002; 2002US-0378131P.
XX (DEVG-) DEVGEN NV.
XX PA
XX PI Kaletta TJ, Dewulf NE, Plaetnick GKM;
XX WPI; 2004-061981/06.
DR P-PSDB; ADF91398.
XX
XX PT New nematode worm expressing a heterologous nucleotide sequence encoding
PT a functional voltage-gated potassium channel of the Kv4 family, useful
PT for determining compounds that interact with the voltage-gated potassium
PT channel.
XX
XX PS Example 1; SEQ ID NO 4; 82bp; English.
XX
CC The invention relates to a nematode worm that expresses a heterologous
CC nucleotide sequence encoding a functional voltage-gated potassium channel
CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,
CC part or fragment. The nematode worm is useful in determining whether a
CC compound interacts with the voltage-gated potassium channel of the Kv4
CC family or whether a compound is an agonist, antagonist, opener and/or
CC blocker of the voltage-gated potassium channel expressed by the nematode
CC worm. The methods are used for identifying and developing compounds that
CC interact with voltage-gated potassium channels of the Kv4 family. The
CC compounds may be used in the development and/or preparation of
CC compositions for pharmaceutical, agrochemical and/or veterinary use.
CC These may be used in preparing compositions for preventing or treating
CC diseases or conditions such as arrhythmia, tachycardia, congestive heart
CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,
CC Alzheimer's disease or Parkinson's disease. The current sequence
CC represents wild-type hkv4.3 cDNA.
XX
XX Sequence 1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;
Query Match 92.4%; Score 1960; DB 12; Length 1968;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1963; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 73 ATGGCGGCGGAGTTGGCGGCTGCTGCTTTGGCGGCGGCTGCGGCATCGGGTGATG 132
DB 1 ATGGCGGCGGAGTTGGCGGCTGCTGCTTTGGCGGCGGCTGCGGCATCGGGTGATG 60
QY 133 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGCGCAGACAGAACAGCGGAGATGAG 192
DB 61 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGCGCAGACAGAACAGCGGAGATGAG 120
QY 193 CTGATTGTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGAGACCACTGAGCGC 252
DB 121 CTGATTGTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGAGACCACTGAGCGC 180
QY 253 TACCCGAGACCTCTGCTGGGACAGACGAGAGAGATTCTTTCAACGAGAGACCAAG 312
DB 181 TACCCGAGACCTCTGCTGGGACAGACGAGAGAGATTCTTTCAACGAGAGACCAAG 240

QY 313 GAGTACTTCTTCGACCGGAGACCCCGAGGTGTTCCGTGGGTGCTCAACTTACCGGACG 372
DB 241 GAGTACTTCTTCGACCGGAGACCCCGAGGTGTTCCGTGGGTGCTCAACTTACCGGACG 300
QY 373 GGGAGCTGCACTACCCCGGCTACGAGTGATCTGTGCTTACGACGAGCTGGCCTTC 432
DB 301 GGGAGCTGCACTACCCCGGCTACGAGTGATCTGTGCTTACGACGAGCTGGCCTTC 360
QY 433 TACGGCATCTCCCGGAGATCATCGGGGACTGTCTACGAGAGTACAGAGACCGCAAG 492
DB 361 TACGGCATCTCCCGGAGATCATCGGGGACTGTCTACGAGAGTACAGAGACCGCAAG 420
QY 493 AGGAGAACCGCGGAGCTCATGACGACAAAGACTCGGAGAACCAACGAGTCCATG 552
DB 421 AGGAGAACCGCGGAGCTCATGACGACAAAGACTCGGAGAACCAACGAGTCCATG 480
QY 553 CCCTGCTCAGCTTCCCGCAGACCATGTGGCGGCTTTCGAGAACCCCGACACGACG 612
DB 481 CCCTGCTCAGCTTCCCGCAGACCATGTGGCGGCTTTCGAGAACCCCGACACGACG 540
QY 613 CTGGCCCTGCTCTTCTACTACGTGAGTGGCTTCTTCATCGCTGTCTCGGTATCAACCA 672
DB 541 CTGGCCCTGCTCTTCTACTACGTGAGTGGCTTCTTCATCGCTGTCTCGGTATCAACCA 600
QY 673 GTGTGAGACGCTGCTCCGCGGACGCTCCCGGAGAGAGAGCTGCGGGGAG 732
DB 601 GTGTGAGACGCTGCTCCGCGGACGCTCCCGGAGAGAGAGCTGCGGGGAG 660
QY 733 CGCTACTGCTGCTCTTCTGCTGAGACGCGGCTGATGATCTTCAACGAGAG 792
DB 661 CGCTACTGCTGCTCTTCTGCTGAGACGCGGCTGATGATCTTCAACGAGAG 720
QY 793 TACCTCTGCGGCTCTTCCGCGGCTCCGAGCGCTTACCGCTTACCGAGCTCATGAC 852
DB 721 TACCTCTGCGGCTCTTCCGCGGCTCCGAGCGCTTACCGCTTACCGAGCTCATGAC 780
QY 853 ATCATGACGTGCTGCGCATCATGCTTCTTACATGCTGTGTATGACCAACAGAG 912
DB 781 ATCATGACGTGCTGCGCATCATGCTTCTTACATGCTGTGTATGACCAACAGAG 840
QY 913 GAGTGTCCGCGCTTCTGTCACGCTCCGCGCTTCCGCTTTCAGAGATCTTCAAGATT 972
DB 841 GAGTGTCCGCGCTTCTGTCACGCTCCGCGCTTCCGCTTTCAGAGATCTTCAAGATT 900
QY 973 TCCCGCACTCCAGGCGCTGCGGATCTTGGCTTACACACTGAGAGCTGTGCTCGGA 1032
DB 901 TCCCGCACTCCAGGCGCTGCGGATCTTGGCTTACACACTGAGAGCTGTGCTCGGA 960
QY 1033 CTGGGCTTCTTCTTCTTCTGCTTACCATGAGCATCATCTTGGCAGCTGATGTTT 1092
DB 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
QY 1093 TATGCCGAGAGGCTCTCTGCGGCGCAGAGTTCACAAGCATCCCTGCTGTTGGTAC 1152
DB 1021 TATGCCGAGAGGCTCTCTGCGGCGCAGAGTTCACAAGCATCCCTGCTGTTGGTAC 1080
QY 1153 ACCATTGTACCATGACCACTGAGATACGAGACATGTGCTTAAAGACATTTGACAGG 1212
DB 1081 ACCATTGTACCATGACCACTGAGATACGAGACATGTGCTTAAAGACATTTGACAGG 1140
QY 1213 AAGATCTTCCGCTCATCTGCTCTTGAAGTGGCGCTCTGCTCATTTGCCCTGCAAGTCCCT 1272
DB 1141 AAGATCTTCCGCTCATCTGCTCTTGAAGTGGCGCTCTGCTCATTTGCCCTGCAAGTCCCT 1200
QY 1273 GTGATTGTTTCAACTTTAGCGGAGTTTACCAACAAGATCAGAGCTGATTAACGACG 1332
DB 1201 GTGATTGTTTCAACTTTAGCGGAGTTTACCAACAAGATCAGAGCTGATTAACGACG 1260
QY 1333 GCACAAAGAGGCGCTTGCAGAGATCCGTGTGCGCAAAACAGGAGTTCGAATGCA 1392
DB 1261 GCACAAAGAGGCGCTTGCAGAGATCCGTGTGCGCAAAACAGGAGTTCGAATGCA 1320

QY	1393	TACCTGCACAGCAAGCGCAACGGGCTCTCTCAACGAGCGCTGGAGCTGAAGGGGCAACCCCA	1452
Db	1321	TACCTGCACAGCAAGCGCAACGGGCTCTCTCAACGAGCGCTGGAGCTGAAGGGGCAACCCCA	1380
QY	1453	GAAGAGGAGCACAATGGGGAGAGACCACTCACTCATGGAGAGCGAGCATCATCCTGTCTG	1512
Db	1381	GAAAGAGGAGCACAATGGGGAGAGACCACTCACTCATGGAGAGCGAGCATCATCCTGTCTG	1440
QY	1513	CACCTGCTGAAAAAACCACCTGGGTGTCTATCTTGTGATGATCCCTGTATCTGTA	1572
Db	1441	CACCTGCTGAAAAAACCACCTGGGTGTCTATCTTGTGATGATCCCTGTATCTGTA	1500
QY	1573	CGAACCTTCACCATCAAGAACCAGAGTTTATTGATGAGCAGATGTTTGAAGCAACTGC	1632
Db	1501	CGAACCTTCACCATCAAGAACCAGAGTTTATTGATGAGCAGATGTTTGAAGCAACTGC	1560
QY	1633	ATGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA	1692
Db	1561	ATGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA	1620
QY	1693	GGCCTCACTACCACTGCTGCTGCCGTCCGTAGTAAGAAGACACACACTGCCCCAATTCT	1752
Db	1621	GGCCTCACTACCACTGCTGCTGCCGTCCGTAGTAAGAAGACACACACTGCCCCAATTCT	1680
QY	1753	AACTGCCAGCTACTCGCTGCGCAGCATGCAAGAGCTCAGACGATCCACATCCAGGGC	1812
Db	1681	AACTGCCAGCTACTCGCTGCGCAGCATGCAAGAGCTCAGACGATCCACATCCAGGGC	1740
QY	1813	AGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCAGCTTAATTGAAAGCAGACGACGGA	1872
Db	1741	AGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCAGCTTAATTGAAAGCAGACGACGGA	1800
QY	1873	CTGAGACCAAACTGCAAAAATCCAGATCACCAAGCCATCATCAGCATCCCACTCCC	1932
Db	1801	CTGAGACCAAACTGCAAAAATCCAGATCACCAAGCCATCATCAGCATCCCACTCCC	1860
QY	1933	CCAGCGCTAACCCAGAGGGGGAAAGTCGSCCACCCTGCGCAGCCGAGGCCCAACACG	1992
Db	1861	CCAGCGCTAACCCAGAGGGGGAAAGTCGSCCACCCTGCGCAGCCGAGGCCCAACACG	1920
QY	1993	AACATTCCCTTCATACCAAGCAATGTTGTCAAGTCTCTGTTGTA 2040	
Db	1921	AACATTCCCTTCATACCAAGCAATGTTGTCAAGTCTCCGCTTGTAA 1968	
RESULT 5			
AAV61571			
ID	AAV61571	standard; cDNA; 2104 BP.	
XX	AC	AAV61571;	
XX	DT	11-JAN-1999 (first entry)	
XX	DE	Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.	
XX	KM	Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;	
XX	KM	therapy; diagnosis; ss.	
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	1..1908	
FT		/*tag= a	
XX	PN	MO9842833-A2.	
XX	PD	01-OCT-1998.	
XX	PF	23-MAR-1998; 98WO-EP001901.	
XX	PR	27-MAR-1997; 97GB-00006377.	
XX	PR	09-DEC-1997; 97EP-00402971.	
XX	PR	11-DEC-1997; 97EP-00403007.	

Query Match	Beet Local Similarity	Matches 1914	Conservative	Mismatches	Indels	Gaps
86.7%; Score 1838; DB 2; Length 2104;	96.4%; Pred. No. 0;	0;	15;	57;	1	
Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other;						
73	ATGCGCGCGGAGTTGCGGCGCTGTCCTTTGCCCCGGGCTGGGGCCATCGGGTGGATG	132				
1	ATGCGCGGAGAGTTGACGCTGCTGCTTTTGCCCGGGCTCGGCATCGGGTGGATG	60				
133	CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCGGCCGACAAAGAAACAAGCGGAGAGTATG	192				
61	CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCGGCCGACAAAGAAACAAGCGGAGAGTATG	120				
193	CTGATTGTCCTCAACGTAGTGGGGCGAGTTTCCAGACTGAGAGACCACTGAGAGCCG	252				
121	CTGATTGTCCTCAACGTAGTGGGGCGAGTTTCCAGACTGAGAGACCACTGAGAGCCG	180				
253	TACCCGGACACCCGTGGGCGAGCAGGAGAGGATCTTCTTCAACGAGACCAAG	312				
181	TACCCGGACACCCGTGGGCGAGCAGGAGAGGATCTTCTTCAACGAGACCAAG	240				
313	GAGTACTTCTTGAACCGGGAACCCCGAGGTGTTCCGTGCTCAACTTCTACCGCAGC	372				
241	GAGTACTTCTTGAACCGGGAACCCCGAGGTGTTCCGTGCTCAACTTCTACCGCAGC	300				
373	GGGAAGCTGCACTAACCCGCGCTACGAGTGCATCTCTGCTTACGACGAGCTGGCTTC	432				
301	GGGAAGCTGCACTAACCCGCGCTACGAGTGCATCTCTGCTTACGACGAGCTGGCTTC	360				
433	TACCGCATCTCCCGGAGATCATCGGGGACTGTGCTGCTTACGAGAGTACAAAGACCGCAG	492				
361	TACCGCATCTCCCGGAGATCATCGGGGACTGTGCTGCTTACGAGAGTACAAAGACCGCAG	420				
493	AGGAGAGACGCGGAGCGGCTCATGAGACGACAAAGACTTCGAGAAACAAGAGATTCATG	552				
421	AGGAGAGACGCGGAGCGGCTCATGAGACGACAAAGACTTCGAGAAACAAGAGATTCATG	480				
553	CCCTGCTCAGCTTCCGCGACGACATGTGGGGGCTTTCGAGAAACCCCAACACGACGACG	612				
481	CCCTGCTCAGCTTCCGCGACGACATGTGGGGGCTTTCGAGAAACCCCAACACGACGACG	540				
613	CTGGCCCTGGTCTTCTACTACGTGACTGCTTCTTCACTGCTGCTCGGTATCAACCAAC	672				

Db 541 CTGGCCCTGCTCTTCTACTAGCTGACTGAGCTTCTTCATCGCTGTCTCGGTCAATCCAAAC 600
 QY 673 GTGCTGAGAACGGTGCCTGTCGGCAGCGGTCCCGGCGAGCAAGAGCTGCCGTGCGGGAG 732
 Db 601 GTGCTGAGAACGGTGCCTGTCGGCAGCGGTCCCGGCGAGCAAGAGCTGCCGTGCGGGAG 660
 QY 733 CGCTACTCGGTGGCCCTTCTTCTGCTGACACGGGCTGCGTCAATGATCTTCAACCGTGAG 792
 Db 661 CGCTACTCGGTGGCCCTTCTTCTGCTGACACGGGCTGCGTCAATGATCTTCAACCGTGAG 720
 QY 793 TACCTCTGCGGCTCTTCTGCGGCTCCAGCCGCTACCGCTTCATCCGACGCTCATGAGC 852
 Db 721 TACCTCTGCGGCTCTTCTGCGGCTCCAGCCGCTACCGCTTCATCCGACGCTCATGAGC 780
 QY 853 ATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGTCTGTCTGATGACCAACAGAG 912
 Db 781 ATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGGTCTGTCTGATGACCAACAGAG 840
 QY 913 GACGTGTCCGGCGCCTTCTGCTCAAGCTCCGGGCTTCTCGGCTTCAAGATCTTCAAGTTT 972
 Db 841 GACGTGTCCGGCGCCTTCTGCTCAAGCTCCGGGCTTCTCGGCTTCAAGATCTTCAAGTTT 900
 QY 973 TCCCGCCACTTCCAGGCGCTGCGGATCTGCGGCTTACACACTGAAGAGCTGTGCTCCGA 1032
 Db 901 TCCCGCCACTTCCAGGCGCTGCGGATCTGCGGCTTACACACTGAAGAGCTGTGCTCCGA 960
 QY 1033 CTGGGCTTCTCTCTCTCTCCCTACCAATGGCCATCATCTTTGCCATGTGATGTTT 1092
 Db 961 CTGGGCTTCTCTCTCTCTCCCTACCAATGGCCATCATCTTTGCCATGTGATGTTT 1020
 QY 1093 TATGCCGAGAGGGCTCTCTCGGCGAGCAAGTTCAGAGCATCCCTGCTGTTTGTAC 1152
 Db 1021 TATGCCGAGAGGGCTCTCTCGGCGAGCAAGTTCAGAGCATCCCTGCTGTTTGTAC 1080
 QY 1153 ACCATTGTCAACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGACAGG 1212
 Db 1081 ACCATTGTCAACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGACAGG 1140
 QY 1213 AAGATCTTGGGCTCCATCTGCTCTTGAAGTGGCGCTGCTGATTTGCCAGTCCCT 1272
 Db 1141 AAGATCTTGGGCTCCATCTGCTCTTGAAGTGGCGCTGCTGATTTGCCAGTCCCT 1200
 QY 1273 GTGATTTGTTTCCACTTTAGCCGGAATTTACACCAATCAGAGAGCTGATTAAGCAGG 1332
 Db 1201 GTGATTTGTTTCCACTTTAGCCGGAATTTACACCAATCAGAGAGCTGATTAAGCAGG 1260
 QY 1333 GCACAAAAGAGGCGCGCTTGGCAGATCCGTGTGGCCAAAACAGGAGTTGCAATGCA 1392
 Db 1261 GCACAAAAGAGGCGCGCTTGGCAGATCCGTGTGGCCAAAACAGGAGTTGCAATGCA 1320
 QY 1393 TACCTGCACAGCAAGGCGCTCTTCAACGAGGCGCTGAGCTGACGGGCAACCCCA 1452
 Db 1321 TACCTGCACAGCAAGGCGCTCTTCAACGAGGCGCTGAGCTGACGGGCAACCCCA 1380
 QY 1453 GAAGAGAGGACATGGGCAAGACCACTCACTCATCGAGAGCAGCATCATCCTGCTG 1512
 Db 1381 GAAGAGAGGACATGGGCAAGACCACTCACTCATCGAGAGCAGCATCATCCTGCTG 1440
 QY 1513 CACTGCTGAAAAAACCACTGGGTGTCTTATCTGTGATGATCCCTGTATCTGTA 1572
 Db 1441 CACTGCTGAAAAAACCACT----- 1461
 QY 1573 CGAACCTCCACCATCAAGAACCAAGTTTATGATGAGCAGATGTTTGAGCAGAACTGC 1632
 Db 1462 -----AACCAAGATTATTGATGAGCAGATGTTTGAGCAGAACTGC 1503
 QY 1633 ATGAGAGATTCAATGACGAAGTACCATCCACAAGAGTCCCTCACTGTCCAGCACCCA 1692
 Db 1504 ATGAGAGATTCAATGACGAAGTACCATCCACAAGAGTCCCTCACTGTCCAGCACCCA 1563
 QY 1693 GGCTCTACTACCACTGCTGCTCGTCTGTAAGTAAGAACCAACACACTGCCAATTCT 1752
 Db 1564 GGCTCTACTACCACTGCTGCTCGTCTGTAAGTAAGAACCAACACACTGCCAATTCT 1623

QY 1753 AACCTGCCAGTACTCGCTCGCGCAGCATGCAAGAGCTCAGCAGATCCACATCCAGGCG 1812
 Db 1624 AACCTGCCAGTACTCGCTCGCGCAGCATGCAAGAGCTCAGCAGATCCACATCCAGGCG 1683
 QY 1813 AGTAGAGAGCCCTTCCCTCAACACAGTGTCTCCAGCCTTAATTGAAAGCAGACGAGCGA 1872
 Db 1684 AGTAGAGAGCCCTTCCCTCAACACAGTGTCTCCAGCCTTAATTGAAAGCAGACGAGCGA 1743
 QY 1873 CTGAGACCAAACTGCAAAACATCCAGATCACCAGATCATGAGCATGCCACTCC 1932
 Db 1744 CTGAGACCAAACTGCAAAACATCCAGATCACCAGATCATGAGCATGCCACTCC 1803
 QY 1933 CCAGCGCTAACCCAGAGGGGAAAAGTCCGCCACCCCTGCCAGCCAGGCCCAACAG 1992
 Db 1804 CCAGCGCTAACCCAGAGGGGAAAAGTCCGCCACCCCTGCCAGGCCCAACAG 1863
 QY 1993 AACATTCTTCCATTAACCAAGATGTTGCAAGGTCTGTCTTGTAAATAATCCCGGCG 2052
 Db 1864 AACATTCTTCCATTAACCAAGATGTTGCAAGGTCTGTCTTGTAAATAATCCCGGCG 1923
 QY 2053 CATGGC 2058
 Db 1924 GAGGGC 1929

RESULT 6
 AAV61573
 ID AAV61573 standard, cDNA; 2104 BP.
 XX
 AC AAV61573;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human Kv potassium channel hkv4.3 cDNA.
 XX
 KW Potassium channel; Kv; hkv4.3; human; Alzheimer's disease; arrhythmia;
 KW therapy; diagnosis; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1911
 FT /*tag= a
 XX
 PN W09842833-A2.
 XX
 PD 01-OCT-1998.
 XX
 PF 23-MAR-1998; 98WO-EP001901.
 XX
 PR 27-MAR-1997; 97GB-00006377.
 PR 09-DEC-1997; 97EP-00402971.
 PR 11-DEC-1997; 97EP-00403007.
 XX
 PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.
 XX
 PI Bril AMA, Calmels TPB, Faivre JSP, Javre J, Rouanet S;
 XX
 DR WPI; 1998-542277/46.
 DR P-PSDB; AAW79591.
 XX
 PT New potassium channel polypeptides, hkv4.3 - and hkv4.3-encoding
 PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
 PT arrhythmias and Alzheimer's disease.
 XX
 PS Claim 18; Page 27; 47pp; English.
 XX
 CC This cDNA sequence codes for human Kv potassium channel hkv4.3 (see
 CC AAW79591). It was isolated using expressed sequence tag analysis. The
 CC sequence has about 91% identity in 1914 nucleotide residues with rat
 CC Kv4.3 potassium channel. Full-length hkv4.3 cDNA clones (see AAV61571-72)
 CC are also claimed. The invention relates to hkv4.3 polynucleotides and

CC polypeptides and to methods for producing such polypeptides by
 CC recombinant techniques. Also claimed are methods for utilizing hkv4.3
 CC polynucleotides for the treatment of subjects in need of enhanced or
 CC reduced activity or expression of hkv4.3 polypeptide. These include the
 CC treatment of cardiac arrhythmias and Alzheimer's disease. The invention
 CC can also be used to identify agonists and antagonists of hkv4.3, and to
 CC detect disease associated with inappropriate hkv4.3 expression or
 CC activity

XX Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;

Query Match 86.3%; Score 1830; DB 2; Length 2104;

Best Local Similarity 96.1%; Pred. No. 0;

Matches 1909; Conservative 0; Mismatches 20; Indels 57; Gaps 1;

QY 73 ATGCGCGCCGAGTTGGCGCTGCTGCTTTTGGCCCGGCTGCGCCATGGGTGATG 132
 DB 1 ATGCGCGCAGAGTTGCAGCTGCTGCTTTTGGCCCGGCTGCGCCATGGGTGATG 60
 QY 133 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCCGGCGCAAGAACAAGCGGAGATGAG 192
 DB 61 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCCGGCGCAAGAACAAGCGGAGATGAG 120
 QY 193 CTGATGTCTCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGACCAAGCTGAGCGC 252
 DB 121 CTGATGTCTCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGACCAAGCTGAGCGC 180
 QY 253 TACCCGAGACACCTGCTGGGCGAGCAGGAGAGAGTTCTTTCAACGAGAGACCAAG 312
 DB 181 TACCCGAGACACCTGCTGGGCGAGCAGGAGAGAGTTCTTTCAACGAGAGACCAAG 240
 QY 313 GAGTACTTCTTCGACCCGGAACCCCGAGGTTCCTGCTGCTCAACTTACCCGACG 372
 DB 241 GAGTACTTCTTCGACCCGGAACCCCGAGGTTCCTGCTGCTCAACTTACCCGACG 300
 QY 373 GGAAGCTGCATACCCCGGCTACGAGTGCATCTTGCTTACGACGACGAGCTGCTTC 432
 DB 301 GGAAGCTGCATACCCCGGCTACGAGTGCATCTTGCTTACGACGACGAGCTGCTTC 360
 QY 433 TAGGCACTCTCCCGAGAGATCATCGGGGACTGCTGCTACGAGAGTACAAGACCGGAG 492
 DB 361 TAGGCACTCTCTCCCGAGAGATCATCGGGGACTGCTGCTACGAGAGTACAAGACCGGAG 420
 QY 493 AGGAGAACCGCGAGCGGCTCATGAGCAGCAACGACTCGGAGAACCAACGAGATCCATG 552
 DB 421 AGGAGAACCGCGAGCGGCTCATGAGCAGCAACGACTCGGAGAACCAACGAGATCCATG 480
 QY 553 CCCTCGCTCAGCTTCGCGACAGACCATGTGGGGGCTTCGAGAACCCCGCACACGACGAG 612
 DB 481 CCCTCGCTCAGCTTCGCGACAGACCATGTGGGGGCTTCGAGAACCCCGCACACGACGAG 540
 QY 613 CTGGCCCTGCTTCTACTACGTGAGTGTCTTCTCATCGCTGCTCGGTATCAACCAAC 672
 DB 541 CTGGCCCTGCTTCTACTACGTGAGTGTCTTCTCATCGCTGCTCGGTATCAACCAAC 600
 QY 673 GTGTGGAGACGGTGCCTGCGGCGGACAGTCCCGGGGCGAGAGAGCTGCGGGGAG 732
 DB 601 GTGTGGAGACGGTGCCTGCGGCGGACAGTCCCGGGGCGAGAGAGCTGCGGGGAG 660
 QY 733 CGTACTCGGTGCTTCTTCTGCTGAGACAGGGGCTGATGATCTTCAACCGTGGAG 792
 DB 661 CGTACTCGGTGCTTCTTCTGCTGAGACAGGGGCTGATGATCTTCAACCGTGGAG 720
 QY 793 TACCTCTGCGGCTCTTCTGCGGCTCCAGCGCTTACCTCGGAGGTCATGAGC 852
 DB 721 TACCTCTGCGGCTCTTCTGCGGCTCCAGCGCTTACCTCGGAGGTCATGAGC 780
 QY 853 ATCATGACGAGTGGTGCATCATGACCTTACATCGGTCTGTCATGACCAACAGAG 912
 DB 781 ATCATGACGAGTGGTGCATCATGACCTTACATCGGTCTGTCATGACCAACAGAG 840
 QY 913 GACGTGTCCGGGCTTCTGTCACGCTCCGGGCTTCTCGGCTTTCAGAGTCTTCAAGTTT 972

DB 841 GACGTGTCCGGGCTTCTGTCACGCTCCGGGCTTCCGGGCTTTCAGAGATCTCCAAGTT 900
 QY 973 TCCCGCACTCCAGAGGCTGCGGATCTGGGCTACACACTGAGAGAGCTGTGCTCCGAA 1032
 DB 901 TCCCGCACTCCAGAGGCTGCGGATCTGGGCTACACACTGAGAGAGCTGTGCTCCGAA 960
 QY 1033 CTGGGCTTCTTCTCTTCTCCCTCAACCATGGCCATCATCTTTGGCCACTGTGATGTT 1092
 DB 961 CTGGGCTTCTTCTCTTCTCCCTCAACCATGGCCATCATCTTTGGCCACTGTGATGTT 1020
 QY 1093 TATGCGGAGAGAGGCTCTCTGCGGACGCAAGTTCAGAACATCCCTGCTGTTTGTAC 1152
 DB 1021 TATGCGGAGAGAGGCTCTCTGCGGACGCAAGTTCAGAACATCCCTGCTGTTTGTAC 1080
 QY 1153 ACCATGTCAACATGACCACTGGGATACGAGACATGCTGCTTAAGACGATTGACAGG 1212
 DB 1081 ACCATGTCAACATGACCACTGGGATACGAGACATGCTGCTTAAGACGATTGACAGG 1140
 QY 1213 AAGATTTGCGCTCCATCTGCTCTTGAAGTGGCTGCTGTCATTTGCCCTGCAATCCCT 1272
 DB 1141 AAGATTTGCGCTCCATCTGCTCTTGAAGTGGCTGCTGTCATTTGCCCTGCAATCCCT 1200
 QY 1273 GTGATGTTTCCAACTTTAGCCGATTTACCAACGAAATCAGAGCTGATTAACCCAGG 1332
 DB 1201 GTGATGTTTCCAACTTTAGCCGATTTACCAACGAAATCAGAGCTGATTAACCCAGG 1260
 QY 1333 GCACAAAAGAAAGCCCGCTTGCAGATCCGTGTGCGCAAAACAGGCACTTCAATGCA 1392
 DB 1261 GCACAAAAGAAAGCCCGCTTGCAGATCCGTGTGCGCAAAACAGGCACTTCAATGCA 1320
 QY 1393 TACCTGACAGAGAGCGCAACGGGCTCTTCAACGAGGCTGAGCTGACGGGACCCCA 1452
 DB 1321 TACCTGACAGAGAGCGCAACGGGCTCTTCAACGAGGCTGAGCTGACGGGACCCCA 1380
 QY 1453 GAAGAGAGACATGGGGAAGACCACTCATGAGAGCGGACATCACTGCTG 1512
 DB 1381 GAAGAGAGACATGGGGAAGACCACTCATGAGAGCGGACATCACTGCTG 1440
 QY 1513 CACTGCTGAAAAAACCACTGGGTGCTCTATCTTGTGATGATCCCTGTATCTGTA 1572
 DB 1441 CACTGCTGAAAAAACCACT----- 1461
 QY 1573 CGAAGCTCCACCATCAAGAACCAAGAGTTTATGATGAGCAGATGTTGAGCAGAACTGC 1632
 DB 1462 -----AACCAGAGTTTATGATGAGCAGATGTTGAGCAGAACTGC 1503
 QY 1633 ATGAGAGTTCAATGACAGAACTACCATCAACAAGAGTCCCTCACTGTCCAGCCCA 1692
 DB 1504 ATGAGAGTTCAATGACAGAACTACCATCAACAAGAGTCCCTCACTGTCCAGCCCA 1563
 QY 1693 GGCCTACTACCACTGCTGCTCCCGTGTGTAAGAAAGCACAACCTGCCCCAATTCT 1752
 DB 1564 GGCCTACTACCACTGCTGCTCCCGTGTGTAAGAAAGCACAACCTGCCCCAATTCT 1623
 QY 1753 AACCTGCAGCTACTGCGCTGCGGACGATGCAAGAGCTCAGACGATCCATCCAGGGC 1812
 DB 1624 AACCTGCAGCTACTGCGCTGCGGACGATGCAAGAGCTCAGACGATCCATCCAGGGC 1683
 QY 1813 AGTGACAGCCCTCCCTCAACAACGATCGCTCAGGCTTAATTGAAAGCAGACGAG 1872
 DB 1684 AGTGACAGCCCTCCCTCAACAACGATCGCTCAGGCTTAATTGAAAGCAGACGAG 1743
 QY 1873 CTGAGACCAAACTGCAAAACATCCAGATGACCAAGCCATCATCAGCATCCCACTCCC 1932
 DB 1744 CTGAGACCAAACTGCAAAACATCCAGATGACCAAGCCATCATCAGCATCCCACTCCC 1803
 QY 1933 CCAGGCTAACCCAGAGAGGGAAGTGGCCACCCCTGCGAGCCCAAGGCCCAACAG 1992
 DB 1804 CCAGGCTAACCCAGAGAGGGAAGTGGCCACCCCTGCGAGCCCAAGGCCCAACAG 1863
 QY 1993 AACATTCTTCATACAGCAATGTGTCAAGTCTCTGTTGTAATAATCCCGCGGC 2052
 DB 1864 AACATTCTTCATACAGCAATGTGTCAAGTCTCTGTTGTAATAATCCCGCGGC 1923

QY 2053 CATGGC 2058
 Db 1924 GAGGGC 1929

RESULT 7

AAH21247 standard; cDNA; 2351 BP.

AAH21247;

13-SEP-2001 (first entry)

Human Kv4.2 cDNA.

Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy; neurodegenerative disease; ischemia; stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory; learning capacity; protein kinase activator; anti-arrhythmic; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 433..2322
 FT /*tag= a
 FT /product= "Kv4.2 alpha subunit"

DE19963612-A1.

12-JUL-2001.

29-DEC-1999; 99DE-01063612.

29-DEC-1999; 99DE-01063612.

(GENT-) FORSCHUNGSGESELLSCHAFT GENTON MBH.

WPI: 2001-426637/46.

P-PSDB; AAB86319.

New potassium channel subunit proteins, useful for identifying and testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological agents.

Claim 11; Page 18-21; 50pp; German.

This invention describes a novel potassium channel protein (I) that is either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium channels containing (I) are used to identify and test: (i) compounds for treatment of neurodegenerative diseases (autism, epilepsy, ischemia, stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac arrhythmia, or those that improve learning capacity and memory; and (ii) activators of protein kinases. Host cells that express (I) can identify agents that do not interact significantly with channels and control I_{to} (a quickly activated transient current), so lack the side effects of known anti-arrhythmic agents. They also eliminate, or reduce, the need for testing on organ cultures

Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Query Match 44.1%; Score 935.4; DB 4; Length 2351;
 Best Local Similarity 70.7%; Pred. No. 8.4e-176;
 Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTCAACATGCGCGCGAGTTGCGGCTGCTTTGCGCGCGGCTGCGGCATCGG 125
 Db 423 AGTATCATGCGCGCGGCGGTGCGAGCGTGGCTGCTTTGCAAGGCGCGGCTATCGG 482
 QY 126 GTGATGCCGCTGCGCACTGCCCCCATGCGCGCGCGCGCGCGCGCGCGCGCG 182
 Db 483 GTGATGCCCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 542

QY 183 GCAGATGATGCTGATGCTCTCAACGCTGAGTGGCGGAGGTTCCAGACCTGAGAGCAC 242
 Db 543 CCAAGATGCTCTGATGCTGTAATGAGTGGCAACCGCTTCCAGACGCTGGCAGAGCAC 602
 QY 243 GCTGAGCGCTTACCCGAGACCTGCTGGGCGAGCAGCAGAGAGAGGTTCTTCTCAACA 302
 Db 603 CTTGAGAGGTTTACCGAGACTCTACTGCGGAGTTCTGAGAGGAGCTTTTCTACACCC 662
 QY 303 GGACACCAAGAGTACTTCTTCCAGCGGAGACCCGAGGTTCCGCTGCTCAACTT 362
 Db 663 AGAACTCAGCAGATTTCTTGTACCGGTGACCCAGACATCTTCCGCCACATCTGTAATT 722
 QY 363 CTACCGCAGCGGAGAGCTGCACTACCCGCTTACGAGTGCATCTTGTCTTACGACGCA 422
 Db 723 CTACCGCAGCTGGAGAGCTCACTATCTCTGCCACGAGTGCATCTTGTCTTACGATGAGA 782
 QY 423 GCTGCGCTTCTACGGCATCTCCCGAGATCATCGGGACTGCTGCTACGAGAGTCA 482
 Db 783 ACTGCGCTTCTTGGCTCTCATCCCGAATCATCGGCACTGCTGTTATGAGAGTCA 842
 QY 483 GGACCGCAGAGAGAGAGAGCGCGGCGCTCATGACGACCAACGACTCGGAGAACCA 542
 Db 843 GATTCGAGCGAGAGAGAGCGCGGCGCTGACGAGACGCGGATACCGACCGCTGG 902
 QY 543 GGAG--TTCATGCGCTCGCTCAGCTTCCGCAACCATGTGGCGGCTTCCAGAACCC 599
 Db 903 GGAAGCGCGCTTCCCAACATGACTGCAAGGAGAGAGGCTGAGAGGCGCTTCCAGAACCC 962
 QY 600 CCACACGACGACGCTGCGCTGCTTCTTACTAGTGACTGCGCTTCTTCAATCGCTGCTC 659
 Db 963 CCACACGACGACGATGCGCGCTGCTTCTTACTAGTGACTGCGCTTCTTCAATCGCTGCTC 1022
 QY 660 GGTATCATCAACGCTGAGAGAGCGGTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 716
 Db 1023 TGTCTATCGCGAATGTGTGGAACAGTCCGCTGCGGATCAAGCCAGGTCACATTAAAGA 1082
 QY 717 GCTGCGCGCGGAGAGCGCTACTCGGTGCGCTTCTTCTGCTGAGCAGCGGCTGCGCAT 776
 Db 1083 ACTGCGCGGTGAGAGCGGTATGCTGCGCTTCTTCTGCTGAGCAGCGGCTGCGCAT 1142
 QY 777 GATCTTCAACGCTGAGTACTCTGCGGCTTCTGCGGCTTCCAGCGGCTTCAACGCTTCA 836
 Db 1143 GATCTTCAACGCTGAGTACTCTGCGGCTTCTGCGGCTTCCAGCGGCTTCAACGCTTCA 1202
 QY 837 CCGCAGCGCTATGACATCATCGAGGTGCGCATCATGCCCTACTACATCGCTGCTGCT 896
 Db 1203 GCGTATGCTATGATATCATCGAGGTGCGCATCGCTTCTTATCATGCGGCTGCTGCT 1262
 QY 897 CATGACCAACAAGAGAGCTGCTGCGGCTTCTGCTACGCTGCGGCTTCCAGCGGCTTCA 956
 Db 1263 GATGACAGCAATGAGAGAGCTGCGGAGCTTGTGACACTCCGAGTCTTCCGCGCTT 1322
 QY 957 CAGGATCTTCAAGTTTCCGCGCACTTCCAGGCGCTGCGGATCTTGGGCTTACACACTGAA 1016
 Db 1323 CAGGATCTTCAAGTTTCCGCGCACTTCCAGGCGCTGCGGATCTTGGGCTTACACACTGAA 1382
 QY 1017 GAGCTGCTGCTCCGAACTGCGCTTCTTCTCTCTCTCCCTACCATGCGCATCATCTT 1076
 Db 1383 GAGTGTGCTCAGAAATGCGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1442
 QY 1077 TGGCCTGCTGATGTTTATGCGGAGAGAGGCTCTCGGCGAGCAAGTTACAGCATCC 1136
 Db 1443 CGTTACAGTTATGTTCTACGAGAGAGAGGCTTCTCGGCTTACAGATTACAGCATCC 1502
 QY 1137 TGGCTGTTTGTGATACCATGCTGACCATGACCACTGCGGATACGAGACATGTGCC 1196
 Db 1503 TGCAGCTTCTGTATACCATGCTGACCATGACCACTGCGGATACGAGACATGTGCC 1562
 QY 1197 TAAGACGATGAGAGAGAGATCTTGGCTCATCTGCTCTTGAAGTGGCTGCTGAT 1256
 Db 1563 AAAAACCATAGCAGAGAGAGATTTTGTCTATCTGTGCTGAGTGGGCTTGTGAT 1622
 QY 1257 TGGCTGCGAGTCCCTGTGATGTTTCCAACTTACCGGATTTACCAACGAGATCAGAG 1316

QY	600	CCACACACGACGCTGGCCCTGGTCTTCTACTACGTGACGTGGCTTCTTCATCGCTCTC	659
Db	963	CCACACACGACGATGGCCCTGGTGTCTACTATGTCACGGGGTTTTCAATTGCCGTCTC	1022
QY	660	GGTCATCACCAACGTGGTGGAGA	716
Db	1023	TGTCATCGCGAATGTGGGAAACAGTGCCTGGCATCAAGCCAGGTCACTTAAAGA	1082
QY	717	GCTGCGGTGCGGGAGCGCTACTCTGGTGGCTTCTTCTGCTGGACA	776
Db	1083	ACTGCCCTGTGGAGAGCGGTATCTGTGGCCCTTCTTCTGCTTGGACA	1142
QY	777	GATCTTCACCGTGGAGTACCTCTGCGGCTCTTGCGGGCTTCCAGCCGCTAC	836
Db	1143	GATCTTCAAGTTGAGTATTTGCTTCGCTGGCTGACGCGCTAGTCTTACCGTTTGT	1202
QY	837	CCGACGGTCATGAGCATCATCGAGTGGTGGCCATCATGGCCCTACTACATCGTCTGGT	896
Db	1203	GCGTAGTGCATGAGTATCATCGAGTGGGCCATCTCTGCTTATTACATGGGCTGGT	1262
QY	897	CATGACCAACAA	956
Db	1263	GATGACAGACAA	1322
QY	957	CAGAGTCTTCAAGTTTTCGCCCACTCCAGAGGCGTGGCATCTTGGGGCTACAC	1016
Db	1323	CAGAGTCTTAAAGTTTTCGCCCACTCAAGGCGTGGCATCTTGGGGTACAC	1382
QY	1017	GAGCTGTGCTCCGAACGTGGGCTTCTTCTTCTCTCCCTACCATGGCCATCATCTT	1076
Db	1383	GAGTGTGCTCAGAAATGGGCTTCTTCTTCTCTCCCTACCATGGCCATCATCTT	1442
QY	1077	TGCCACTGTGATGTTTATGCCGAGAGGGCTCCTCGGCAAGAA	1136
Db	1443	CGCTACGTTATGTTCTACGAGAGAGGGGCTTTCGGCTTAGCAATTCACAGCATCC	1502
QY	1137	TGCCGTGTTTGGTACACCATTTGTCACCATGACCACTGGGATACGAGACATGTGCC	1196
Db	1503	TGCAGCCTTCTGGTATACATCGTCAACCATGACCACTAGGGTATGTGACATGTGCC	1562
QY	1197	TAAGACGATTGACGAGAAATCTTCGGCTCCATCTGCTCCTTAGTGGCGTCTGTGCAT	1256
Db	1563	AAAAACCATAGCAGGAAAGATTTTGGTCTTATCTGTTCGTGAGTGGGGCTTGTGCAT	1622
QY	1257	TGCCCTGCCAGTCCCTGTGATTTGTTTCCAACTTAAAGCCGGAATTTACACCAAGATCAGAG	1316
Db	1623	TGCTCTACCTGTTCGGGTGATGTATCCAACTTCACTGCGCATCTACCA	1682
QY	1317	AGCTGATTAACGACGAGGACAAAGAGGGCCGCTTGGCCAGATCCGTGTGCCAAAC	1376
Db	1683	AGCAGACAAACGAAAGGACAAAGAAAGTTAGACTGGCCAGGATCCGGGACCCAAAG	1742
QY	1377	AGGCAGTTTGAATGCACTACCTGCA	1436
Db	1743	CGGAAGCGCAATGTCTTACATGACAGACAAAGAAATGTTTACTCAGTAATCAGCTGCA	1802
QY	1437	GCTGACGGGCA	1496
Db	1803	GTCTCTCAGAGGA	1859
QY	1497	GCATCATCACTGTGCACTGCTGTGAAAAAACCACTGGGTGTCTTATCTTGTGATGA	1556
Db	1860	GCAACCAACCTGCTTCACTGCTGAAAAAACCA	1895
QY	1557	TCCCTGTTATCTGTACGAACCTCCACATCAAGAACCAAGATTATTTGATGACAGAT	1616
Db	1896	GAATCACGAGTTGTGAGCAACAAAGT	1922
QY	1617	GTTTGACAGAACTGCATGAGAGTTTCAATGACAGAACTAACCATCCAAAGAGTCCCTC	1676
Db	1923	CTTTGAAGAAAGCTGCATGAGAGTTTGCAACTGTTAATCGTCTTCAAGTCA	1982
QY	1677	ACTGTCCAGCCACCGGCTCACTAACCACTGCTGCTCCCGTCTGATGTAAGAACCAAC	1736

Accession	Gene	Species	Length (bp)	Source	Notes
D011252	standard	Human	2351	GenBank	ADJ11252 standard; DNA; 2351 BP.
D011252	ADJ11252	Human	2351	GenBank	ADJ11252; 15-APR-2004 (first entry)
D011252	ADJ11252	Human	2351	GenBank	Human ovarian tumour antigen DNA SeqID 253.
D011252	ADJ11252	Human	2351	GenBank	human, ds; ovarian cancer; immunogenic; antibody; antigen presenting cell; APC; immune system cell; T cell; tumourigenic; cytostatic; gene.
D011252	ADJ11252	Human	2351	GenBank	Homo sapiens.
D011252	ADJ11252	Human	2351	GenBank	US2003232056-A1.
D011252	ADJ11252	Human	2351	GenBank	18-DEC-2003.
D011252	ADJ11252	Human	2351	GenBank	14-FEB-2003; 2003US-00369186.
D011252	ADJ11252	Human	2351	GenBank	10-SEP-1999; 99US-00394374.
D011252	ADJ11252	Human	2351	GenBank	01-MAY-2000; 2000US-00561778.
D011252	ADJ11252	Human	2351	GenBank	15-AUG-2000; 2000US-00640173.
D011252	ADJ11252	Human	2351	GenBank	07-SEP-2000; 2000US-00656668.
D011252	ADJ11252	Human	2351	GenBank	14-NOV-2000; 2000US-00713550.
D011252	ADJ11252	Human	2351	GenBank	03-APR-2001; 2001US-00825294.
D011252	ADJ11252	Human	2351	GenBank	02-OCT-2001; 2001US-00970966.
D011252	ADJ11252	Human	2351	GenBank	02-AUG-2002; 2002US-00212677.
D011252	ADJ11252	Human	2351	GenBank	05-FEB-2003; 2003US-00361811.
D011252	ADJ11252	Human	2351	GenBank	(CORI-) CORIXA CORP.
D011252	ADJ11252	Human	2351	GenBank	Fanger GR, Fling SP;
D011252	ADJ11252	Human	2351	GenBank	WPI; 2004-178717/17.
D011252	ADJ11252	Human	2351	GenBank	P-PSDB; ADJ11258.
D011252	ADJ11252	Human	2351	GenBank	Novel isolated ovarian tumor polynucleotide encoding ovarian tumor polypeptide, useful as probes of primers for detecting presence of cancer in a patient.
D011252	ADJ11252	Human	2351	GenBank	Example 12; SEQ ID NO 253; 222pp; English.
D011252	ADJ11252	Human	2351	GenBank	This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/or expanding T cells specific for a tumourigenic protein (i.e. T cell

CC therapy). Furthermore, compositions can be used for the diagnosis, treatment and/or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polynucleotide is a human ovarian tumour antigen DNA sequence given in an exemplification of the invention.

XX Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Query Match 44.1%; Score 935.4; DB 12; Length 2351;
Best Local Similarity 70.7%; Pred. No. 8.4e-176;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

Qy	66	AGTACCATGGGCGCCGAGTGTGCGCTGCTGCTTTGCCCCGGGCTGGGCCATCGG	125
Db	423	AGTAATCATGGGCGCGGGGTGGCAGCGTGGCTGCTTTGCAAGGGCAGGGGCTATCGG	482
Qy	126	GTGATGCGCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAGAACAGCG	182
Db	483	GTGATGCGCTGTGGCCCTGGGGGCTTATGCCCCGCTCCCGAGGCAAGAGAGAGAGAG	542
Qy	183	GCAGATGAGCTGATTTGCTCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGACAC	242
Db	543	CCAAGATGCTCTATTTGCTGTAATGTAGTGGCACCCTTCCAGACGTGGCAGAGAC	602
Qy	243	GCTGAGCGCTACCCGAGACCCCTGCTGGGCGACACGAGAGAGAGAGTCTTCTTCAACA	302
Db	603	CCTGAAACGTATACCCAGACACTTACTGCGCAGTTCTGAGAGGAGACTTTTCTACACAC	662
Qy	303	GGACACCAAGAGTACTTCTTGACCGGGAGCCCGAGGTGTTCCGCTGCTGCTCACTT	362
Db	663	AGAACTCAGCAGTATTTCTTGACCGTGACCCAGACATCTTCCGCCACATCTTGAATTT	722
Qy	363	CTACCCGACGGGAGAGTGCATACCCGCGCTACGAGTGCATCTTCCCTACGACGACGA	422
Db	723	CTACCGCACTGGGAAAGCTCACTATCTCGCAAGTGCATCTTCTGCTTACGATGAGA	782
Qy	423	GCTGCGCTTCTACGCACTCTCCCGAGATCACTGGGAGCTGCTGTACGAGAGTAA	482
Db	783	ACTGCGCTTCTTTGGCTCTATCCCGAAATCATCGGCACTGCTGTATGAGAGATCA	842
Qy	483	GGACCGCAAGAGGAGAAAGCCCGAGCGGCTCATGAGCAACAAGTCTGGAGAACCA	542
Db	843	GGATCGCAGCGCAGAGAAAGCCCGAGCGGCTGAGAGACGACGCGATACCGACACCG	902
Qy	543	GGAG--TCCATGCGCTGCTCAGCTTCCGCCAGACCATGTGGCGGCGCTTGAGAACCC	599
Db	903	GGAGAGCGCTTGGCCACCATGACTGCAAGGCGAGAGGCTCTGAGAGGCGCTTGAGAAC	962
Qy	600	CCACACGACGAGCGTGGCGCTGCTTCTTACTACGTAAGTGGCTTCTTCAATGCTGCTC	659
Db	963	CCACACGACGAGTGGCGCTGCTTCTTACTATGTAACGAGGCTTTTCAATGCGCTCTC	1022
Qy	660	GGTCAATCACCAAGTGTGGAGAGCGGTGCGGCGGACCGGTCCCGG--CAGCAAGA	716
Db	1023	TGTCAATCGCAATGTGTGGAAACAGTGGCGGTGGATCAAGCCAGGTCAATTAAGA	1082
Qy	717	GCTGCGGTGGGCGGAGCGCTACTGCTGCTGCTTCTTCTGCTGGAACAGCGCTGCTCAT	776
Db	1083	ACTGCGCTGTGGAGAGCGGTATGCTGTGGCTTCTTCTTGTGGACACGCGCTGCTCAT	1142
Qy	777	GATCTTCAACCGTGGAGTACTCTGCGGCTCTTGGCGGCTCCAGCGCTTACCGCTTCT	836
Db	1143	GATCTTCAACAGTGTAGTATTTGCTTGGCGCTGCTGCAAGCGCTTGTGTTACCGTTTGT	1202
Qy	837	CCGACGCTGATGAGCATCATGAGTGTGGCCATCATGCGCTTACTACTACATGCTGTGT	896
Db	1203	GCGTATGTCAATGATATCATGAGTGTGGCCATCTGCTTATTAATTAATTTGGGCTGT	1262
Qy	897	CATGACCAACAAGAGAGTGTCCGCGCTTCTGTCACGCTCCGGGCTTTCGCGCTCTT	956
Db	1263	GATGACAGACAAATGAGAGTGTAGGAGGCTTGTGTACACTCGAGTCTTCCGCGCTCTT	1322
Qy	957	CAGATCTTCAAGTTTCCCGCACTCCAGGCGCTGGGATCTGGGCTAACACACTGAA	1016

Db	1323	CAGATCTTTAAGTTTCCCGCACTCTCAAGGCTGGCGCATCTCGGGTACACACTGAA	1382
Qy	1017	GAGCTGTGCTTCGAACTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1076
Db	1383	GAGTGTGCTTCAGAAATGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1442
Qy	1077	TGCCATGTGATGTTTATGCGGAGAGGCTCCCTGGCCAGAGTTCACAAGATCCC	1136
Db	1443	CGCTACAGTTATGTTCTACGAGAGAGGCGTCTTGGCTAGCAAGTTACACAGATCCC	1502
Qy	1137	TGCCCTGTTTGTGTACACCATTTGTCACCATGACACACTGGGATTAACGAGATGTGCC	1196
Db	1503	TGCAGCTTCTGTATACCATCGTCACCATGACACACTAGGGTATGTGACATGTGCC	1562
Qy	1197	TAAACGATTGAGAGGAAAGATCTTGGCTCATCTGCTCTTGAAGTGGCTCTGCTCAT	1256
Db	1563	AAAAACATAGCAGGAAAGATTTTGTGTATCTGTTCGCTGAGTGGGCTCTGTCTAT	1622
Qy	1257	TGCCCTGCGCAGTCCCTGATTTGTTTCCAACTTACCGGATTTACACAGAAATCAGAG	1316
Db	1623	TGCTTACCTGTTCGGTATGTATCCAACTTACGTCATCTTACACAGAAATCAACG	1682
Qy	1317	AGCTGATAACGCGAGGAGCAAAAGAGGCGCTTGGCAGATCCGTGGCCAAAC	1376
Db	1683	AGCAGACAAAGAGGAGCAAAAGAGGCTGAGTACCTGCGCAGATCCGCGCAGCCAAAG	1742
Qy	1377	AGGCAATTGCAATGATATCTGCAACAGACGCAACGGGCTCTCAACGAGGCGCTGGA	1436
Db	1743	CGAAGCGCAATGCTTATCATGAGAGCAACGAAATGTTTACTAGTAATCAGCTGCA	1802
Qy	1437	GCTGACGGGACCCCGAGAGAGGACCATGAGCAACCACTTCACTATCGAGAGCA	1496
Db	1803	GTCTCAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCCGCTCCAGCTTGTGAACCA	1859
Qy	1497	GCATATCACTGCTGCTGCACTGCTGGAAGAAACCACTGGGTTGTCTTATCTTGTGATGA	1556
Db	1860	GCACCACTGCTGCTTCACTGCTGGAAGAAACCACTGGGTTGTCTTATCTTGTGATGA	1895
Qy	1557	TCCCTGTTATCTGTACGAACCTCCACCATCAAGAACCAAGAGTTTATGATGACAGAT	1616
Db	1896	-----GAATCAGAGTTTGTGGACGAACAAGT	1922
Qy	1617	GTTTGAAGAGAACTGCATGAGAGTCAATGCAAGAACTAACCTTCAAGAGTCCCTC	1676
Db	1923	CTTTGAAGAAAGCTGCATGGAAGTTGCACTGTTAATCGTCTTCAAGTCAAGTCTTTC	1982
Qy	1677	ACTGTCCAGCAACCGAGGCTCACTACCACTGCTGCTCCGCTGCTGTAAGAGAACCA	1736
Db	1983	ACTGTCTTCAACAAGAGAGTCAACAGCACTGCTGTTTCAAGAGAGCACAAAAGAACTTT	2042
Qy	1737	ACACCTGCCCAATTCTAACCCTGCGAGTCTGCGCTGCGCAGATGCAAGAGCTCAGCAC	1796
Db	2043	TGCGATCCCAATGCAATGTATGAGAGAGCCATCAAGGTATGATACAAAGAACTCAGCAC	2102
Qy	1797	GATCCATATCAGGAGGAGTGAAGAGCCCTTCTTCAACACAGTGCCTTCAATTT	1856
Db	2103	GATTCAGATGATGTGTGAAGAGAACACTTGTCTTAAACAGCCGATCAGTTTAAATGC	2162
Qy	1857	GAAAGCAGAGAGAGTGAAGACCAAACTGCAAAACATCCAGATCAGACAGCATCAT	1916
Db	2163	CAAAATGGAAGAGTGTAACTTAACTGTAACCACTTATGTGACTTACAGCATTAAT	2222
Qy	1917	CAGATCCCACTCCCGAGCGCTAACCCAGAGGAGGAAAGTGGGCA	1965
Db	2223	AAGCATCCCAACACTTCAATCAACACACAGAGAGAGCATAGGCCA	2271

RESULT 10
ADM43513
ID ADM43513 standard; DNA; 2351 BP.
XX
AC ADM43513;

XX 03-JUN-2004 (first entry)
DT Human ovarian cancer cDNA homologous DNA #7.
DE ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.
XX Homo sapiens.
OS
XX US2003129192-A1.
XX 10-JUL-2003.
XX 02-AUG-2002; 2002US-00212677.
XX 10-SEP-1999; 99US-00394374.
XX 01-MAY-2000; 2000US-00561778.
XX 15-AUG-2000; 2000US-00640173.
XX 07-SEP-2000; 2000US-00656668.
XX 14-NOV-2000; 2000US-00713550.
XX 03-APR-2001; 2001US-00825294.
XX 02-OCT-2001; 2001US-00970966.
XX (CORI-) CORIXA CORP.
XX Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
XX WPI; 2004-051070/05.
XX P-PSDB; ADM43519.
XX New isolated polynucleotide encoding an ovarian tumor protein for use in
XX diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX
XX Claim 1; SEQ ID NO 253; 220bp; English.
XX
XX The invention relates to an isolated polynucleotide. The invention is
XX used to diagnose, prevent or treat cancer, particularly ovarian cancer.
XX The present sequence represents a human ovarian carcinoma cDNA homologous
XX DNA.
SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
Query Match 44.1%; Score 935.4; DB 12; length 2351;
Best Local Similarity 70.7%; Pred. No. 8.4e-176;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
QY 66 AGTACCATGCGCGCGAGATTGCGGCTGCTTTCGCCGCGGCTGCGGCATCGG 125
DB 423 AGTAATCATGCGCGCGGCGGTGCGAGCGTGCCTTTGCAAGGCGAGCGGTATCGG 482
QY 126 GTGATGCGCGGTGCGCAACTGCGCCCATGCGCCCTGGCCCC---GGCGACAAGACAAGCG 182
DB 483 GTGATGCGCTGTGCGCTCGGGGCTATGCGGCTCCCGAGGCAAGAGAAAGGAC 542
QY 183 GCAGATGAGCTGATGCTTCTCAAGTGAAGTGGGAGGTTCCAGACTGAGAGACGAC 242
DB 543 CCAAGATGCTCTCATTTGTGATGATGAGTGCACCCGCTTCCAGAGTGGAGAGAC 602
QY 243 GCTGAGCGCTACCCGACACCTGCTGGGAGCAGCAGAGAAAGATTCTTCAACGA 302
DB 603 CTTGGAACTTACCCAGACACTCTACTGCGGAGTTCTGAGAGGACTTTTCTAACACCC 662
QY 303 GGACACCAAGAGTACTTCTTTCGACCGGAGACCCCGAGGTTCGCTGCTCAACTT 362
DB 663 AGAACTCAGCAATATTTCTTTCGACCGGAGACCCAGACATCTTCGCCCATCTGAATTT 722
QY 363 CTACCGCAGCGGGAAGTGCATACCCGCGCTACAGAGTGCATCTGCTACAGACGA 422
DB 723 CTACCGCAGCGGGAAGTGCATACCTGCGCACAGTGCATCTCTGCTTACGATGAGA 782
QY 423 GCTGGCTTCTTACGCGGATCTTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACA 482
DB 783 ACTGGCTTCTTGTGGCTCTATCCCGGAATCATCGGCGACTGCTGTATAGAGAGTACAA 842

QY 483 GGACCGCAGAGGAGAACGCCGAGCGCTCATGAGACACAGACTCGGAGAACACCA 542
DB 843 GGATCGCAGCGGAGAACGCCGAGCGCTGCAGACGACGCGATACCGACACCGCTGG 902
QY 543 GGAG---TCCATGCGCTCGCTCAGCTTCGCGACAGACCATGTGGCGGCTTCGAGAACCC 599
DB 903 GGAAGCGGCTTGGCCACCATGACTGCAAGGCGAGGGCTTGAGGGCTTCGAGAACCC 962
QY 600 CCACACCAAGCAGCTGGCGCTGCTTCTTACTAGCTGACTGCTTCTTCACTGCTGCTC 659
DB 963 CCACACCAAGCAGATGCGCTGCTGCTTCTTACTAGTCAAGGGGTTTTCATGCGCTC 1022
QY 660 GGTTCATCAACGATGATGAGAGCGGCTGCGGACCGGCTCCGCGG---CAGCAAGA 716
DB 1023 TGTTCATCGCGAATGTGTGAGAAACAGTCCGCGATCAAGCCAGTCACTTAAGA 1082
QY 717 GCTGCGGCGGAGCGCTTACTCGGTGCTTCTTCTGCTGACACAGGCTGCTCAT 776
DB 1083 ACTGCGCTGTGAGAGCGGATGCTGTGCTTCTTCTGCTTGAACAAGGCTGCTCAT 1142
QY 777 GATCTTCAACGATGATGATGAGAGCGGCTGCGGCTTTCGCGGCTCCAGCGGCTTCTCAT 836
DB 1143 GATCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
QY 837 CCGCAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896
DB 1203 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
QY 897 CATGACCAACAG 956
DB 1263 GATGACAGACAGATGAG 1322
QY 957 CAGATCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1016
DB 1323 CAGATCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
QY 1017 GAGCTGTGCTCCGAACTGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1076
DB 1383 GAGTGTGCTCAGATGATGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1442
QY 1077 TGCCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1136
DB 1443 CGCTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1502
QY 1137 TGCTCTGTTTGTGATACCAATGTTGATGATGATGATGATGATGATGATGATGATGAT 1196
DB 1503 TGCAAGCTTCTGATATACCACTGCTACCATGACAACTAGAGGTATGATGATGATGAT 1562
QY 1197 TAAGACGATGACAGGAGAGATCTTCCGCTCACTGCTCTGCTGATGATGATGATGAT 1256
DB 1563 AAAAACCATAGCAGGAGAGATTTTGGTTCTATCTGTTGCTGAGTGGGCTTGTGAT 1622
QY 1257 TGCCCTGCGAGTCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1316
DB 1623 TGCTTACCTGTTCCGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
QY 1317 AGCTGATTAACGAGGAGGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1376
DB 1683 AGCAGACAAAGAGAGGAGGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1742
QY 1377 AGGAGTTGCAATGATACCTGACAGCAAGGCAAGGAGGCTCTCAAGAGGCGCTGGA 1436
DB 1743 CGAAGCGCAATGCTTACATGACAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1802
QY 1437 GCTGAGGAGCAGCAG 1496
DB 1803 GTCTCTAGAGGA---TGAAGAGGCTTTTGTAGCAAAATCCGCTTCAAGCTTTGAA 1859
QY 1497 GATCATCACTGCTGACATGCTGCTGAGAAAGCACTGGGTTGTCTATCTTGTGATGA 1556
DB 1860 GAACCAACACTGCTTCACTGCTGCTGAGAAAGCACTGCTGCTGCTGCTGCTGCTGCTG 1895

QY 1557 TCCCTGTATCTGTAGAACCTCCACATCAAGAACGAGTTTATGATGACGAT 1616
 Db 1896 -----GAATCAGAGTTTGTGACGACCAAGT 1922
 QY 1617 GTTTGACGAGAACTGATGAGAGTTCAATGACAGAACTACCCATCCACAAAGTCCCTC 1676
 Db 1923 CTTGAAGAAAGCTGATGAGAGTTGCAACTGTATCGTCTTCAAGTCAAGTCTTTC 1982
 QY 1677 ACTGTCCAGCCACCCAGGCTCTACACTACCTGCTGCTCCGCTGTAAGTAAGAACAC 1736
 Db 1983 ACTGTCTTCAACAAGAGAGTCAACCCAGCAGCTGTTTCAAGCAGACACAAAAAATTT 2042
 QY 1737 ACACCTGCCCAATCTTAACCTGCAGCTACTGCTGCGAGCATGACAGAGCTCAGAC 1796
 Db 2043 TCGCATCCCAATGCCAATGATGATCAGAGAACCATCAAGGTATATACAAAGACTCAGCAG 2102
 QY 1797 GATCCACATCCAGGAGAGTGAAGAGCCCTCCCTCACAACAGTCCGCTCAGCCTTAATT 1856
 Db 2103 GATTCAATCAGATGTGTGAGAGAAACCTCTGTCTTAACAGCCGATCCAGTTTAAATGC 2162
 QY 1857 GAAAGCAGACGAGGAGTGAAGACCAAACTGCAAAACATCCAGATCAACACAGCCATCAT 1916
 Db 2163 CAAATGAGAGAGTGTGTAACTAACTGTAACAACCTTATGTAAGTACAGCAATTAAT 2222
 QY 1917 CAGCATCCCACTCCCTCCAGCGCTAACCCAGAGGAGGAAAGTCCGCCA 1965
 Db 2223 AAGCATCCCAACACTCTCCAGTAAACCAACAGAGAGAGATGAGCCA 2271

RESULT 11

ADM10923
 ID ADM10923 standard; cDNA; 5333 BP.

AC ADM10923;

XX 20-MAY-2004 (first entry)

DE Human O647SgenomicContig3 homologue cDNA #5.

XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;

KW cytosolic; gene therapy; human; ss.

XX Homo sapiens.

PN US2003206918-A1.

XX 06-NOV-2003.

PF 05-FEB-2003; 2003US-00361811.

XX 10-SEP-1999; 99US-00394374.

PR 01-MAY-2000; 2000US-00561778.

PR 15-AUG-2000; 2000US-00640173.

PR 07-SEP-2000; 2000US-00656668.

PR 14-NOV-2000; 2000US-00713550.

PR 03-APR-2001; 2001US-00825294.

PR 02-OCT-2001; 2001US-00970966.

PR 02-AUG-2002; 2002US-00212677.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Fling SP;

XX WPI; 2003-901037/82.

XX P-PSDB; ADM10929.

XX New polynucleotides encoding tumor proteins, treating or inhibiting the

XX development of cancer, particularly ovarian cancer, and for stimulating

XX and/or expanding T cells specific for a tumor protein.

CC to detecting the presence of an ovarian cancer in a patient by
 CC stimulating and/or expanding T cells specific for the tumor protein. The
 CC products of the invention can also be used in a method to inhibit the
 CC development of a cancer in a patient comprising (a) incubating CD4+
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian
 CC tumour protein, such that T cell proliferate and (b) administering to the
 CC patient the proliferated T cells. The cytosolic polynucleotides or
 CC polypeptides described in the invention are useful for treating or
 CC inhibiting the development of cancer, particularly ovarian cancer and for
 CC stimulating and/or expanding T cells specific for a tumour protein or for
 CC gene therapy.
 XX
 SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
 Query Match 44.1%; Score 935.4; DB 11; Length 5333;
 Best Local Similarity 70.7%; Pred. No. 9.4e-176;
 Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
 QY 66 AGTACCATGCGCGCGGAGTTGCGGCTGCTGCTTTTGGCCGCGGCGCATCGG 125
 Db 959 AGTAATCATGCGCGCGGAGTTGCGGCTGCTGCTTTTGGCAAGGCGCGCATTCGG 1018
 QY 126 GTGATGCGCGGCGGCGGAGTTGCGGCTGCTGCTTTTGGCAAGGCGCGCATTCGG 182
 Db 1019 GTGATGCGCGGCGGCGGAGTTGCGGCTGCTGCTTTTGGCAAGGCGCGCATTCGG 1078
 QY 183 GCAGATGAGCTGATTTCTTCAACGTGAGTGGCGGAGTTTCCAGACCTGAGAGACAC 242
 Db 1079 CCAAGATGCTTCAATTTGCTGTAATGTGAGTGGCACCCGCTTCCAGACCTGAGAGAC 1138
 QY 243 GCTGAGCGCTTACCGGAGACCTGCTGCGGAGCAGCAGAGAAAGTCTTCTTCAACA 302
 Db 1139 CCTGGAACGTTTACCGGAGACCTTCACTGCGGAGTTTCTGAGAGGAACTTTTCTACACC 1198
 QY 303 GGACACCAAGAGTACTTCTTCAACCGGAGACCCCGAGGTGTTCGCTGCTCAACTT 362
 Db 1199 AGAACTCAGAGATATTCTTTGACCGTACCCAGACATCTTCCGACATCTGTAATT 1258
 QY 363 CTACCGCAGCGGAGAGTCACTACCTCCGCTATGAGTGCATCTCTGCTACGACGAGA 422
 Db 1259 CTACCGCAGCGGAGAGTCACTACCTCCGCTATGAGTGCATCTCTGCTTACGATGAAGA 1318
 QY 423 GCTGCGCTTCTACCGGAGTCTCCGCGAGATCATCGGAGACTGCTGTAAGAGATCAA 482
 Db 1319 ACTGCGCTTCTTGGCGCTCATCCGGAATATCATCGGAGACTGCTGTAAGAGATCAA 1378
 QY 483 GGACCGCAGAGGAGAGAGCGCGGAGTCTATGAGCAGCAACGACTCGGAGAAACA 542
 Db 1379 GATGCGCAGAGGAGAGAGCGCGGAGTCTATGAGCAGCAGCGGATACGACACGCGTGG 1438
 QY 543 GGAG--TCCATGCCCTGCTCAGCTTCCGCGAGACCATGTGGCGGCGCTTGGAGAACCC 599
 Db 1439 GGAGAGCGCTTGGCGCGGAGTCTGAGCAGAGAGGCTTGGAGAGGCGCTTGGAGAACCC 1498
 QY 600 CCACACGAGCAGCGTGGCGCTGCTTCTACTAGCTGAGTGGCTTCTTCACTGCTGCTC 659
 Db 1499 CCACACGAGCAGATGCGCGGAGTCTTCTACTATGACGCGGCTTTCATGCGCTC 1558
 QY 660 GGTATCACCACAGTGTGAGAGAGCGTGGCGGAGTCCCGG--CAGCAAGGA 716
 Db 1559 TGTATCGCAATGTGTGAGAAAGTGGCGGATCAAGGCCAGGTCAATTAAGA 1618
 QY 717 GCTGCGGCGGAGGAGCTACTGCTGCTTCTTCTGCTGAGACAGGCGTGGCTCAT 776
 Db 1619 ACTGCCCTGTGAGAGCGGTATGCTGCTTCTTCTGCTTGGAGACAGGCGCTGGCTCAT 1678
 QY 777 GATCTTACCGTGAAGTACTCTGCGGCTTCTTCCGCGCTCCAGCGCTACCGCTTCAT 836
 Db 1679 GATCTTACAGTTAGATTTGCTTCCGCTGCTGCTGAGCGGCTTACCTGTTTGT 1738
 QY 837 CCGACCGTATGAGCATCATCAAGTGTGGCATCATGCTTACTACTCATCGTGTGT 896
 Db 1739 GCGTGTGTATGATATCATCAAGTGTGGCATCATGCTTACTACTCATGCTGTGT 1798

This invention describes a novel ovarian tumour protein which can be used

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QY 897 CATGACCAACAGAGAGAGCGTGTCCGGCCCTTCGTCACGCTCCGGGTCTTCCGGCTCTT 956
DB 1799 GATGACAGACGATGAGAGAGCGTGTCCGGCCCTTGTGTCACTCCGAGTCTTCCGGGTCTT 1858
QY 957 CAGGATCTTCAAGTTTCCCGCCACTCCAGAGGCGCTGCGGATCCCTGGGCTACACACTGAA 1016
DB 1859 CAGGATCTTAAAGTTTCCCGCCACTCTCAAGGCGCTGCGGATCCCTGGGCTACACACTGAA 1918
QY 1017 GAGTGTGCTCCGAACTGGGCTTCTTCTTCTTCCCTCACTAGGCGATCATCTT 1076
DB 1919 GAGTGTGCTCCGAACTGGGCTTCTTCTTCTTCCCTCACTAGGCGATCATCTT 1978
QY 1077 TGCACCTGTGATGTTTATGCGAGAGAGGCGCTCCGCGCAGCAAGTTCAACAACATCCC 1136
DB 1979 CGCTACAGTTATGTTCTTACGAGAGAGAGGCGCTCCGCGCAGCAAGTTCAACAACATCCC 2038
QY 1137 TGCTCTGTTTGTATACCATTTGTCACTGACCACTAGGAGTACGAGACATGTGCC 1196
DB 2039 TGCAGCCTTGTGTATACCATTTGTCACTGACCACTAGGAGTATGTGACATGTGCC 2098
QY 1197 TAAGACGATTCAGGAGAGATCTTCCGCTCCATCTGCTCTTGAAGGCGCTCCGTGTGAT 1256
DB 2099 AAAAACCATGAGAGAGAGATTTTGGTTCTATCTGTTCCGTGAGTGGGCTCTTGTGAT 2158
QY 1257 TGCCCTGCGAGTCCCTGTGATGTTTCCAACTTACCGGATTTACCAACAGATTCAGAG 1316
DB 2159 TGCTCTACCTGTTCCGCTGATTTGTATCCAACTTCACTGCGATCTACCAACAGATTCAGAG 2218
QY 1317 AGCTGATTAACGAGGCGCAAAAGAGGCGCGCTTCCAGAGATCCGTGTGCCAAAC 1376
DB 2219 AGCAGACAAACGAGGCGCAAAAGAGGCGCAAAAGAGTACGAGTCCGAGATCCGGGCGAGCAAAAG 2278
QY 1377 AGGCGATTCGATGATGATCTTACCTGACAGCAAGCGGCTCCCTCAACGAGGCGCTGGA 1436
DB 2279 CGGAAGCGCAATGCTTACATGAGAGCAAAAGGATGTTTACTCACTGATTCAGCTGGA 2338
QY 1437 GCTGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1496
DB 2339 GTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2395
QY 1497 GCATCATCACTGCTGAGTGTGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1556
DB 2396 GCACCAACCACTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2431
QY 1557 TCCCTGTATCTGTACGAACCTCCACCATCAAGAACCAAGAGTTTATGATGAGCAGAT 1616
DB 2432 -----GATTCACGAGTTTGTGAGCAGCAAGT 2458
QY 1617 GTTTGAGCAGAACTGATGAGAGTTCAATGACAGAACTAACCATCCCAAGAGTCCCTC 1676
DB 2459 CTTTGAAGAAAGCTGATGAGAGTTGCACTGTATATGCTCTTCAAGTCAAGTCCCTTC 2518
QY 1677 ACTGTCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
DB 2519 ACTGTCTTCAACAAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2578
QY 1737 ACACCTGCCCCAATTCTAACCTGCACTGCTGCGGCGAGATGCAAGAGCTCAGCAC 1796
DB 2579 TCGCATCCCAATGCAATGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2638
QY 1797 GATCCACATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
DB 2639 GATTCAGATCAGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2698
QY 1857 GAAAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
DB 2699 CAAATGGAAGAGTGTGTTAACTTAACTGTGAACAACCTTATGTGATTCAGAGAGATTAAT 2758
QY 1917 CAGCATCCCACTCCCAAGCGCTTAAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1965
DB 2759 AAGCATCCCAACACCTCAAGTAAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807

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RESULT 12
ADM10921
ID ADM10921 standard; cDNA; 5333 BP.
XX
AC ADM10921;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue cDNA #3.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytosolic; gene therapy; human; ss.
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2003-901037/82.
DR P-PSDB; ADM10927.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 252; 221bp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
Query Match 44.1%; Score 935.4; DB 11; Length 5333;
Best Local Similarity 70.7%; Pred. No. 9,4e-176;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
QY 66 AGTCACCATGCGCGCGAGTTGCGGCTGCTGCTTGTGCCCCGGGCTGCGGCATCGG 125
DB 959 AGTAATCATGCGCGCGGGGTGGCAGAGTGTGCTTTTGAAGGCGAGCGGCTATCGG 1018
QY 126 GTGGATCGCGGTGGCCCACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAAGAACCG 182
DB 1019 GTGGATGCTGTGGCTTCCGGGCTTATGCCGGCTCCCCGAGGAGAGAGAGAGAGAGAG 1078
QY 183 GCAGATGAGCTGATTTCTCAACGATGAGTGGCGGAGGTTCCAGAGAGAGAGAGAGAG 242

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Db 1079 CCAAGATGCTCTCATTTGTGCTGATGTGAGTGGACACCCGCTTCCAGACGTGGCAGGACAC 1138
Qy 243 GGTGAGGGCTACCCGGACACCCCTGCTGGGACGACCGGAGAGAGTCTTCTTCAACGA 302;
Db 1139 CCTGGAAGCTTACCAGACCTCTACTCTGAGAGTCTTGAAGAGGAGCTTTTCTACCAACC 1198
Qy 303 GGACACCAAGAGTACTTCTTCGACCGGACCCCGAGGTGTTCCGCTGCGCTCAACTT 362
Db 1199 AGAACTCAGCAGATTTCTTTGACCGGTGACCAGACATCTTCCGCCACATCTTGAAATT 1258
Qy 363 CTACCGCAGCGGGAAGCTGCACTACCCGCTACGAGTGCATCTTGTCTACGACGCA 422
Db 1259 CTACCGCAGCTGGGAAGCTCCTACTATCTCCGACGAGTGCATCTGTCTTACGATGA 1318
Qy 423 GCTGCGCTTCTACGCACTCTCCCGGAGATCATCGGGGACTGTGCTTACGAGAGTACA 482
Db 1319 ACTGGCTTCTTTGGCTTCATCCCGAAATCATCGGCGACTGTGTTATGAGAGTACAA 1378
Qy 483 GGACCGCAAGAGGAGAAAGCCGAGCGGCTCATGACGACAAACGACTCGGAGAACAA 542
Db 1379 GGATCGCAGGCGGAGAGACGCCGAGCGCTGCAAGACGACCGGATACCGACACCGCTGG 1438
Qy 543 GGAG---TCCATGCCCTCGCTCAGCTCCCGACAGACCATGTGGCGGGCTTCGAGAACCC 599
Db 1439 GGAGAGCGCCTTGCCACCATGACTGCAAGGAGAGAGGCTGTGAGAGGCTTCGAGAACCC 1498
Qy 600 CCACACGACGACGCTGCGCTGTCTCTACTACGTGACTGGCTTCTTCACTGCTGTCTC 659
Db 1499 CCACACGACGACGATGGCCCTGTGTTCTACTATGTCAAGGGGTTTTCATGTGCCGTCTC 1558
Qy 660 GGTATTCACCAAGTGTGTGAGACGGTCCGTGCGGACGGTCCCGGG---CAGCAAGGA 716
Db 1559 TGTCAATGGCGAATGTGTGAGAAACAGTCCCGCGGATCAAGCCAGGTCACTTAAGA 1618
Qy 717 GCTGCGGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGACACGGCGTGGCGTAT 776
Db 1619 ACTGCCCTGTGAGAGCGGATGTGTGTGCTTCTTCTGCTTGAACAGCGCTGCGTAT 1678
Qy 777 GATCTTCAACCGTGAATCTCTGCGGCTCTTCTGCGGCTCCAGCGCTAACCGCTTAT 836
Db 1679 GATCTTCAAGTTGATTTTGTCTTCTGCTGCGCTGACGCGCTGATGCTTACCGTTTGT 1738
Qy 837 CCGCAGGCTCATGACATCATGACGCTGTGGCCATCATGCCCCATCACTACGCTGTGT 896
Db 1739 GCGTAGTGTCAATGATATCATCGAGCTGTGGCCATCCTGCTTATTAATGATGGGCTGT 1798
Qy 897 CATGACCAACACGAGACGTGTCCGGCGCTTCTGTCACGCTCCGGGTCTTCCGCTT 956
Db 1799 GATGACAGACAAATGAGAGCTCAGCGGAGCTTGTGTCACTCCGAGTCTTCCGGTCTT 1858
Qy 957 CAGATCTTCAAGTTTCCCGGCACTCCAGGGGCTGCGGATCTGCGCTACACACTGAA 1016
Db 1859 CAGATCTTAAAGTTTCCCGGCACTCTCAAGGCTGCGCATCTGCGGTAACACACTGAA 1918
Qy 1017 GAGCTGTGCTCGAAGTGGGCTTCTTCTTCTCTCCCTACCAATGGCCATCATCTT 1076
Db 1919 GAGTGTGCTCAGAAATGGGCTTCTTCTTCTCTGCTCACCATGCTATCATCTT 1978
Qy 1077 TGCCACTGTGATGTTTATGCGAGAGGGCTCTCGGCCAGCAAGTTTCAAGCATCC 1136
Db 1979 CGCTACAGTTATGTTCTACGACAGAGAGGGGTCTTGGGCTAGCAAGTTCAACGACATCC 2038
Qy 1137 TGCCGTGTTTGGTACACATGTGACCATGACCAACTGGGATACGAGACATGTGCC 1196
Db 2039 TGCAAGCTTCTGTATACATGTCATCAACATGACCTAGGATATGTGATGATGTC 2098
Qy 1197 TAAAGCATTTGAGGGAGATCTTGGGCTCATCTGCTCTTGAAGTGGCGTCTGTCT 1256
Db 2099 AAAAACCATAGCAGGGAAGATTTTGGTCTTATCTGTGTGCTGAGTGGGTCTTGTCT 2158
Qy 1257 TGCCCTGCACTGCTGTGATGTTTCAACTTTAGCGGATTTACCAACAGAAATCAG 1316
Db 2159 TGCTTAACCTGTTCCGGTGTATGTATCCAATTCAGTGCATTAACACAGAAATCAACG 2218

Qy 1317 AGCTGATTAACGAGGGACAAAGAGCCCGCTTGGCAGAGATCCGTGTGCCAAAC 1376
Db 2219 AGCAGCAAAAGAGGGACAAAGAAAGCTTGAATCTGGCCAGAGATCCGGCAGCCAAAG 2278
Qy 1377 AGGCAATTGCAATGATATCTGACAGCAAGCGCAAGCGGCTCTCAACGAGCGCTGGA 1436
Db 2279 CGGAAGCGCAATGCTTATCATGCAAGCAACGGAATGTTTACTGATTAATCAGCTGCA 2338
Qy 1437 GCTGACGGGACCCAGAGAGACATGAGGACCAACCTCACTCATCGAGAGCA 1496
Db 2339 GTCCATAGAGA---TGAAGAGGCTTTTGTTAAGAAATCCGGCTCCAGCTTGAACCCA 2395
Qy 1497 GCATCATCACCTGCTGCACTGCTGAAAAAAACCACTGGGTTGTCTTATGTGATGA 1556
Db 2396 GCACCAACCACTGCTTCACTGCTGAAAAAACCACTGCTGCTTGAACCCA 2431
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Db 2432 -----GAATCAAGAGTTTGTGAGCAAGCAAGT 2458
Qy 1617 GTTTGACAGAACTGATGAGAGTCAATGCAAGAACTAACCAAGCAAGAGTCCCTC 1676
Db 2459 CTTTGAAGAAAGCTGATGAGAGTGAAGTTGCAACTGTTAATGCTTCAAGTCAAGTCTTC 2518
Qy 1677 ACTGTCCAGCAACCAAGGCTCACTACCACTGCTGCTCCGCTGTGATGAAGAACCA 1736
Db 2519 ACTGTCTTCAACAAGAGTACACAGCACTGCTGTTTCAAGCAAGCAAGAAACTTT 2578
Qy 1737 ACACCTGCCCAATTCTAACTGCAAGTACTGCTGCGCAGCATGCAAGAGCTCAGCAC 1796
Db 2579 TCGATATCCCAATGCAATGTATGATGAGAAAGCATCAAGTATGATTAACAAGAACTCAGCAC 2638
Qy 1797 GATTCATATCAGGGCAGTGAAGAGCCCTCTCCACAAACAGTGTCTCAGCCTTAATT 1856
Db 2639 GATTGATATCAGATGTGTGAGAGAAACCTCTGTCTTACAGCCGATCAGTTTAATGC 2698
Qy 1857 GAAAGAGACGACGAGCTGAGACCAACTGCAAAACATCCAGATACACAGCCATCAT 1916
Db 2699 CAATAATGGAAGTGTGTTAACTGAACCTGTAACAACTTATGTGACTTACAGCAATAT 2758
Qy 1917 CAGCATCCCACTCCCGCAGCGCTTAACCCAGAGGGGAAAGTGGCCA 1965
Db 2759 AAGCATCCCAACCTCCAGTAAACACACAGAGAGAGCATGAGCCA 2807

RESULT 13
ADJ11253
ID ADJ11253 standard; DNA; 5333 BP.
XX
AC ADJ11253;
XX
DT 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SeqID 254.
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumorigenic;
XX cytosolic; gene.
OS Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
XX
PF 14-FEB-2003; 2003US-00369186.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.

PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2004-178717/17.
DR P-PSDB; ADU11259.
XX
PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
XX
XX Example 12; SEQ ID NO 254; 222pp; English.
XX
XX This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide is a human ovarian tumour antigen DNA
CC sequence given in an exemplification of the invention.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
Query Match 44.1%; Score 935.4; DB 12; Length 5333;
Best Local Similarity 70.7%; Pred. No. 9.4e-176;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
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QY 126 GTGATGCGCGTGGCCAACTGCGCCATGCGGCTGGCCCC--GGCCGACAAGACAAGCG 182
DB 1019 GTGATGCGCGTGGCGCTCGGCGCTATGCGGCTGCGGCGGCGAGAGAGAAAAGAC 1078
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QY 303 GGAACACCAAGAGTACTTCTTGAACCGGAGACCCGAGGTGTTCCGCTGCTCAACTT 362
DB 1199 AGAAACTCAGCAGTATTTCTTGAACCGTACCCAGACATCTTCGACCATCTGAATTT 1258
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DB 1439 GGAAGAGCGCTTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1498

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DB 1559 TGTCAATCGCAATGTGTGAGAAACAGTCCGTCGAGATCAAGCCAGGTACATTAAGA 1618
QY 717 GCTGCGGCTGCGGAGCGCTACTCGGTGCGCTTCTTCTGCTGAGCAAGGCTGCTCAT 776
DB 1619 ACTGCGCTGTGAGAGCGGATATGCTGTGCGCTTCTTCTGCTGAGCAAGGCTGCTCAT 1678
QY 777 GATCTTCAACGCTGAGTACCTCTGCGGCTTTCGCGGCTCCAGCGCTTACCGCTTCA 836
DB 1679 GATCTTCAACGCTGAGTATTTGCTTGGCTGCTGAGCGCTTACGCTTACCGTTTGT 1738
QY 837 CCGCAGCTCATGACATCATGACGTGTGCGCATATGCGCTTACTACATCGCTGCT 896
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DB 1799 GATGACAGACATAGAGAGCTGACGCGGCTTGTGCTACACTCCAGTCTTCCGCTT 1858
QY 957 CAGGATCTTCAAGTTTCCCGCACTTCCAGGCGCTGCGGATCTGCGGCTTACACTGAA 1016
DB 1859 CAGGATCTTCAAGTTTCCCGCACTTCCAGGCGCTGCGGATCTGCGGCTTACACTGAA 1918
QY 1017 GAGCTGTGCTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1076
DB 1919 GAGTGTGCTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1978
QY 1077 TGCCACGTGATGTTTATGCGGAGAGAGGCTCTGCGGCGAGAGTTCAAGCATGCC 1136
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DB 2039 TGACGCTTGTGATACCATTTGTCACCATGACCACTGGGATACGAGACATGCTCC 2098
QY 1197 TAAAGCATGTCAGGAGAGATCTTCCGCTCACTGCTCTTGAAGTGGCGCTGCTCAT 1256
DB 2099 AAAAACCATAGCAGGAGAGATTTTGTGTTCTTCTGCTGCTGAGTGGGCTTGTGCTAT 2158
QY 1257 TGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
DB 2159 TGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2218
QY 1317 AGCTGATTAAGCAGGAG 1376
DB 2219 AGCAGACAAAG 2278
QY 1377 AGCAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1436
DB 2279 CGGAAAGCGCAATGCTTACATGACAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2338
QY 1437 GCTGACGCGGACCCAG 1496
DB 2339 GTCCTCAGAGAG--TGAGAGAGGCTTTGTTAGCAATTCGCGCTCAAGCTTTGAACCA 2395
QY 1497 GCATCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
DB 2396 GACACACCACTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2431
QY 1557 TCCCTGTTATCTGTAAGAACTTCCACATCAAGAACCAAGAGAGAGAGAGAGAGAT 1616
DB 2432 -----GATCAGAT 2458
QY 1617 GTTGAAGAT 1676
DB 2459 CTTTGAAGAT 2518

QY 957 CAGGATCTTCAAGTTTCCCGCACTCCGAGGCTGCGGATCCCTGGGCTACACTGAA 1016
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 QY 1017 GAGCTGTGCTCCGAACCTGGGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1076
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 QY 1557 TCCCTGTATCTGTACGAACCTCCACCATCAAGAACCAAGTTTATGATGACAGAT 1616
 DB 2432 -----GAATCAGAGTTTGTGACGCAACAGT 2458
 QY 1617 GTTTGAGCAGAACTGATGAGAGTTCAATGCAAGAACTAACCATCCCAAGAGTCCCTC 1676
 DB 2459 CTTTGAAGAAAGCTGATGAGAGTTGCACTGTTAATCGTCTTCAAGTCAAGTCCCTTC 2518
 QY 1677 ACTGTCCAGGCAACCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1736
 DB 2519 ACTGTCTTCAACAAGAGAGTCAACGAGCACTGCTGTTTCAAGAGCACAAAAAAATCTT 2578
 QY 1737 ACACCTGCGCAATTTCAACTGCGAGCTACTGCGCTGCGCAGCATGCAAGAGTCAAGAC 1796
 DB 2579 TCGCATCCCAATGCGCAATGTATCAAGAGCCATCAAGGTATATCAAGAACTCAGCAC 2638
 QY 1797 GATCCACATCCAGGAGTGAAGAGCCCTCCCTCAACAACGCTGCTCCAGCTTAATTT 1856
 DB 2639 GATTCAGATCAGATGTTGTGAGAGAAACCTCTGTCTAACAAGCCGATCCAGTTAAATGC 2698
 QY 1857 GAAAGCAGACGAGCTGAGACCAAACTGCAAAAATCCCAAGATCAACAGCATCAT 1916
 DB 2699 CAAATGGAAGAGTGTGTTAACTAACTGTGAACAACTTATGTGACTACAGCAATTAAT 2758
 QY 1917 CAGATCCCACTCCCAAGCGCTTAACCCCAAGAGGGGAAAGTCCGCCA 1965
 DB 2759 AAGCATCCCAACACTCAGTAACACACCAAGAGAGAGATAGGCCA 2807

RESULT 15
 ADM43512
 ID ADM43512 standard; DNA; 5333 BP.
 XX

AC ADM43512;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human ovarian cancer cDNA homologous DNA #6.
 XX
 KW ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.
 XX
 OS Homo sapiens.
 XX
 PN US2003129192-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 02-AUG-2002; 2002US-00212677.
 XX
 PR 10-SEP-1999; 99US-00394374.
 PR 01-MAY-2000; 2000US-00561778.
 PR 15-AUG-2000; 2000US-00640173.
 PR 07-SEP-2000; 2000US-00656668.
 PR 14-NOV-2000; 2000US-00713550.
 PR 03-APR-2001; 2001US-00825294.
 PR 02-OCT-2001; 2001US-00970966.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
 XX
 DR WPI; 2004-051070/05.
 DR P-PSDB; ADM43518.
 XX
 PT New isolated polynucleotide encoding an ovarian tumor protein for use in
 PT diagnosing, preventing or treating cancer, particularly ovarian cancer.
 XX
 PS Claim 1; SEQ ID NO 252; 220pp; English.
 XX
 CC The invention relates to an isolated polynucleotide. The invention is
 CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.
 CC The present sequence represents a human ovarian carcinoma cDNA homologous
 CC DNA.
 XX
 SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
 XX
 Query Match 44.1%; Score 935.4; DB 12; Length 5333;
 Best Local Similarity 70.7%; Pred. No. 9.4e-176;
 Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
 QY 66 AGTCACCATGCGGCGGAGTTGGGCTGCTGCTTTTGGCCGGGCTGGCCATCGG 125
 DB 959 AGTAATCATGCGGCGGAGTTGGGCTGCTGCTTTTGGCAAGGCGAGGCTATCGG 1018
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Db 1439 GGAGAGCGCCTTGCCACCATGACTGCAAGGAGAGAGGCTTGAGAGGCGCTTCGAGAACCC 1498
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Db 2099 AAAAACCATAGCAGGGAAGATTTTGGTCTATCTGTCTGAGTGGGCTTGTGTCAT 2158
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Job time : 2517.09 secs

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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 15:08:54 ; Search time 2190.94 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

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	Maximum Match	100%
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- 22: /cgn2_6/ptodataa/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1997	94.2	2064	13	US-10-062-879-3
3	935.4	44.1	2351	15	US-10-112-677-253
4	935.4	44.1	2351	17	US-10-161-811-253
5	935.4	44.1	2351	17	US-10-169-186-253
6	935.4	44.1	5333	15	US-10-112-677-252
7	935.4	44.1	5333	15	US-10-112-677-254
8	935.4	44.1	5333	17	US-10-161-811-252
9	935.4	44.1	5333	17	US-10-161-811-254
10	935.4	44.1	5333	17	US-10-169-186-252
11	935.4	44.1	5333	17	US-10-169-186-254

12	798.2	37.6	3424	14	US-10-121-746-9	Sequence 9, Appli
13	795.4	37.5	2578	17	US-10-296-115-373	Sequence 373, App
14	679	32.0	5404	15	US-10-212-677-255	Sequence 255, App
15	679	32.0	5404	17	US-10-361-811-255	Sequence 255, App
16	679	32.0	5404	17	US-10-369-186-255	Sequence 255, App
17	634.2	29.9	1121	16	US-10-029-386-24777	Sequence 24777, A
18	354.4	16.7	1597	15	US-10-212-677-256	Sequence 256, App
19	354.4	16.7	1597	17	US-10-361-811-256	Sequence 256, App
20	354.4	16.7	1597	17	US-10-369-186-256	Sequence 256, App
21	338	15.9	612	9	US-09-864-761-26304	Sequence 26304, A
22	266	12.5	2882	18	US-10-377-139-19	Sequence 19, Appli
23	259.2	12.2	3254	15	US-10-212-677-251	Sequence 251, App
24	259.2	12.2	3254	17	US-10-361-811-251	Sequence 251, App
25	259.2	12.2	3254	17	US-10-369-186-251	Sequence 251, App
26	240	11.3	3303	18	US-10-322-281-95	Sequence 95, Appli
27	240	11.3	3303	19	US-10-372-636-9	Sequence 9, Appli
28	240	11.3	23055	18	US-10-322-281-94	Sequence 94, Appli
29	230	10.8	1408	16	US-10-029-386-20260	Sequence 20260, A
30	221.2	10.4	2555	17	US-10-435-935-10	Sequence 10, Appli
31	221.2	10.4	3756	18	US-10-377-139-18	Sequence 18, Appli
32	216	10.2	2483	13	US-10-143-002-3	Sequence 3, Appli
33	216	10.2	2483	14	US-10-325-891-3	Sequence 3, Appli
34	215.6	10.1	1747	10	US-09-804-014A-7	Sequence 7, Appli
35	214.6	10.1	1371	9	US-09-974-712-1	Sequence 1, Appli
36	214.6	10.1	1792	9	US-09-974-712-3	Sequence 3, Appli
37	213	10.0	1341	10	US-09-875-321-7	Sequence 7, Appli
38	213	10.0	1341	14	US-10-162-012-7	Sequence 7, Appli
39	213	10.0	1341	17	US-10-162-102-7	Sequence 7, Appli
40	213	10.0	1341	19	US-10-916-061-7	Sequence 7, Appli
41	213	10.0	6883	9	US-09-989-920-16	Sequence 16, Appli
42	211.4	10.0	4372	9	US-09-993-811-1	Sequence 1, Appli
43	211.4	10.0	4372	15	US-10-254-010-3	Sequence 3, Appli
44	207.6	9.8	1587	18	US-10-322-281-92	Sequence 92, Appli
45	207.6	9.8	21587	18	US-10-322-281-91	Sequence 91, Appli

ALIGNMENTS

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RESULT 1
US-10-062-879-1
; Sequence 1, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang, Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062, 879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178, 109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-10-062-879-1

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Query Match	100.0%;	Score 2121;	DB 13;	Length 2121;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 GATTGCTGAACCTAACTCCAGAGCTGGTGTGCTAGCGTCCGCGCGGCTGCGCCCAAGA 60

Db 1 GATTGCTGAACCTAACTCCAGAGCTGGTGTGCTAGCGTCCGCGCGGCTGCGCCCAAGA 60

QY 61 GCTGAGTCACCATGCGCGCCGGAATTGCGGCTGGCTGCTTTGCCCCGGGCTGGGCC 120

Db 61 GCTGAGTTCACCATGCGCGCGGAGTTGCGGCTGCTGCTTTTGCCCGGCTGCGCC 120
QY 121 ATCGGTGATGCGGTGCGCAACTGCCCCCATGCCCCCTGCGCCCGCGCAAGAACAG 180
Db 121 ATCGGTGATGCGGTGCGCAACTGCCCCCATGCCCCCTGCGCCCGCGCAAGAACAG 180
QY 181 CCGCAGATGAGCTGATTTGCTCAACGTGAGTGGCGGAGTTCCAGACCTGGAGACC 240
Db 181 CCGCAGATGAGCTGATTTGCTCAACGTGAGTGGCGGAGTTCCAGACCTGGAGACC 240
QY 241 AGCTGAGAGCTTACCCGAGACCCCTGCGGAGCAGCAGAGAGAGTTCTTCTCAAC 300
Db 241 AGCTGAGAGCTTACCCGAGACCCCTGCGGAGCAGCAGAGAGAGTTCTTCTCAAC 300
QY 301 GAGGACACCAAGAGATCTTCTTCCAGCCCGAGAGTGTCCGCTGCTGCTCAAC 360
Db 301 GAGGACACCAAGAGATCTTCTTCCAGCCCGAGAGTGTCCGCTGCTGCTCAAC 360
QY 361 TTCTACCGACGCGGAGAGTGTGCTACCCGCGCTACGAGTGCATCTGCTTCAAC 420
Db 361 TTCTACCGACGCGGAGAGTGTGCTACCCGCGCTACGAGTGCATCTGCTTCAAC 420
QY 421 GAGCTGCGCTTCTACCGCATCTCCCGAGATCATCGGGAATGCTGCTACGAGAGTAC 480
Db 421 GAGCTGCGCTTCTACCGCATCTCCCGAGATCATCGGGAATGCTGCTACGAGAGTAC 480
QY 481 AAGGACCGCAAG 540
Db 481 AAGGACCGCAAG 540
QY 541 CAGAGATCCATGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 600
Db 541 CAGAGATCCATGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 600
QY 601 CACACCAAGACGCTGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 660
Db 601 CACACCAAGACGCTGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 660
QY 661 GTCATCACCAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 GTCATCACCAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CCGTGGCGGAG 780
Db 721 CCGTGGCGGAG 780
QY 781 TTCAACCGTGAATCTCTGCGGCTCTTCCGCGCTCCAGCGCTTCCATCCGC 840
Db 781 TTCAACCGTGAATCTCTGCGGCTCTTCCGCGCTCCAGCGCTTCCATCCGC 840
QY 841 AGCGTCAATGAGATCATGACGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 AGCGTCAATGAGATCATGACGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACCAACAACAG 960
Db 901 ACCAACAACAG 960
QY 961 ATCTTCAAGTTTTCGCGCACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 ATCTTCAAGTTTTCGCGCACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 TGTGCTTCCGAACTGGCTTTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1021 TGTGCTTCCGAACTGGCTTTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1081 ACTGTGATGTTTATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 ACTGTGATGTTTATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 TCGTTTGTGTAACCAATGTGTCAACATGACACATGAGAGAGAGAGAGAGAG 1200
Db 1141 TCGTTTGTGTAACCAATGTGTCAACATGAGAGAGAGAGAGAGAGAGAGAGAG 1200

QY 1201 ACGATTGCAAGGAGAGATCTTCCGCTCCATCTGCTCTTGAAGTGGCGTCCGTGATG 1260
Db 1201 ACGATTGCAAGGAGAGATCTTCCGCTCCATCTGCTCTTGAAGTGGCGTCCGTGATG 1260
QY 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGGAATTACCAACAGAAATCAGAGCT 1320
Db 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGGAATTACCAACAGAAATCAGAGCT 1320
QY 1321 GATTAACGAG 1380
Db 1321 GATTAACGAG 1380
QY 1381 AGTTGGAATGATACCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 AGTTGGAATGATACCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 ACGGCAACCCAG 1500
Db 1441 ACGGCAACCCAG 1500
QY 1501 CATCACTGCTGCACTGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 CATCACTGCTGCACTGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 CTGTTATCTGTAGAACTTCCACCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 CTGTTATCTGTAGAACTTCCACCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GAGCAGAACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 GAGCAGAACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 TCCAGCAACCCAG 1740
Db 1681 TCCAGCAACCCAG 1740
QY 1741 CTGCGCAATTTCAACTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CTGCGCAATTTCAACTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CACATCCAG 1860
Db 1801 CACATCCAG 1860
QY 1861 GCAG 1920
Db 1861 GCAG 1920
QY 1921 ATCCCACTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 ATCCCACTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 GGGCCCAACAG 2040
Db 1981 GGGCCCAACAG 2040
QY 2041 AAATCCCGGAG 2100
Db 2041 AAATCCCGGAG 2100
QY 2101 AGTCGATTAAGCCGAATTC 2121
Db 2101 AGTCGATTAAGCCGAATTC 2121

RESULT 2

US-10-062-879-3
; Sequence 3, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.

```

; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-10-062-879-3

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Query Match	94.2%	Score 1997;	DB 13;	Length 2064;
Best Local Similarity	97.3%	Pred. No. 0;		
Matches 2064; Conservative	0;	Mismatches	0;	Indels 57; Gaps 1;

OY	1	GATTGTGAACTAACTCCAAAGCTGCTGTGCTTAAGCGTCCGGCGGCTGCTCCGCCAAGA	60
Db	1	GATTGTGAACTAACTCCAAAGCTGCTGTGCTTAAGCGTCCGGCGGCTGCTCCGCCAAGA	60
OY	61	GCTGAGTCACCAATGGCGCGGAGTTGGCGGCTGCGCTCTTTTGGCCGGGCTGGCGCC	120
Db	61	GCTGAGTCACCAATGGCGCGGAGTTGGCGGCTGCGCTCTTTTGGCCGGGCTGGCGCC	120
OY	121	ATCGGGTGGATGCCGTGGGCCAACTGCCCCCATGCCCCCTGCCCCCGGCCGAAGAACAAG	180
Db	121	ATCGGGTGGATGCCGTGGGCCAACTGCCCCCATGCCCCCTGCCCCCGGCCGAAGAACAAG	180
OY	181	CGGCAGATGAGCTGATTGTCTCAACGTGAGTGGCGGAGGTTCCAGACTGGAGAGCC	240
Db	181	CGGCAGATGAGCTGATTGTCTCAACGTGAGTGGCGGAGGTTCCAGACTGGAGAGCC	240
OY	241	ACGCTGGAGCGCTACCCCGGACACCCTGCTGGCGAGACAGAGAGAGATTCTTCTTCAAC	300
Db	241	ACGCTGGAGCGCTACCCCGGACACCCTGCTGGCGAGACAGAGAGAGATTCTTCTTCAAC	300
OY	301	GAGGACACCAAGAGATATTCTTCCAGCCGGGACCCCGAGGTGTTCCGCTGCTCAAC	360
Db	301	GAGGACACCAAGAGATATTCTTCCAGCCGGGACCCCGAGGTGTTCCGCTGCTCAAC	360
OY	361	TTCTACCGCACGGGGAAAGTGCACATACCCGCGTACGAGTGCACTCTGCTTACGACGAC	420
Db	361	TTCTACCGCACGGGGAAAGTGCACATACCCGCGTACGAGTGCACTCTGCTTACGACGAC	420
OY	421	GAGCTGGCTTCTACCGGCATCTCCCGGAGATCATCGGGGACGTGCTACGAGAGTAC	480
Db	421	GAGCTGGCTTCTACCGGCATCTCCCGGAGATCATCGGGGACGTGCTACGAGAGTAC	480
OY	481	AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGAGCAACAAGACTCGAGACAAC	540
Db	481	AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGAGCAACAAGACTCGAGACAAC	540
OY	541	CAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCTTTCAGAAACCC	600
Db	541	CAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCTTTCAGAAACCC	600
OY	601	CACACCAAGACGCTGGCCCTGATCTTCTACTACGTGAGTGGCTTCTCATCGCTGCTCG	660
Db	601	CACACCAAGACGCTGGCCCTGATCTTCTACTACGTGAGTGGCTTCTCATCGCTGCTCG	660
OY	661	GTCAATCAACCAAGTGTGAGACGGTGCCTGCGGACGGTCCCGGGCAGCAAGGAGCTG	720
Db	661	GTCAATCAACCAAGTGTGAGACGGTGCCTGCGGACGGTCCCGGGCAGCAAGGAGCTG	720
OY	721	CCGTGCGGGAGCGCTACTCGTGGCCTTCTTGCTGAGACAGGGCGTGCATGATC	780
Db	721	CCGTGCGGGAGCGCTACTCGTGGCCTTCTTGCTGAGACAGGGCGTGCATGATC	780

QY	781	TTCAACGCTGGAAGTACCTCTCTCGGGCTCTTTCGGGGCTCCCAAGCCGCTACCGCTTCATCCGC	840
Db	781	TTCAACGCTGGAAGTACCTCTCTCGGGCTCTTTCGGGGCTCCCAAGCCGCTACCGCTTCATCCGC	840
QY	841	AGCGTCAATGAGCATCATCGACGTGGTGGCCATCATGCCCCCTACTACATCGGTCTGTGATG	900
Db	841	AGCGTCAATGAGCATCATCGACGTGGTGGCCATCATGCCCCCTACTACTATCGGTCTGTGATG	900
QY	901	ACCAACAACGAGGACGTCTCCGGCGCTTCGTACAGCTCCGGGTCTTCCGGCTTCAAG	960
Db	901	ACCAACAACGAGGACGTCTCCGGCGCTTCGTACAGCTCCGGGTCTTCCGGCTTCAAG	960
QY	961	ATCTTCAAGTTTCCCGCCACTCCAGGGCTCGCGGATCTGGGCTACACATGAAGAC	1020
Db	961	ATCTTCAAGTTTCCCGCCACTCCAGGGCTCGCGGATCTGGGCTACACATGAAGAC	1020
QY	1021	TGTGCTCTCCGAACCTGGGCTTCTTCTCTCTCCCTCAACCATGGCCATCATCTTTGCC	1080
Db	1021	TGTGCTCTCCGAACCTGGGCTTCTTCTCTCTCCCTCAACCATGGCCATCATCTTTGCC	1080
QY	1081	ACTGTGATGTTTATGCGGAGAAAGGCTCCTCGGCGAGAAAGTTACAAAGCATCCCTGCC	1140
Db	1081	ACTGTGATGTTTATGCGGAGAAAGGCTCCTCGGCGAGAAAGTTACAAAGCATCCCTGCC	1140
QY	1141	TGCTTTTGGTACACCATTTGTACCATGACCAACATGGGATACGAGACATGTGCTTAAG	1200
Db	1141	TGCTTTTGGTACACCATTTGTACCATGACCAACATGGGATACGAGACATGTGCTTAAG	1200
QY	1201	ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCTTGAATGGCGCTCTGCTCATTTGCC	1260
Db	1201	ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCTTGAATGGCGCTCTGCTCATTTGCC	1260
QY	1261	CTGCCAGTCCCTGTGATGTTTCCAACTTAAAGCCGGAATTTACACAGAAATCAGAGAGCT	1320
Db	1261	CTGCCAGTCCCTGTGATGTTTCCAACTTAAAGCCGGAATTTACACAGAAATCAGAGAGCT	1320
QY	1321	GATAAACGACAGGGCACAAGAAGAGGCCCGCTTGGCAGAGATCCGTGTGGCCAAAACAGGC	1380
Db	1321	GATAAACGACAGGGCACAAGAAGAGGCCCGCTTGGCAGAGATCCGTGTGGCCAAAACAGGC	1380
QY	1381	AGTTGCAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGCGCTGAGCTG	1440
Db	1381	AGTTGCAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGCGCTGAGCTG	1440
QY	1441	ACGGGCAACCCAGAGAGAGACATGGGCAAGAACCTTCACTCATTCGAGAGCCAGCAT	1500
Db	1441	ACGGGCAACCCAGAGAGAGACATGGGCAAGAACCTTCACTCATTCGAGAGCCAGCAT	1500
QY	1501	CATCACTGCTGCTCACTGCTGAAAAAACCACTGGGATGTCTATCTTGTGATGATCCC	1560
Db	1501	CATCACTGCTGCTCACTGCTGAAAAAACCACT-----	1533
QY	1561	CTGTATCTGTACGAACCTCCACATCAAGAACCAAGATTTATGATGAGCAGATGTTT	1620
Db	1534	-----AACCAAGATTTATGATGAGCAGATGTTT	1563
QY	1621	GAGCAGAACTGCATGAGAGATTCAATGCAAGAACTAACCCATCCACAAGAGTCCCTCACTG	1680
Db	1564	GAGCAGAACTGCATGAGAGATTCAATGCAAGAACTAACCCATCCACAAGAGTCCCTCACTG	1623
QY	1681	TCCAGCCACCCAGGCTCACTACCACTGCTGCTCCGTCGTAGTAAGAAAGACCAACAC	1740
Db	1624	TCCAGCCACCCAGGCTCACTACCACTGCTGCTCCGTCGTAGTAAGAAAGACCAACAC	1683
QY	1741	CTGCCCAATTCTAACCTGCCAGCTACTGCGCTGCGGACGATGCAAGAGCTACGACGATC	1800
Db	1684	CTGCCCAATTCTAACCTGCCAGCTACTGCGCTGCGGACGATGCAAGAGCTACGACGATC	1743
QY	1801	CACATCCAGGGCAGTGAAGAGCCCTCCCTCAACAACAGTGGCTCCAGCCTTAATTGAAA	1860
Db	1744	CACATCCAGGGCAGTGAAGAGCCCTCCCTCAACAACAGTGGCTCCAGCCTTAATTGAAA	1803
QY	1861	GCAGAGACCGGACTGAGACCAAACTGCAAAACATCCAGATCAACCAAGCCATCATCAGC	1920

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Db      1804 GCAGACGACGAGCTGAGACCAAACTGCAAAACATCCCAATCAACACAGCCATCATAGC 1863
Qy      1921 ATCCCACTCCCGCCAGCGCTAAACCCAGAGGGGAAAGTCGGCCACCCCTGCCAGCCCA 1980
Db      1864 ATCCCACTCCCGCCAGCGCTAAACCCAGAGGGGAAAGTCGGCCACCCCTGCCAGCCCA 1923
Qy      1981 GGGCCCAACAGAACTTCTCTTCAATACCAAGATGTGTCAAGGTCTGTCTTGTAA 2040
Db      1924 GGGCCCAACAGAACTTCTCTTCAATACCAAGATGTGTCAAGGTCTGTCTTGTAA 1983
Qy      2041 AAATCCCGGGCCATGCGCGCGGAGCATGCGAGTCCGGGCCCAATTCGCCCTATAGTG 2100
Db      1984 AAATCCCGGGCCATGCGCGCGGAGCATGCGAGTCCGGGCCCAATTCGCCCTATAGTG 2043
Qy      2101 AGTCGATTAAAGCCGAATTC 2121
Db      2044 AGTCGATTAAAGCCGAATTC 2064
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RESULT 3

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US-10-212-677-253
; Sequence 253, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-677-253
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Query Match 44.1%; Score 935.4; DB 15; Length 2351;
Best Local Similarity 70.7%; Pred. No. 2.6e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

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Qy      66 AGTCACCACTGGCGCGCGGAGTTGCGGCTGCTGCTTTGCCCGGCTGCCGCAATCGG 125
Db      423 AGTAATCATGGCGCGGAGTTGCGGCTGCTGCTTTGCCCGGCTGCCGCAATCGG 482
Qy      126 GTGGATGCGGTCGCAACTGCCCCCATGCCCCCTGAGCCC---GGCCGACAAGAAACGCG 182
Db      483 GTGGATGCTGTGCGCTCGGGGCTATGCGGCTGCCCGGAGGAGAGAGAAAGGAC 542
Qy      183 GCAGATGAGCTGATGTCTCTCAACGTGAGTGGCGGAGTTCCAGACTGTGAGAGAC 242
Db      543 CCAAGATGCTCTCATTTGTGTAATGTGAGTGCAACCCGCTTCCAGAGCTGGCAGAGAC 602
Qy      243 GCTGGAGCGCTACCGGAGCACTGCTGGGAGAGCAGAGAGAGAGTTCTTCAACGA 302
Db      603 CCGGAACTGTAACCAAGACACTCTACTGGGAGTTCTGAGAGGAGACTTTTCTAACACCC 662
Qy      303 GGAACCAAGAGATCTTCTTGAACCGGAGCCCGAGGTGTTCCGCTGCTGCTCAACTT 362
Db      663 AGAACTCAGCAGATTTCTTGAACCGGAGCCCGAGCATCTTCCGCACTCTGAATTT 722
Qy      363 CTACCGCAGGGGAGAGCTGCACTACCCGCTAGAGTGAATCTGTGCTTACAGAGCA 422
Db      723 CTACCGCAGGGGAGAGCTGCACTACCCGCTAGAGTGAATCTGTGCTTACAGAGCA 782
Qy      423 GCTGGCTTCTACGAGCATCTCCCGAGATCATGGGAGCTGTGCTACGAGAGTACAA 482
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Db      783 ACTGCGCTTCTTTGGCCCTCATCCCGAAATCATCGGCGACTGCTGTATAGAGAGTACAA 842
Qy      483 GGAACCGAAGAGGAGAAAGCGCCGAGCGGCTCATGAGCAGCAACGACTCGAGAAACCA 542
Db      843 GGATCGCAGGCGAGAGAACCGCGAGCGCTTCAAGAGCAGACCGGATACCGACACCGTGG 902
Qy      543 GGAG---TCCATGCCCTCGCTCAGCTTCCGCAAGACATGTGGGGGCGCTTGAAGAACCC 599
Db      903 GGAGAGCGCTTCCACCATGACTGCAAGGAGAGAGGTCTGAGAGGCGCTTGAAGAACCC 962
Qy      600 CCACACGACGACGCTGCGCTGTCTTCTACTACGTGACTGCTTCTTCAATGCTGTCTC 659
Db      963 CCACACGACGACGATGCGCTGTGTTCTACTATGTCACGGGGTTTTCATTTGCCGCTTC 1022
Qy      660 GGTATACCAACAGTGTGAGAGACGCTGCGCGGAGCAGGTCCTCCGG---CAGCAAGGA 716
Db      1023 TGTCAATCGGAATGTGTGAACAGTCCGCGGATCAAGCCAGGTCACTTAAGA 1082
Qy      717 GCTGCGTGGCGGAGCGCTACTCGGTGCGCTTCTTCTGCTGACACGCGGCTGCTCAT 776
Db      1083 ACTGCCCTGTGAGAGCGGTATGTGTGCGCTTCTTCTGCTGACACGCGCTGCTCAT 1142
Qy      777 GATCTTACCGTGAATACCTCTGCGGCTCTTCCGCGCTCCAGCGCTACCGCTTCTAT 836
Db      1143 GATCTTACAGTGAATATTTGCTGCGCTGCTGCTGACGCGCTTACCGTTCGTTTGT 1202
Qy      837 CCGACGCTCATGAGCATCATCGAGTGTGCGCATCATGCCCTACTACATCGGTGCTGT 896
Db      1203 GCGTAGTCTCATGATGATCATCATGAGTGTGCGCATCTGCTTATTAATCATGCGTGT 1262
Qy      897 CATGACCAACAGAGAGCGTGTGCGCGCTTCTGTCACGCTCGGGTCTTCCGCTCTT 956
Db      1263 GATGACAGACAAATGAGAGCGTCAAGCGAGCTTGTGACACTCCGAGTCTTCCGGCTT 1322
Qy      957 CAGGATCTTCAAGTTTCCCGGCACTCCCAAGGCGCTGCGATCCGTGGGCTACACATGAA 1016
Db      1323 CAGGATCTTCAAGTTTCCCGGCACTCCCAAGGCGCTGCGATCCGTGGGCTACACATGAA 1382
Qy      1017 GAGCTGTGCTCCGAACTGGGCTTCTTCTCTTCTCCCTACCAATGGCCATCATCTT 1076
Db      1383 GAGTGTGCTCCGAAATTTGGGCTTCTTCTTCTCCCTACCAATGGCCATCATCTT 1442
Qy      1077 TGCCACTGTGATGTTTATGCGGAGAGGCTCTCGGCAAGCAATTCACAAAGCATCC 1136
Db      1443 CGCTACAGTATGTTCTACGACAGAGAGGCTCTCGGCTAGCAAGTTACACAGATCCC 1502
Qy      1137 TGCTCTGTTTGTATACACATGTTGACCATGACCACTGGATGAGATGAGAGCATGTGCC 1196
Db      1503 TGCAAGCTTCTGTATACCATGTCACATGACCAACATGAGGTATGTGATGTGCC 1562
Qy      1197 TAAAGCATTTGAGGAGAGATCTTGGGCTCATCTGCTCTTGAATGGCTGCTGTGAT 1256
Db      1563 AAAAACCATAGCAGGAGAGATTTTGGTCTTATCTGTCTGAGTGGGCTTGTGAT 1622
Qy      1257 TGCCCTGCAAGTCCCTGTGATGTTTCCACTTACCGGATTTACCAAGCAATCATGAG 1316
Db      1623 TGCTTACCTGTTCCGCTGATTTGATTCACATTCAGTGCATCTACACAGAAATCAACG 1682
Qy      1317 AGCTGATTAACGAGGAGCAAAAGAGAGGCGCTTGCAGAGATCCGTGTGSCCAAAAC 1376
Db      1683 AGCAGACAAAGAGAGGAGCAAAAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1742
Qy      1377 AGGCAAGTTCGAATGCTATCTGCAACAGAGGCAACGGGCTCTTCAACGAGGCGTGA 1436
Db      1743 CGGAAGCGCAATGCTTACATGAGAGCAACGGAATGTTTACTAGTAATCAAGTGA 1802
Qy      1437 GCTGACGGGCAACCCAGAGAGAGCAATGGGCAAGCACTCATCTCATGAGAGCCA 1496
Db      1803 GTCTTCAAGAGA---TGAGCAGGCTTTTGTAGCAAAATCCGCTCAGCTTTGAAAACCA 1859
Qy      1497 GCATCATCACTGTGCACTGCTGAGAAACCACTGGGTTGTCTATCTTGTGATGA 1556
Db      1860 GCAACCAACCTGCTTCACTGCTGAGAAAAAACCAAC----- 1895
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QY 1557 TCCCTGTTATCTGTACGAACCTCCATCAAGAACAAGAGTTTATGATGAGAGAT 1616
 Db 1896 -----GAAATCAAGAGTTTGTGAGCAAGCAAGT 1922
 QY 1617 GTTGAAGCAACTGATGAGAGTTTCAATGCAAGAACTAACCCATCCACAAGAGTCCCTC 1676
 Db 1923 CTTTGAAGAAGCTGATGAGAGTTGCAACTGTTAATGCTCTTCAAGTCAAGTCTTTC 1982
 QY 1677 ACTGTCAGCAACCCAGGCTCTCACTAACCACTGCTGCTCCGCTGATGTAAGAAGCAAC 1736
 Db 1983 ACTGCTTCAACAACAAGAGTCAACCAAGCACTGCTGTTCAAGCAAGCAACAAAACTTT 2042
 QY 1737 ACACCTGCCCCAATTCTAACTTGCAGCTACTGCTGCGGAGATGCAAGAGTCAAGCAC 1796
 Db 2043 TCGCATCCCAATGCAATGTATCAAGAGCCATCAAGGTAGTATACAAAGAACTCAAGCAC 2102
 QY 1797 GATCAATCCAGGAGAGAGAGAGCCCTCCCTCAACAACAGTGGCTCCAGCCTTAATTT 1856
 Db 2103 GATCAGATCAGATGTGTGAGAGAGAACACCTGCTGTAAACAGCCGATCCAGTTTAAATGC 2162
 QY 1857 GAAAGCAGACGAGCTGAGAGCAAACTGCAAAACATCCAGATCACCAAGCCATCAT 1916
 Db 2163 CAAATGGAAGGTGTGTTAACTGAACTGAAACAACCTTATGTGATCAAGCAATTAAT 2222
 QY 1917 CAGCATCCCACTCCCCAGCGCTAACCCCAAGAGGGGAAAGTCCGCCA 1965
 Db 2223 AAGCATCCCAACACTCTCAAGTAACCAACAGAGAGAGATAGGCCA 2271

RESULT 4
 US-10-361-811-253

; Sequence 253, Application US/10361811
 ; Publication No. US20030206918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.484C8
 ; CURRENT APPLICATION NUMBER: US/10/361,811
 ; NUMBER OF SEQ ID NOS: 293
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 253
 ; LENGTH: 2351
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-361-811-253

Query Match 44.1%; Score 935.4; DB 17; Length 2351;
 Best Local Similarity 70.7%; Pred. No. 2.6e-248;
 Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTACCATGGCGCGGAGTGGCGGCTGCTTTTGGCCGGGCTGGCGCATCGG 125
 Db 423 AGTAATCATGGCGCGGAGTGGCGGCTGCTTTTGGCGGAGCGGCTATCGG 482
 QY 126 GTGATGCCGCTGGCAACTGCCCATGCCCCCTGGCCCC--GGCGACAAGAACAGCG 182
 Db 483 GTGATGCCCTGTGGCTTGGGGGCTTATGCGGCTCCCCGAGGAGAGAGAAAGGAC 542
 QY 183 GCAGATGAGTGTATGCTCTCAAGTGAAGTGGCGGAGGTTCCAGACTGAGAGCAC 242
 Db 543 CCAAGATGCTCTCATTTGTGCTGAATGTAGTGGCAACCGCTTCAAGCTGGCAGAGAC 602
 QY 243 GCTGAGCGCTAACCCGAGACCCCTGCTGGGAGCAAGAGAGAGTCTTCTTCAACGA 302
 Db 603 CTTGGAACGTTAACCCAGACACTTACTGGGAGTTCTGAGAGGGAATTTTCTTCAACCC 662
 QY 303 GGACACCAAGAGTACTTCTTCAAGCGGAGACCCGAGTGTTCGCTGGCTGCTCAACTT 362
 Db 663 AGAACTCAGAGTATTTCTTGAACGCTGACCCAGACATCTTCCGACACATCTCTGATTT 722

QY 363 CTACCGCAGCGGGAAGCTGCACTTACCAGCGCTACAGTGCATCTCTGCTACGACGCA 422
 Db 723 CTACCGCAGCTGGGAAGCTTCACTATCTCTGCGCAGAGTGCATCTCTGCTTACGATGAAGA 782
 QY 423 GCTGGCTTTTACCGGATCTCTCCGGAGATCATCGGGGACTGTGCTTACGAGAGTACAA 482
 Db 783 ACTGGCTTCTTGGCTCATCCGGGAATCATCGGGGACTGTGTTATGAGAGTACAA 842
 QY 483 GGACGCAAGAGGAGAGAGCGCGGAGCTCATGAGAGCAACAGACTCGGAGAACCA 542
 Db 843 GGATCGAGGAGAGAGAGAGCGCGGAGCTTGCAGAGAGAGCGGATACCAACCGCTGG 902
 QY 543 GGAG---TCCATGCTCTGCTCACTTCCGCGAGACCATGTGGCGGCTTGAAGAACCC 599
 Db 903 GGAAGAGCGCTTGGCCACCATGACTGCAAGGAGAGAGGCTTGGAGAGGCTTTCAGAACCC 962
 QY 600 CCACACAGCAGCTGGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 659
 Db 963 CCACACAGCAGATGGGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1022
 QY 660 GGTATCACCAACGTGTGAGAGAGCGTGGCGGCTCCAGCGGCTACCGGCTTCTAT 716
 Db 1023 TGTATCGCAATGTGTGAAACAGTGGCGGATCAAGCCAGGCTACATTTAAAGA 1082
 QY 717 GCTGCGCTGGGGAAGCGCTACTTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 776
 Db 1083 ACTGCTCTGTGAGAGCGGTATGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1142
 QY 777 GATCTTCAACCGGAGATCTCTCTGCGGCTCTTCCGGGCTCCAGCGGCTACCGGCTTCTAT 836
 Db 1143 GATCTTCAAGTGTGATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTGT 1202
 QY 837 CCGCAGCTCATGAGCATCATGAGCGTGTGCGCATCATGCTTCTTCTTCTTCTTCTTCTTCTTCT 896
 Db 1203 GCGTGTGCTATGATGATCATGAGCGTGTGCGCATCATGCTTCTTCTTCTTCTTCTTCTTCTTCT 1262
 QY 897 CATGACCAACAAGAGAGCGTGTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 956
 Db 1263 GATGACAGACATGAGAGCGTGTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1322
 QY 957 CAGATCTTCAAGTTCCTCCGCACTCCAGGCGCTGCGGATCTTGGGCTACACACTGAA 1016
 Db 1323 CAGATCTTCAAGTTCCTCCGCACTCCAGGCGCTGCGGATCTTGGGCTACACACTGAA 1382
 QY 1017 GAGCTGTGCTTCCGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1076
 Db 1383 GAGTGTGCTTCCGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1442
 QY 1077 TGCCATGTGATGTTTATGCGGAGAGGCTCTGCGGCGCAAGTTTCAACAGCATCC 1136
 Db 1443 CGCTACAGTTATGTTTACGAGAGAGGCTTCTGCGCTGAGCAAGTTTCAACAGCATCC 1502
 QY 1137 TGCTGCTTGTGATACCATGTCACCATGACCACTGGGATACGAGACATGTGCTC 1196
 Db 1503 TGCAGCTTCTGTGATACCATGTCACCATGACCACTAGGATATGTGACATGTGCTC 1562
 QY 1197 TAAACGATTCAGAGGAGATCTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1256
 Db 1563 AAAAACATAGCAGGAGATTTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1622
 QY 1257 TGCCCTGCAAGTCTGCTGATGTTTCAACTTACCGGATTTACCAACGAAATCAGAG 1316
 Db 1623 TGCTTACCTGTTCCGCTGATGTTTCAACTTACCGGATTTACCAACGAAATCAGAG 1682
 QY 1317 AGCTGATTAACGAGGAGCAAAAGAGGCGCTTGGCAGAGTCCGTGTGCGCAAAAC 1376
 Db 1683 AGCAGACAAAGAGGAGCAAAAGAGGCTTGAAGTGTGCTGCGGAGGAGCAAAAG 1742
 QY 1377 AGGAGTTTCAATGATACCTGACAGAGAGCGCAAGCGGCTCTTCAAGAGGCGCTGGA 1436
 Db 1743 CGGAAGCGCAATGCTTATGATGAGAGCAAGGAGATGTTTACTAGTATACGCTGCA 1802

QY	1437	GCTGACGGGCACCCCCAGAGAGACACATGGGCAAGACCACTCTCATCGAGACCA	1496
Db	1803	GTCTCTAGAGGA---TGAGCAGGCTTTGTGTAGCAATCCGGCTCCAGCTTTGAAACCCA	1859
QY	1497	GCATCATCACTCGTGCACCTGCTGGAAAAAACCACTGGGTGTCTATCTTGTGATGA	1556
Db	1860	GCACCACCACTGCTTCACTGCTGGAAAAAACCACTGGGTGTCTATCTTGTGATGA	1895
QY	1557	TCCCCTGTATCTGTACGAACCTCCACCATCAAGAACCAAGAGTTTATTTGATGAGCAGAT	1616
Db	1896	-----GATACAGAGTTTGTGACGACCAAGT	1922
QY	1617	GTTTGAGCAGAACTGCATGAGAGATTCAATGCAGAACTACCCTCACAAGAGTCCCTC	1676
Db	1923	CTTTGAGAAAGCTGCATGGAAGTTGCACATGTTAATCGTCTTCAAGTCACAGTCCCTTC	1982
QY	1677	ACTGTCCAGCCACCCAGGCTCACTACCACTGCTGCTCCCGTCTGTAAGTAAGAAGACCAC	1736
Db	1983	ACTGTCTTCACACAAGAGAGTCAACAGCACTGCTGTTCAAGCAGCACACAAAAAATTTT	2042
QY	1737	ACACCTGCCCAATTCTAACTGCGCAGTACTGCGCTGCGCAGATGCCAAGAGCTCAGCAC	1796
Db	2043	TCCGATCTCCAAATGCCAATGTATTCAGAAAGCCATCAAGGTAGTATTCAAAGAACTCAGCAC	2102
QY	1797	GATCCACATCCAGGGGACAGTGAAGACGCCCTCCCTCAACAACCAAGTGGCTCCAGCTTAATTT	1856
Db	2103	GATTGATTCAGATGTGTGAGAGAAACACTCTGTCTAACAAGCCGATCCAGTTTAATGTC	2162
QY	1857	GAAAGCAGACGACGACCTGAGACCAAACTGCAAAAATCCAGATCAACACAGCCATCAT	1916
Db	2163	CAAAATGGAAAGAGTGTGTAACTTAACCTGTGAACAACCTTTATGTGACTACAGCAATPAT	2222
QY	1917	CAGCATCCCCCACTCCCCCAGCGCTAACCCACAGAGGGGGAAGTCCGGCCA	1965
Db	2223	AAGCATCCCCAACCTCCAGTAAACACACCCAGAAAGAGACGATAGGCCA	2271

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RESULT 5
US-10-369-186-253
; Sequence 253, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-253

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Query Match	44.1%;	Score 935.4;	DB 17;	Length 2351;
Best Local Similarity	-70.7%;	Pred. No. 2.6e-248;		
Matches 1349;	Conservative 0;	Mismatches 491;	Indels 69;	Gaps 5
OY	66	AGTCACCATGGCGCGCCGAGTTGGCGCTGCTGCTTTTGCCCGGCGCCATCG	125	
Db	423	AGTAATCATGGCGCGCGGGGTGGCAGCGTGCTGCTTTTGCAAGGGCAGCGGCTATCG	482	
OY	126	GTGGATGCCGGTGGCCAATGCCCCATGCCCTTGCGCCC---GGCCGACAAGACAAGG	182	
Db	483	GTGAATGCTGTGGCTTCGGGGCTTATGCCGCTCCCCGAGGCAAGAGAGAAAGGAC	542	
OY	183	GCAGATGAGCTGATTTGTCTCAACGTGATGGGGGAGGTTCCAGACTTGAGAGACAC	242	
Db	543	CCAAGATGCTCTCATTTGCTCTGATGTGAGGGCACCCGCTTCCAGACTGGCAGACAC	602	

QY	243	GCTGAGCGCTAACCCCGACACCTTGCTGGGACACGAGAAAGAGTTCTTCTTCAACGA	302
Db	603	CTTGAACGTTAACCCAGACACTCTACTGGGCACTTCTGAGAGGGACTTTTCTTACCAACC	662
QY	303	GGACACCAAGAGTACTTCTTGACCGGGAGCCCCGAGGTGTTCGCTGCTCAACTT	362
Db	663	AGAACTCAGAGATTTCTTGACCGGTGACCCAGACACTTCCGCCACATCTGAAATTT	722
QY	363	CTACCGCAGCGGGGAAGCTGACTACCCGGCGCTACGAGTGCACTCTGCTTACGACGACGA	422
Db	723	CTACCGCACTGGGAAGCTCCACTATCTCTGCGCAGAGTGCACTCTGCTTACGATGAGA	782
QY	423	GCTGGCTTTCTACGGCATCTCTCCGGAGATCATCTGGGGACTGTGCTACGAGAGTACAA	482
Db	783	ACTGGCTTTTGGCTCTATCCGGAAATCATCGCGCACTGCTGTATAGAGAGTACAA	842
QY	483	GGACCGCAAGAGGGAGAACGCCGAGCGCTCATGAGACCAACGACTCGGAGAACACCA	542
Db	843	GGATCGCAGGGGAGAGAACGCCGAGCGCTTGAGAGACGACGCCGATACCGACACCGCTGG	902
QY	543	GGAG---TCCATGGCCCTCGCTCAGCTTCCGCCAGACCAATGTGGCGGCTTTGAGAACCC	599
Db	903	GGAGAGCGCTTGGCCCACTATGTCGAAGCAGAGGGTCTGAGAGGCTTGCAGAACCC	962
QY	600	CCACACGACGACGCTGGCCCTGTCTTCTACTACGTGACTGGCTTCTTCATCGTGTCTC	659
Db	963	CCACACGACGACGATGGCCCTGTGTCTACTATGTACAGGGGTTTTTCAITTGCCGTCTC	1022
QY	660	GGTCATCACCAACGTGTGAGAGACGCTCCGTGCGGACAGCTCCCCGG---CAGCAAGGA	716
Db	1023	TGTCAATCGCGAATGTGTGGAACAGTCCGTGGGATCAAGCCAGGTCACTTAAGA	1082
QY	717	GCTGCGGTGCGGGAGCGCTACTCGTGGGCTTCTTCTGCTTGGACACGGCGTGCCTCAT	776
Db	1083	ACTGCGCTGTGAGAGCGGTATGCTGTGGCTTCTTCTTGTGACACGGCGCTGCCTCAT	1142
QY	777	GATCTTCAACCGTGAAGTACTCTCGCGCTTTTCGCGGCTCCAGCCGCTAACCGCTTCAT	836
Db	1143	GATCTTCAAGTTGAGTATTTGCTTCCGCTTGCTGACGCGCTTATGTCTTACCGCTTTTGT	1202
QY	837	CCGACCGCTCATGAGCATCATGACGCTGTGCGCATCATGCCCTACTACATCGCTGTGT	896
Db	1203	CGGTATGTCAATGAGTATCATGACGCTGTGCGCATCTGCCCTTATTAATTTGGGCTGT	1262
QY	897	CATGACCAACAAGAGAGCTGTCCGGGCTTCTGTACAGCTCCGGGCTTTCGGGCTT	956
Db	1263	GATGACAGACAATGAGAGCTGACGGAGCCTTGTTCACACTCGAGTCTTCCGGGCTT	1322
QY	957	CAGATCTTCAAGTTTCCCGGCACCTCCAGGGCGTGGGATCTGGGCTTACACACTGAA	1016
Db	1323	CAGATCTTAAAGTTTCCCGGCACCTCTCAAGGCTGGCATCTGGGGTACACACTGAA	1382
QY	1017	GAGCTGTGCTTCGGAACGTGGGCTTCTTCTCTCTCCCTTCAACCATGCGCATCATCTT	1076
Db	1383	GAGTGTGCTTCAGAAATGGGCTTCTTCTCTCTCCCTTCAACCATGCGCATCATCTT	1442
QY	1077	TGCCACTGTGATGTTTTATGCGAGAGAGGGCTCTCGGCGACGCAAGTTCAACGACTCCC	1136
Db	1443	CGCTACAGTTATGTTCTTACGACAGAAAGGGGTCTTCGGGTAGCAAGTTTCAACGACTCCC	1502
QY	1137	TGCCGTGTTTGGTATCAACATTTGTCAACCATGACCAACATGGGATACGAGACATGTGCC	1196
Db	1503	TGCAGCTTCTGGTATTAACATGTCAACCATGACCAACATAGGGTATGTGTACATGTGCC	1562
QY	1197	TAAAGACATTGACGGGAAGATCTTGGGCTTCATCTGCTCTTGAATGGCGTCTGTGCAT	1256
Db	1563	AAAAACCATAGCAGGGAAAGATTTTGGTCTTATCTGTTCGTGAGTGGGGCTTGTGCAT	1622
QY	1257	TGCCCTGCCAGTCCCTGTGATTTGTTTCCAATTAGCGGATTTTACCAACGAATCAGAG	1316
Db	1623	TGCTTCACTGTTCGGGTGATGTATCCAACCTCAGTGCATTTACCAACGAATCAGAG	1682
QY	1317	AGCTGATTAACGACGGGACAAAGAAGGCCCGGCTTGGCCAGATCCGTGTGGCCAAAC	1376

Db 1683 AGCAGACAAA CGAAGGGG CAAAAGAAAGCTTAGACTGGCCAGATTCGGGCGAGCCAAAAG 1742

Qy 1377 AGGCA GTT CGAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGA 1436

Db 1743 CGGAAGCGCAAAATGCTTACATGTCAGAGCAAAACGGAATGGTTTACTCAGTAATCAGCTGCA 1802

Qy 1437 GCTGACGGGACCCCGAAGAGGACACATGGGGCAAGACCACTTCATCTCATCGAGACCA 1496

Db 1803 GTCTCTCAGAGGA---TGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAACCCA 1859

Qy 1497 GCATCATCACCTGCTGCTGCACTGCTGAAAAAAACCATCTGGGTTGTCTTATCTTGTGATGA 1556

Db 1860 GCACCAACCACTGCTTCACTGCTGGAAAAAACACAC----- 1895

Qy 1557 TCCCTGTATCTGTAGCAACCTCCACCATCAAGAACCAAGAGTTTATTTGATGACAGAT 1616

Db 1896 -----GAATCAGAGTTTGTGACGACGAACAAGT 1922

Qy 1617 GTTTGAGCAGAACTGCATGAGAGTTTCAATGACAGAACTAACCCATCCACAAGAGTCCCTC 1676

Db 1923 CTTTGAAAGAAAGCTGCATGGAAGTTGCAACGTTAATCGTCTTCAAGTCAACAGTCCCTTC 1982

Qy 1677 ACTGTTCAGCCACCCAGGCTCACTACCACTGCTGCTCCCGTGTAGTAAGAGACCAAC 1736

Db 1983 ACTGTCTTCAACAACAAGAGATCACCAAGCACTGCTGTTCACGACGACACAAAAAACTTT 2042

Qy 1737 ACACCTGCCCAATTCTTAACCTGCCAGCTACTCGCCCTGGGACAGATGCAAGAGCTCAGCAC 1796

Db 2043 TCGCATCCCAATGCCAAATGTATGATAGAGAGGACATCAAGTAGTATACAAAGAACTCAGCAC 2102

Qy 1797 GATTCACATCCAGGGCAGGTGAGCAGCCCTCCCTCACAAACGATCGCTCCAGCCTTAATTT 1856

Db 2103 GATTCAGATCAGATGTGTGAGAGACAACCTCTGTCTTAACAGCCGATCCAGTTTAAATGC 2162

Qy 1857 GAAGCAGACGACGAGCTGAGACCAAACTGCAAAACATCCAGATCACCAAGCCATCAT 1916

Db 2163 CAAATGGAAGAGTGTGTAACTTAACCTAAGTGAACAACCTTATGTAGCTACAGCATATAT 2222

Qy 1917 CAGCATCCCACTCCCGCAGCGCTAACCCAGAGGGGGAAGTCCGCCA 1965

Db 2223 AAGCATCCCAACACCTCCAGTAACCAACAGAGGAGAGATAGGCCA 2271

RESULT 6

US-10-212-677-252

Sequence 252, Application US/10212677

Publication No. US20030129192A1

GENERAL INFORMATION:

APPLICANT: Chenault, Ruth A.

APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 252

LENGTH: 5333

TYPE: DNA

ORGANISM: Homo sapiens

US-10-212-677-252

Query Match	44.1%;	Score 935.4;	DB 15;	Length 5333;
Best Local Similarity	70.7%;	Pred. No. 3.2e-248;		
Matches 1349;	Conservative 0;	Mismatches 491;	Indels 69;	Gaps 5;

QY 66 AGTCACCATGGCGCGCGAGTGTGGCGCTGCTTTTGGCCCGGCGTGGCGGCATGG 125

|||||

D	959	AGTAATCATGGCGCGGGGTGGCAGCGTGGCTGCTTTTGCAAGGGCAGCGGCTATTCG	1018
Q	126	GTGGATGCCGTGGCCMACTGCCCATGCCCCCTGGCCCC--GGCCGACAAGAACAGCG	182
D	1019	GTGGATGCTGTGGCCCTCGGGGCTTATGCCGCTCCCCCGAGGCAGAGAGAGAAAGAC	1078
Q	183	GCAGATGAGCTGATGTTCCTCAACGTGAGTGGCGGAGGTTCCAGACTCGAGGACCA	242
D	1079	CGAAGATCTCTCATTTGTGCTGAATGTGAGTGGCACCCGCTTCAAGACGTGGCAGACAC	1138
D	243	GCTGAGCGCTACCCCGACACCCTGCTGGCAGCACGAGAGAGAGTTCCTTCAACGA	302
D	1139	CTGGAAAGTTACCCAGACACTTACTGCGCAGTTCTGAGAGGAGCTTTTCTACACACC	1198
Q	303	GGACACCAAGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCTCACTT	362
D	1199	AGAAACTAGCAGTATTTCTTGACCGTGAACCCAGACATCTTCGCACATCTGAATTT	1258
Q	363	CTAACCGCAGGGGAGCTGCACTACCCGCTACGAGTGACATCTGCTCTACAGACGA	422
D	1259	CTAACCGCATGGGAAGCTCACATATCTCGCCACAGATGCATCTGCTTACGATGAAGA	1318
Q	423	GCTGGCTTCTTACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACA	482
D	1319	ACTGGCTTCTTTGGCTCTATCCGGAATCATCGCGACTGCTGTTATGAGAGTACAA	1378
Q	483	GGACCGCAAGAGGAGAACGCCCGAGCGCTCATGACGACACGACTCGGAGAACACCA	542
D	1379	GGATCGCAGGCGAGAGAACGCCCGAGCGCTGCAAGACGACCGGATACCGACACCGCTGG	1438
Q	543	GGAG--TCCATGCCCTCGCTCAGCTTCGCCAAGCATGTGGCGGGCTTGGAGAACCC	599
D	1439	GGAGAGCGCTTCCGCCCATGACTGCAAGGACGAGGGTCTGGAGGGCTTGGAGAACCC	1498
Q	600	CCACACGACGACGCTGGCCCTGCTTCTACTAGTGACTGGCTTCTCATCGCTGCTC	659
D	1499	CCACACGACGACGATGGCCCTGCTGTTCTACTATGTACAGGGGTTTTCATATGCCGCTCC	1558
Q	660	GGTCATCAACCAAGTGTGGAGACGGTGCCTGGCGGACCGGTCCCGGG--CAGCAAGCA	716
D	1559	TGTCAATCGGAATGTGTGGAAACAGTGCCTGGCGGATCAAGCCGAGTCACTTAAGA	1618
Q	717	GCTGCCGTGGGGAGCGCTACTGGTGGCTTCTTCTGCTGAGACGGCGTGGCTCAT	776
D	1619	ACTGCCCTGTGGAGAGCGGTATGTGTGGCTTCTTCTGCTTGAACAGCGCTGGCTCAT	1678
Q	777	GATCTTCAACCGTGGAGTACTCTGCGGCTCTTGCGGCTTCCAGCGCTACCGCTTCAT	836
D	1679	GATCTTCAACAGTATGATTTGCTTCCGCTGGCTGACCGCTAGTCTGTTACCGTTTGT	1738
Q	837	CCGACGCTCATGAGCATTCGACGTGTGGCCATCATGCGCTTACTATCATGCTGTGT	896
D	1739	GCGTAGTGTCAATGATATCATCGAGTGTGGCCATCTGCGCTTATTAATTGAGGCTGTGT	1798
Q	897	CATGACCAACAAGAGACGTGTCCGGCGCTTGTCACGCTCCGGGTCTTCCGCTCTT	956
D	1799	GATGACGACAAATGAGAGCGTCAAGCGAGCTTGTCACACTCCGAGTCTTCCGGCTCTT	1858
Q	957	CAGGATCTTCAAGTTTCCCGCACTCCAGAGGCTGCGGATCTGGGCTACACATGAA	1016
D	1859	CAGGATCTTAAAGTTTCCCGCACTTCAAGGCTTCCGATCTGGGGTACACATGAA	1918
Q	1017	GAGCTGTGCTCCGAACCTGGGCTTCTTCTTCTTCCCTTCAACCATGCGCATCATCTT	1076
D	1919	GAGTTGTGCTCAGAAATGGGCTTCTTCTTCTTCTGCTTCAACCATGCGTATCATCTT	1978
Q	1077	TGCCACTGTGATGTTTATGCGCAGAGAGGGCTCTCGGCGACGAAGTTCAACAAGATCCC	1136
D	1979	CGCTACAGTTATGTTCTAAGCAGAGAGAGGGGTCTTCGGCTAAGAGTTCAACAAGATCCC	2038
Q	1137	TGCCCTGTTTGTATACCATTTGTCAACCATGACCAACTGGGATACGAGACATGTGCC	1196
D	2039	TGCAGCTTTGTGTATACCATGTCATGACCAACTAAGGATATGTTGATCATGTGTCC	2098

QY	107	TGCCACCTGTGATGTTTATGCCCAGAAAGGACCTCTCGSCACGCAAGTTCACAAACATCCC	1136
Db	1979	CGCTACAGTTATGTTCTTACGCAAGAAAGGGGTCTTCGGCTAAGCAAGTTCAACGACATCCC	2038
QY	1137	TGCGTCGTTTTTGATACACCATTTGCACCACTGACCAACATCGGAGATACGAGACATGTGTCC	1196
Db	2039	TGCAGCCCTTCTGTATACCATCGTCACCATGACACACTAGGGTATGTTGTCATGTGTGCC	2098

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QY 1197 TAAGACGATTGACGGGAAGATCTCGGCTCCATCTGCTCTTGAGTGGCGTCTGTAT 1256
DB 2099 AAAAAACCATAGACGGGAAGATTTTGTCTATCTGTCTGCTGAGTGGGCTTGTGTAT 2158
QY 1257 TGCCTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACCAACCAATCAGAG 1316
DB 2159 TGCCTGAGTCTGTTCCGATGATGATCACTTCACTGATGATCACTTCACTGATCAAG 2218
QY 1317 AGCTGATTAAGCAGAGGAGCAAAAGAGGCGGCTTGCAGAGATCCGTGCGCAAAAC 1376
DB 2219 AGCAGACAAAGAGAGGAGCAAAAGAGAGTAACTGCGCAGATCCGGGAGCCAAAG 2278
QY 1377 AGGAGTTTGAATGATACCTGACAGAGCGGAGCGGCTCTCAACGAGGCGCTGGA 1436
DB 2279 CGGAAGCGCAATGCTTACATGACAGAGAAACGGAATGTTTACTCACTAATCACTGCA 2338
QY 1437 GCTGACGGGACCCCAAGAGGAGACATGGGCAAGACCACTCACTCATGAGAGCA 1496
DB 2339 GTCCCTCAGAGGA---TGAGCAGGCTTTGTTAGCAATCCGGCTCAGCTTTGAAACCA 2395
QY 1497 GCATCATACCTGCTGACCTGCTGAGAAAAAACAATGCTGCTTCTATCTTGATGA 1556
DB 2396 GCACCAACCACTGCTTCACTGCTGAGAAAAACAC----- 2431
QY 1557 TCCCTGTTATCTGTAAGAACTCCACCATCAAGAAACCAAGTTTATGATGAGCAGAT 1616
DB 2432 -----GAAATCAGAGTTTGTGAGCAACAGT 2458
QY 1617 GTTTGAGAGACTGATGAGAGTTCATATGACAGAACTAACCATCCACAAGAGTCCCTC 1676
DB 2459 CTTTGAAGAAAGCTGATGAGAGTTCATATGATGATGATGATGATGATGATGATGATG 2518
QY 1677 ACTGTCCAGCCAGGAGGCTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
DB 2519 ACTGTCTTCACAACAGAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2578
QY 1737 ACACCTGCGCAATTTTAACTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1796
DB 2579 TCGCATCCCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2638
QY 1797 GATCCACATCCAGGAGGAGTGAAGAGGCTTCCCTCAACCAAGTGGCTGAGGCTTAAATT 1856
DB 2639 GATTCAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2698
QY 1857 GAAAGCAGACGAGGAGTGAAGCAAACTGCAAAACATCCAGATCAACCAAGGCTCAT 1916
DB 2699 CAAATGAGAGAGTGTGTTAACTAACTGTAACAACTTATGTACTACGCAATTAAT 2758
QY 1917 CAGCATCCCACTCCCAAGGCTTAAACCCAGAGGAGGAGAGTGGGCA 1965
DB 2759 AAGCATCCCAACCTCCAGTAAACCAACAGAGAGAGATAGGCCA 2807

RESULT 7
US-10-212-677-254
; Sequence 254, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 5333
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TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-254
Query Match 44.1%; Score 935.4; DB 15; Length 5333;
Best Local Similarity 70.7%; Pred. No. 3,2e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTACCATGCGCGCGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 125
DB 959 AGTAATCATGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1018
QY 126 GTGATGCGCGGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 182
DB 1019 GTGATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1078
QY 183 GCAGATGAGCTGATTTGCTCAACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
DB 1079 CCAAGATGCTCTCATTTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1138
QY 243 GCTGAGCGCTACCCGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
DB 1139 CTTGAGAGCTTACCAAGACCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
QY 303 GGAACCAAGAGTACTTCTTTCAGACCGGAGACCCCGAGGAGTTCGCTGCTGCTGCTGCTGCT 362
DB 1199 AGAATCTGACAGATTTCTTTCAGACCGGAGACCCCGAGGAGTTCGCTGCTGCTGCTGCTGCT 1258
QY 363 CTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 422
DB 1259 CTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318
QY 423 GCTGCGCTTCTACCGCATCTTCCCGAGATCATTCGGGAGCTGCTGCTGCTGCTGCTGCTGCTG 482
DB 1319 ACTGCGCTTCTTGGCTTATCCCGAGATCATTCGGGAGCTGCTGCTGCTGCTGCTGCTGCTG 1378
QY 483 GGAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542
DB 1379 GGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1438
QY 543 GGAG--TCCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
DB 1439 GGAGGAGGCTTGGCCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1498
QY 600 CCACACGAGCAGGCTGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 659
DB 1499 CCACACGAGCAGATGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1558
QY 660 GGTATCAACCACTGATGAGAGCGGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
DB 1559 TGTATGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1618
QY 717 GCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 776
DB 1619 ACTGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1678
QY 777 GATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
DB 1679 GATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1738
QY 837 CCGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 896
DB 1739 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1798
QY 897 CATGACCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 956
DB 1799 GATGACCAACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1858
QY 957 CAGGATCTTCAAGTTTCCCGCAGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016
DB 1859 CAGGATCTTCAAGTTTCCCGCAGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1918
QY 1017 GAGCTGTGCTCCGAGAGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1076
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1919 GAGTTGTGCTCAGAAATGGGGCTTCTGCTTTTCTCGCTCACCATTGGCTATCATCTT 1978
 QY 1077 TGCCACTGTGATGTTTATGCGGAGAAAGGCTCTCGGCCAGCAAGTTCAACAAGCATCCC 1136
 Db 1979 CGCTACAGTATGTTCTTACGAGAGAAAGGGCTCTCGGCTAGCAAGTTCAACAAGCATCCC 2038
 QY 1137 TGCCCTGTTTGGTACACCATTTGTCACCATGACCACTGGGATACGGAGATGGTGGCC 1196
 Db 2039 TGACGCTTCTGTATACCATGTCACCATGACCACTAGGAGTATGAGATGATGGTGGCC 2098
 QY 1197 TAAGACGATTGAGGAGAGATCTTGGCTCCATCTGCTCTGAGTGGGCTCGTCTCAT 1256
 Db 2099 AAAAACCATAGCAGGAGAGATTTTGGTTCTATCTGTTCTGCTGAGTGGGCTCTGCTCAT 2158
 QY 1257 TGCCCTGCGCAGTCCCTGATTTGTTTCCAACTTTAGCCGAGTTTACCACCAAGATCAGAG 1316
 Db 2159 TGCTCTACCTGTTCCGGGATTTGATTCACCTTCACTGCTGATCTACACCAAGATCAGAG 2218
 QY 1317 AGCTGATTAAGCGAGGCGCAAAAAGAGGCGCTTGGCCAGGATCCGTTGGCCAAAC 1376
 Db 2219 AGCAGACAAAGAGAGGCGCAAAAAGAGCTAGACTGGCCAGGATCCCGGCGAGCCAAAG 2278
 QY 1377 AGGAGTTTGAATGATGATCTGCAAGCAAGCGGAGGCTCTCAACGAGCGCTGGA 1436
 Db 2279 CGGAAGCGCAAAATGCTTATCATGAGAGCAAAAGGATGTTTACTCAGTAATCAGCTGCA 2338
 QY 1437 GCTGACGGGCAACCCAGAGAGACATGGGCAAGACCACTCACTCATCTGAGAGCCA 1496
 Db 2339 GTCTCTAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAACCCA 2395
 QY 1497 GCATCATCAGCTGCTGCACTGCTGGAAGAAACCACTGGGTTGTTCTATCTTGTGATGA 1556
 Db 2396 GCACACCACTGCTTCACTGCTGGAAGAAACCACTGCTGGAAGAAACCACTGCTGGAAG 2431
 QY 1557 TCCCTGTTATCTGATGCAACCTTCCACCATCAAGAACCAAGATTATGATGAGCAGAT 1616
 Db 2432 -----GAATCAGAGTTTGTGAGAGCAAGT 2458
 QY 1617 GTTGAAGAGATGATGAGAGTTCAATGACAGAACTAACCCATCCACAGAGAGTCCCTC 1676
 Db 2459 CTTTGAAGAAAGCTGCAATGGAAGTTGCAACTGTTAAATGCTTCAAGTCAACAGTCCCTC 2518
 QY 1677 ACTGTCCAGCCACCCAGGCTCTCACTACCACTGCTGCTCCGCTGTAAGTAAAGAACCCAC 1736
 Db 2519 ACTGTCTTCAACAACAAGAGTCAACGACCTGCTGTTCAACGACGACACAAAAAATCTT 2578
 QY 1737 ACACCTGCCCAATTCTAACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1796
 Db 2579 TCGCATCCCAATATGCAATGATATCAAGAGCATCAAGTATGATACAGAACTCAGCAC 2638
 QY 1797 GATCCATCCAGGAGGAGTGAAGACCCCTCTTCAACCAACAGTCCGCTCAGGCTTAATTT 1856
 Db 2639 GATTCAGATCAGATGTTGAGAGAGAACACCTCTGTTAAACAGCGATCCAGTTTAAATGC 2698
 QY 1857 GAAAGCAGACGAGGAGTGAAGACCAACTGCAAAAACATCCAGATCAGCAGGCTCAT 1916
 Db 2699 CAATATGAGAGTGTGTTAACTAACTGGAACAACCTTATGTGATCAGCAGCAATAT 2758
 QY 1917 CAGCATCCCACTCCCGCAGCGCTAACCCAGAGGGGGAAGTCCGCCA 1965
 Db 2759 AAGCATCCCAACACCTCCAGTAACACACAGAGAGAGCATAGGCCA 2807

FILE REFERENCE: 210121.484C8
 ; CURRENT APPLICATION NUMBER: US/10/361,811
 ; CURRENT FILING DATE: 2003-02-05
 ; NUMBER OF SEQ ID NOS: 293
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 252
 ; LENGTH: 5333
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-361-811-252

Query Match 44.1%; Score 935.4; DB 17; Length 5333;
 Best Local Similarity 70.7%; Pred. No. 3.2e-248;
 Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTCAACATGCGCGCGGAGTGGCGGCTGCTGCTTTTGGCCGGGCTGGCCATCGG 125
 Db 959 AGTATCATGCGCGCGGAGTGGCGGCTGCTGCTTTTGGCAAGGCGGCTATCGG 1018
 QY 126 GTGATGCGCGGAGCAACTGCGCCATGCGCCCTGCGCCC--GGCCGACAAAGAACGC 182
 Db 1019 GTGATGCGCTGTGCGCTTGGCGGCTTATGCGGCTCCCGCCGAGGAGAGAGAAAGAC 1078
 QY 183 GCAGATGAGTGAATGTTCTCTCAACGTGATGGCGGAGTTTCCAGACTGAGAGAACAC 242
 Db 1079 CCAAGATGCTCTCATTTGCTGTAATGTGATGGACACCCGCTTCCAGACTGGCAGAGAC 1138
 QY 243 GCTGAGCGCTTACCCGACACCTGCTGGGCAAGCAGGAGAGAGAGTCTTCTTCAAGCA 302
 Db 1139 CTTGGAAGCTTACCCAGACACTTACTGGGCAAGTCTGAGAGGAGACTTTTCTACACCC 1198
 QY 303 GGACACCAAGAGTACTTCTTCAACCGGAGACCCCGAGGTGTTCCGTCGTCATCACTT 362
 Db 1199 AGAACTCAGAGATATTTCTTGAACCGTGAACCCAGACATCTTCCGCACTGTGAATTT 1258
 QY 363 CTACCGCAAGGAGAGTCTGACTTACCCGCTGCTGAGTGAATCTTGGCTTACAGAGCA 422
 Db 1259 CTACCGCAAGGAGAGTCTGACTTACCCGCTGCTGAGTGAATCTTGGCTTACAGAGCA 1318
 QY 423 GCTGCGCTTCTACGCGATCTTCCGAGATCATCGGAGATCTGCTGCTGCTGCTGCTGCT 482
 Db 1319 ACTGCGCTTCTTGGCTTATCCCGGAATCATCGGAGATCTGCTGCTGCTGCTGCTGCT 1378
 QY 483 GGACCGCAAGAGAGAGAGAGCGCGGCTCATGAGCAGAAAGACTGAGAGAGAGAGAGCA 542
 Db 1379 GGATTCGAGGAGAGAGAGAGAGCGCGGCTCATGAGCAGAAAGAGATACCGAGAGAG 1438
 QY 543 GGAG--TCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
 Db 1439 GGAAGCGCTTGGCCACATGATCTGAAAGGAGAGGCTGAGAGGCTTCAAGAGAGAG 1498
 QY 600 CCAACACAGACGCTGCGCTGCTTCTTCACTAGCTGAGTCTTCTTCACTGCTGCTGCTGCT 659
 Db 1499 CCACACAGACGATGCGCTGCTGCTTCTTCACTAGCTGAGTCTTCTTCACTGCTGCTGCT 1558
 QY 660 GGTATCAACCAAGTGTGAGAGAGCGGTGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 716
 Db 1559 TGTATCGCGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1618
 QY 717 GCTGCGTGGGAG 776
 Db 1619 ACTGCGCTGAG 1678
 QY 777 GATCTTCAACGTTGAGTACTTCTGCGGCTCTTCCGCGGCTCCAGCGGCTTACCGCTTCA 836
 Db 1679 GATCTTCAACGTTGAGTACTTCTGCGGCTCTTCCGCGGCTCCAGCGGCTTACCGCTTGT 1738
 QY 837 CCGAGCGTATGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
 Db 1739 GCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1798
 QY 897 CATGACCAACAG 956

RESULT 8
 US-10-361-811-252
 ; Sequence 252, Application US/10361811
 ; Publication No. US20030206918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER


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Db 1799 GATGACAGACAATGAGACGTCAGCGAGCCCTTGTCACTCCGAGTCTTCCGGTCTT 1858
Qy 957 CAGGATCTTCAAGTTTCCCGCCACTCCAGGCGCTGCGATCTGGGCTACACACTGAA 1016
Db 1859 CAGGATCTTAAAGTTTCCCGCCACTCTCAAGGCGCTGCGATCTGGGCTACACACTGAA 1918
Qy 1017 GAGCTGTGCTCCGAATGCGCTTCTTCTCTCTCCCTACCATGGCCATCATCTT 1076
Db 1919 GAGTGTGCTCAGAAATGGGCTTCTGCTTCTCTGCTCCTACCATGGCTATCATCTT 1978
Qy 1077 TGCCACTGTGATGTTTATGCGAGAAAGGCGCTCCGCGCAAGATTCAAGCATCCC 1136
Db 1979 CGCTACAGTATGTTCTACGAGAGAAAGGGGTCTTCGCTAGCAAGTTCAACGATCCC 2038
Qy 1137 TGCCCTGTTTGGTACACCATGTACCATGACACACTGGGATACGAGACATGTGC 1196
Db 2039 TGCAAGCTTCTGTATACCATGCTACCATGACACACTAGGGTATGGTACATGTGC 2098
Qy 1197 TAAAGCATGTCAGGGAAGATCTTGGGCTCCATCTGCTCTTGAAGGCGTCCGTGAT 1256
Db 2099 AAAAAACATAGCAGGGAAGATTTTGGTCTATCTGTTCCGTGAGTGGGGTCTTGTGAT 2158
Qy 1257 TGCCCTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACCAACAGATCAGG 1316
Db 2159 TGCTTACTGTTTCCGCTGATGTTTATCCAACTTCAAGTCCGATCTACCAACAGATCAGG 2218
Qy 1317 AGCTGATAACGACGAGGCACAAAAGAGGCGCGCTTGCCAGATCCGTGTGGCAAAAC 1376
Db 2219 AGCAGACAAACGAAAGGCACAAAAGAACTAGACTGCGCAGATCCGCGAGCCAAAG 2278
Qy 1377 AGGAGTTGCAATGATACCTGTCACAGACGCGCAAGCGGCTCTCAACGAGGCGTGA 1436
Db 2279 CGGAAGCGCAATGCTTACATGACAGAGCAACGAAATGTTTACTCAATACATGCA 2338
Qy 1437 GCTGACGGGCAACCCAGAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCA 1496
Db 2339 GTCTCAGAGGA---TGAGCAGGCTTTTGTAGCAATCCGCGCTCAGGCTTGAACCA 2395
Qy 1497 GCATCATCACTGTGTCAGCTGCTGAAAAAAACCACTGGGTGTCTATCTTGTGATGA 1556
Db 2396 GCACCAACCACTGTCTTCACTGCTGAAAAAACCACT----- 2431
Qy 1557 TCCCCGTATCTGTACGAACCTCCACCATCAAGAACGAGTTTATGTAGACAGAT 1616
Db 2432 -----GATCAGAGTTTGTGAGCAAACT 2458
Qy 1617 GTTTAGCAGACCTGATGAGAGTTCAATGACAACTACCATCCACAAAGATCCCTC 1676
Db 2459 CTTTGAAGAAAGCTGATGAAAGTTGCACTGTATCTTCAAGTCAAGTCCCTTC 2518
Qy 1677 ACTGTCCAGCCACCGAGGCTCTCACTACCTGTGCTCCGCTGTAAGTAAGAACCA 1736
Db 2519 ACTGTCTTCAACAAGAGAGTCACTGCTGTTTCAAGACGACACAAAAAACTTT 2578
Qy 1737 AACCTGCCCAATTTAACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
Db 2579 TCGCATCCCAATGCAATGTATCAGAAAGCCATCAAGGTATATACAAAGAACTCAGC 2638
Qy 1797 GATTCACATCCAGGAGAGTGAAGAGCCCTCCCTCAACCAAGTCCGCTCAGGCTTAATT 1856
Db 2639 GATTTCAGATCAGATGTGTGAGAGAACACTCTGTCTTAAACAGCCGATCCAGTTTAAATGC 2698
Qy 1857 GAAAGCAGACGAGCTGAGACCAAACTGCAAAACATCCAGATCACCAGACCATCAT 1916
Db 2699 CAAATGAGAGAGTGTATTAATTAACCTGTGAACAACCTTATGTGACTACAGCAATAT 2758
Qy 1917 CAGCATCCCACTCCCGAGCGCTAACCCAGAGGGGAAAGTCCGCCA 1965
Db 2759 AAGCATCCCAACACCTCCAGTAAACACACAGAAAGAGCATAGGCCA 2807
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RESULT 9
US-10-361-811-254

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Sequence 254, Application US/10361811
Publication No. US20030206918A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 254
LENGTH: 5333
TYPE: DNA
ORGANISM: Homo sapiens
US-10-361-811-254

Query Match 44.1%; Score 935.4; DB 17; Length 5333;
Best Local Similarity 70.7%; Pred. No. 3.2e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

Qy 66 AGTCACCATGCGCGCCGAGTGGCGGCTGGCTGCTTTTGCCTGGGCTGGGCGCATCGG 125
Db 959 AGTAATATATGCGCGCGGCGGCTGGCGAGCTGGCTGCTTTTGCAGAGGCGAGGCTATCGG 1018
Qy 126 GTGATGCGGCTGCGCACTGCCCATGCGCCCTGCGCCG---GGCGCAAGAAAGAGCG 182
Db 1019 GTGATGCTGTGCGCTCGGCGGCTTATGCGCGCTCCCGAGGAGAGAGAAAGAGAC 1078
Qy 183 GCAGATGAGCTGATGTCTCTCAACGTAGTGGCGGAGGTTCCAGACCTGAGAGACAC 242
Db 1079 CCAAGATGCTCTCATTTGTGTAATGTAGTGCAACCCGCTTCCAGACGTGCGAGAGAC 1138
Qy 243 GCTGAGGCGTACCCGAGACCCCTGCTGGGCGAGACGAGAGAGAGTCTTCTCAACGA 302
Db 1139 CCGGAAGTATACCAAGACCTACTGAGGCGAGTCTGAGAGGAGCTTTTCTACCAACC 1198
Qy 303 GGACACCAAGAGTACTTCTTGAACCGGAGACCCGAGGTGTCGCTGCTGCTCACTT 362
Db 1199 AGAAACTGACAGATATTTCTTTGACCGGTGACCAAGACATCTTCCGACACATCTGAAATT 1258
Qy 363 CTACCGCAGCGGGAAGCTGCACTACCCGCGCTACAGATGATCTTGTCTTACAGACGA 422
Db 1259 CTACCGCAGTGGGAAGCTCACTATCTTCCGACGAGTGCATCTGTCTTACATGAGA 1318
Qy 423 GCTGCGCTTCTACGCGCATCTCCCGGAGATCATGCGGAGCTGCTGCTACGAGAGTAA 482
Db 1319 ACTGGCTTCTTGGCTCTCATCCCGGAATCATTCGCGCATGCTGTATGAGAGTCAAA 1378
Qy 483 GGAACGAGAGAGAGAACGCGGAGGCTCATGAGACCAACGACTCGGAGAACCA 542
Db 1379 GGAATGAGAGGAGAGAACGCGGAGGCTGAGAGACGAGCGGATACCGACACCGCTGG 1438
Qy 543 GGAAG---TCCATGCGCTCGCTCAGCTCCGCGAGACCATGTGCGGCGCTTGAAGAAC 599
Db 1439 GGAAGAGCGCTTGGCCACCAATGACTGCAAGGAGAGAGGTCTGAGAGGCGCTTGAAGAAC 1498
Qy 600 CCAACACGACAGCTGCGCTGTGCTTCTACTAGTGAAGTGGCTTCTTCACTGCTGCTC 659
Db 1499 CCAACACGACAGATGCGCTGTGCTTCTACTAGTGAAGGAGTCTTCTTCACTGCTGCTC 1558
Qy 660 GGTATACCAACGTGTGAGAGCGGTGCGCGGCGGACGCTCCCGG---CAGCAAGA 716
Db 1559 TGTCTATCGGGAATGTGTGAGAAACAGTCCGCGGATCAAGCCAGGTCACTAATAAGA 1618
Qy 717 GCTGCGGTGCGGAGCGCTACTCGGTGCTTCTTCTGCTGAGACAGGCGTGGCTGAT 776
Db 1619 ACTGCCCTGTGAGAGCGGTATGTCTGTGCGCTTCTTCTGCTTGAACAAGCGCTGCGTAT 1678
Qy 777 GATCTTCAACCGTGAATCACTCTGCGGCTCTTTCGCGGCTCCAGCGCTACCGCTTAT 836
Db 1679 GATCTTCAAGTTGATATTGCTTGCCTGCGCTGAGCGGCTTATGCTTACCGTTTGT 1738
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QY 717 GCTGCCGCGGGAGCGCTACTCGGTGGCCCTTCTTCTGCTGAGACAGCGGCGCTGAT 776
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Db 1619 ACTGCCCCCTGTGAGAGCGGTATGCTGTGCGCTTCTTCTGCTTGACACGGCGCTGCGTAT 1678
QY 777 GATCTTCAACCGTGAGTACCTTCCTGCGGCTCTTTCGGGCTTCCAGCCGCTACCGCTTAT 836
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1679 GATCTTCAAGTGAATATTGCTTGGCTGCGCTGAGCGCCCTAGTCGTTACCGTTTGT 1738
QY 837 CCGCAGCGCTCATGAGCATCATCGACGTGTGGCCATCATGCGCTTACTACATCGGTCTGTT 896
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1739 GCGTAGTGTATGATGATCATCGACGTGTGGCCATCCGCTTATTAATGAGGCGTGGT 1798
QY 897 CATGACCAACAACGAGAGCTGTCCGCGCTTCTGTCACGCTCCGCGCTTCTCCGCTT 956
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1799 GATGACAGACAATGAGAGCGCTGACGCGAGCCCTTGTCACTCCGAGCTTCTCCGCTT 1858
QY 957 CAGGATCTTCAAGTTTTCGCGCACTCCAGGCGCTGCGGATCCGAGTCCGAGCTACACTGAA 1016
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1859 CAGGATCTTAAAGTTTTCGCGCACTCAAGGCGCTGCGGATCCGAGTCCGAGCTACACTGAA 1918
QY 1017 GAGCTGTGCTCCGAACCTGGGCTTCTTCTTCTCCCTCAACATGCGCATCATCTT 1076
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1919 GAGTGTGCTCAGAAATGGGCTTCTTCTTCTCGCTCAACATGCGCATCATCTT 1978
QY 1077 TGCCACTGTGATGTTTATGCGCGAAGAGGCTCTCGGCGCAAGTTCAACAAGATCCC 1136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1979 CGCTACAGTATGTTCTACGAGAGAGAGGGGTCTTCGGCTAGACAAATTCACCAAGATCCC 2038
QY 1137 TGCCCTGTTTGTATACACCATTTGTACCATGACCACTGAGATACGAGACATGTTGCC 1196
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Db 2039 TGACGCTTCTGTATACCATCTGTACCATGACCACTAGGATGATGATGATGATGCC 2098
QY 1197 TAAAGCAGTTGACGAGAGATCTTCGCTCCATCTGCTCTTGAAGTGGCGTCTGTAT 1256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2099 AAAAAACCAATAGCAGGAGATTTTGGTTCTATCTGTTCGCTGAGTGGGGTCTTGTAT 2158
QY 1257 TGCCCTGCGAGTCCCTGTGATGTTTCCAACTTAGCCGATTTACCAACAGATCAGAG 1316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2159 TGCTTACTCTGTTCCGGTGTATGTATCCAATTCAGTCCGATCTACCAACAGATCAGAG 2218
QY 1317 AGCTGATTAACGACGAGGACAAAGAGGCGCGCTTGCCAGATCCGTGTGGCCAAAG 1376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2219 AGCAGACAAACGAAAGGACAAAGAAAGCTAGACTGGCCAGATCCGGGCGAGCCAAAG 2278
QY 1377 AGCGAGTTGAATGATACCTGTCACAGACGCGCAACGGGCTCTCAACGAGCGCTGA 1436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2279 CGAAAGCGCAATGCTTACATGACAGACAAACGAAATGTTTACTCAATATCAAGTGA 2338
QY 1437 GCTGACGGGACCCGCAAGAGAGACATGAGGCAAGACCACTCATCTCATGAGAGCCA 1496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2339 GTCCCTCAGAGGA--TGACAGGCGCTTTTGTAGCAAAATCCGGCTCCAGCTTGAAGCCA 2395
QY 1497 GCATCATCACCTGTGCACTGCTGGAAGAAACCACTGGGTTGTCTTATCTTGTGATGA 1556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2396 GCACACCACTGCTTCACTGCTGGAAGAAACCACTGCTGCTGCTGCTGCTGCTGCTGCT 2431
QY 1557 TCCCTGTATATCTGTAAGAACTCCACATCAAGAACACAGATTTATGATGACAGAT 1616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2432 -----GAATCAGAGATTGTGAGCAACAGT 2458
QY 1617 GTTTGACAGAACTGATGAGAGTTCAATGACAGAACTACCATCAACAAGAGTCCCTC 1676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2459 CTTTGAAGAAAGCTGATGAAAGTTGCAACTGTATATGCTTCAAGTCAAGTCTCTTC 2518
QY 1677 ACTGTCCAGCACCGAGGCTCACTACACCTGCTGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 1736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2519 ACTGTCTTCAACAACAGAGATACACAGACCTGCTGCTTCAAGACGACACAAAAAACTTT 2578
QY 1737 ACACTGCGCAATTTAACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2579 TCGCATCCCAAAATGCAATGTATCAGAGAAAGCCATCAAGGATATACAAAGATCAAGCAC 2638
QY 1797 GATCCACATCCAGGAGTGAAGACGCTCCCTCAACAACCAAGTCCGCTCAAGCTTAATT 1856
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Db 2639 GATTCAGATCAGATGTGTGAGAGAGAACACCTCTGTCTTAACAGCGCATCCAGTTAAATGC 2698
QY 1857 GAAAGACAGACGAGCTGAGACCAAACTGCAAAACATCCAGATCAACACAGCCATCAT 1916
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2699 CAAAATGGAAGAGTGTATTAACATAACTGTGAACAACCTTATGTACTACAGCAATTAAT 2758
QY 1917 CAGCATCCCACTTCCCCAGCGCTAAACCCAGAGGGGGAAGTCCGCCA 1965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2759 AAGCATCCCAACCTCCAGTAACCAACACAGAGAGAGATAGGCCA 2807

RESULT 11
US-10-369-186-254
; Sequence 254, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-254

Query Match 44.1%; Score 935.4; DB 17; Length 5333;
Best Local Similarity 70.7%; Pred. No. 3.2e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTACCAATGCGCGCGAGTTGGCGCTGCTGCTTTGCGCGGCTGGGCCATCGG 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 959 AGTAATCATGCGCGCGAGGTGGCAGCGTGGCTGCTTTGCAAGGCGAGCGCTATCGG 1018
QY 126 GTGATGCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAACAAGCG 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1019 GTGATGCTGTGCGCTCGGGGCTTATGCCGCTCCCCGAGGACGAGAGAAAGAGAC 1078
QY 183 GCAAGATAGCTGATTTGTCTCAAGTGAAGTGGCGGAGCTTCCAGACCTGAGAGACAC 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 CCAAGATCTCTCATTTGTGTGAATGTAGTGACACCGCTTCCAGACGTGGCAGACAC 1138
QY 243 GCTGAGCGCTAACCCGACACCTGTGTGGGACAGCAGCAAGAGAGTTCTTCAACGA 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1139 CTTGAAGTTTACCCAGACACTACTGCGGAGTTTGAGAGGAGCTTTTCTACCAACC 1198
QY 303 GGAACCAAGAGTACTTCTTCCAGCCGGAACCCGAGGTGTTCCGCTGCTCAACTT 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1199 AGAAATCAGACAGTATTTCTTGAACCGTGACCAAGACATCTTCCGCCACATCTGAATT 1258
QY 363 CTACCGCAGCGGGAAGCTGACCTACCGCGCTACGAGTGCATCTGCTTACGAGACGA 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1259 CTACCGCACTGGGAAGCTCCACTATCTTCGCAAGAGTCATCTGCTTACGATGAAGA 1318
QY 423 GCTGCGCTTCTACGCGATCTCCCGAGATCATCGGGAAGCTGCTGCTACGAGAGTACA 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1319 ACTGCGCTTCTTGGCTCTCATCCCGGAATCATCGGCGAGCTGCTGTTATGAGAGTACAA 1378
QY 483 GGAACCGAAGAGAGAACCCGAGCGGCTCATGGAACGACAACTCGGAGAACAAACA 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1379 GGATCGAGGCGGAGAAACCGAGGCGCTGACGAGACGCGGATACCGAACCGCTGG 1438
QY 543 GGAG--TCCATGCGCTGCTCAGCTTCCGCAAGACCATGTGGCGGCGCTTGAAGAACCC 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1439 GGAGAGCGCTTGGCCACCATGACTGCAAGGAGAGGCTGTGAGAGGCGCTTGAAGAACCC 1498
QY 600 CCAACACGACACGCTGGCGCTGCTTCTACTACGTGACTGGCTTCTTCAATCGCTGCTC 659
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Db 1499 CCACACGACGATGCGCTGTCTTCTACTATGATGACGCGGTTTTCATTTGCGCTCTC 1558
Qy 660 GGTATCATCAACAGTGTGGAGAGCGGTGCGGCGACGTTCCCGG---CAGCAAGA 716
Db 1559 TGTCTCGCGAATGTGTGGAAACAGTCCGTGCGGATCAAGCCAGGTCACTTAAAGA 1618
Qy 717 GCTGCGGTGCGGGAGCGCTACTGCTGCTTCTTCTGCGCTGGACAAGCGGTGCGTCT 776
Db 1619 ACTGCGCTGTGAGAGCGGTATGCTGTGCTTCTTCTGCTTGGACACGCGCTGCGTCT 1678
Qy 777 GATCTTCAACCGTGAAGTACTCTGCGGCTCTTCCGCGCTCCAGCGCTTACCGCTTCT 836
Db 1679 GATCTTCAAGTTAGTATTTGCTTCCGCTGCGCTGACGCGCTTATGCTTACCGTTTGT 1738
Qy 837 CCGCAGCGTCAATGAGCATCATGACGTGTGGCCATATATGCCCTACTACATCGGTGTGT 896
Db 1739 GCGTAGTGTCAATGAGTATCATGAGTGTGGCCATCTGCTTATTAATGAGGTGCTGT 1798
Qy 897 CATGACCAACAGAGAGCGTGTCCGCGCGCTTCTGTCACGCTCCGGGTCTTCCGCGTCT 956
Db 1799 GATGACAGACATGAGGACGTGACGCGGAGCGCTTGTCTACATCCGAGTCTTCCGCGTCT 1858
Qy 957 CAGATCTTCAAGTTTTCGCGCACTCCAGAGCGCTGCGGATCTTGGGCTACACACTGAA 1016
Db 1859 CAGATCTTCAAGTTTTCGCGCACTCTCAAGCGCTGCGGATCTTGGGCTACACACTGAA 1918
Qy 1017 GAGCTGTGCTCCGACCTGCGGCTTCTTCTTCTTCTCCCTCACCATGGCCATCATCTT 1076
Db 1919 GAGTGTGCTCCAGAAATGCGGCTTCTTCTTCTTCTGCTCACCATGGCTATCATCTT 1978
Qy 1077 TGCCACTGTGATGTTTATGCGGAGAGGCGCTCTCGGACAGCAAGTTTCAAGCATCCC 1136
Db 1979 CGTACAGTTATGTTCTACGAGAGAGGCGCTTCTCGGCTAGCAAGTTTCAAGCATCCC 2038
Qy 1137 TGCTCTGTTTGTGTACACCATTTGTCAACATGACCACTGGGATACGAGACATGTTGCC 1196
Db 2039 TGCAGCTTGTGTATACCATGTCATGACATGACATGAGGATGATGATGATGATGATGAT 2098
Qy 1197 TAAAGCATGAGGAGGAGATCTTGGGCTCCATCTGCTCCTTGAATGGGCTCTGCTCAT 1256
Db 2099 AAAAACATAGAGGAGGAGATTTTGGTCTTATCTGTTGCTGAGTGGGCTCTTGTCTAT 2158
Qy 1257 TGCTCTGCGAGTCTCTGTGATTTTTCAACTTAAAGCGGATTTACACAGATTCAGAG 1316
Db 2159 TGCTCTACCTGTTCCGCTGATTTGATTCACATTTCACTGATTCATCCACAGATTCAGC 2218
Qy 1317 AGCTGATTAACGAGGAGCAAAAGAGGCGCTTGGCAGGATCCGCTGGCCAAAC 1376
Db 2219 AGCAGACAAAGAGGAGCAAAAGAGGAGTACTGAGGAGGAGGAGGAGGAGGAGGAGG 2278
Qy 1377 AGGCACTTGAATGATCTCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1436
Db 2279 CGGAGCGCAATGCTTACATGAGAGCAAAAGGAGTGTACTGATGATGATGATGATGAT 2338
Qy 1437 GCTGACGGGAGCAACCCAGAGAGAGAGACATGGGCAAGACCACTCACTATGAGAGCCA 1496
Db 2339 GTCTCTAGAGGA---TGAGCAGGCTTTTGTAGCAATCCGGCTCCAGCTTTGAACCCA 2395
Qy 1497 GCATCATCACTGCTGACCTGCTGAGAAACCACTGGGTTGTCTATCTTGTGATGA 1556
Db 2396 GCACCAACCACTGCTTCACTGCTGAGAAACCACTGCTGCTGCTGCTGCTGCTGCTG 2431
Qy 1557 TCCCTGTATCTGTAGCAACCTGCAACATCAAGAACCAAGAGTTTATGATGAGAGAT 1616
Db 2432 -----GAATCAAGAGTTTGTGAGCAAGCAAGT 2458
Qy 1617 GTTGTAGAGAACTGATGAGAGTTCAATGAGAACTAACCACTCAAGAGAGTCCCTC 1676
Db 2459 CTTTGAAGAAAGCTGATGAGAGTTGCAAGTGTAAATGCTTCAAGTCAAGTCAAGTCTTC 2518
Qy 1677 ACTGTCCAGCAACCCAGGCTCACTACCACTGCTGCTCCGCTGTAGTAAAGAACCAAC 1736
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Db 2519 ACTGTCTTCAACAAGAGTACACGACCTGCTGTTCACGACGACCAAAAACTTT 2578
Qy 1737 ACACGTGCCCAATTTCTAATCTGCGAGTACTGCGCTGCGAGCATGAGAGCTCAGAC 1796
Db 2579 TCGCATCCCAATGCGAATGTATCAAGAAAGCATCAAGTATATCAAGAACTCAGCAC 2638
Qy 1797 GATTCATCAAGGAGGAGTGAAGAGCGCTTCTTCTCAACCAAGTGTCTCAGCTTAAATT 1856
Db 2639 GATTAGATGATGATGTGTGAGAGAGAACCTCTGTCTTACAGCCGATTCAGTTAAATGC 2698
Qy 1857 GAAAGCAGACGAGCTGAGACCAAACTGCAAAATCCAGATCAGCAGCATCAT 1916
Db 2699 CAAATGGAAGAGTGTGTTAACTGTAACAACTTATGTGACTACAGCAATAT 2758
Qy 1917 CAGCATCCCACTCCCGCAGCGCTTAAACCCAGAGGAGGAGGAGGAGGAGGAGGAG 1965
Db 2759 AAGCATCCCAACCTCCAGTAAACACACAGAGAGAGAGAGATAGGCCA 2807
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RESULT 12

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US-10-121-746-9
; Sequence 9, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-10-121-746-9
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Query Match 37.6%; Score 798.2; DB 14; Length 3424;
Best Local Similarity 72.8%; Pred. No. 2.7e-210;
Matches 1079; Conservative 1; Mismatches 379; Indels 24; Gaps 3;

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Qy 65 GAGTACCATGAGGCGGCGGAGTGTGCGGCTGCTGCTTTTCCCGGCTGCGGCATCG 124
Db 249 GTGCAAGATGCGGCGGAGGCGCTGCGCAAGTGTGCTGCTTTCGCGCAGACAGTGG 308
Qy 125 GTGTGATGCGGTGCGCAACTGCGCCCATGCGCCCGGCGGCGGAGCAAGAACGCGC 184
Db 309 GCTGCTGCGCGCGCGCGCGCAACCCCTGCGCGCGGCGGCGGAGGAGCATCTCGAG 368
Qy 185 AGATGAGCTGATTTGTCTCAAGCTGATGAGGCGGAGGTTCCAGACCTGAGAGCACGCG 244
Db 369 GAGATGAGGTTCTGTGTGTAACGTGAGCGGAGCGGCTTGAAGACTGGAAGATACGC 428
Qy 245 TGAAGCGTACCCGAGCAACCTGCTGGGAGCAGCAGAGAGAGTCTTCTTCAAGAGG 304
Db 429 TGAACGCTTACCCAGACACCTTGTCTGGGAGCTCGGAGAGAGATTTCTTACAGTGTG 488
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OY		303	ACACCAAGAGACTTCTTCGACC GGAA CCCC GAGTGTTCCGCTGCCTCAACTTCT	364
Db		489	ACTCAGGGCGAATCTTTCGAATCGGACCC TGCATATGTTCGCCCATGTGCTGAATTCT	548
OY		365	ACCGCACGGGGAGA CTGCTACT ACCCGCGCTACGAGTG CATCTTGCTTACGACGAGC	424
Db		549	ACCGAACGGGGCGCTGATTTGCCACCGCAGGAGTG CATTCAGGCTTCACGAAGAGC	608
OY		425	TGGCTTCTACGGGCA TCCTCC CGGAGATCATCGGGAGCTGCTGCTACGAGAGTACAAG	484
Db		609	TGGCTTCTACGGGCTGTTC CCAGCTAGTCGGTGACTGCTGCTTGAAGATAATGGG	668
OY		485	ACCGCAAGAGGAGAA CGCCGAGCTGCTATGACAGCAAACGACTGGGAGAACCAAG	544
Db		669	ACCGAAAGAGAGAA TGCCGAGCGCTGGCAGAGGATGAGGAGGACGAGCGCGGG	728
OY		545	AGTCCATG CCTCGC-----TCAGCTTCGGCAGACCATGTGGCGGGCTTCGAGA	595
Db		729	ACGGCCAGCCTCTGCCAGACGACGTCCCTGCGGACGGCTCTGGCGGCTTCGAGA	788
OY		596	ACCCCCACACCA GACCGCTG GCCCTGTCCTTA CTACGTAGCTTGCTTTCATCGCTG	655
Db		789	ATCCACACACGACGACCGCAGCCCTGTTTTCTACTATGTGACCGGCTTTCATCGCG	848
OY		656	TCTCGGTATCA CCAACGTGTGTGAGACGSGTCCGTGCGGACAGTCCCGGACG----	710
Db		849	TGTCGGTATCGCCAA TGTGTGAGAACCATCCCATGCGGGGCTCTGCACGCAAGTCT	908
OY		711	-CAAGAGCTGCGCTGCGGGGAGGCGCTACTCGTGACCTTCTTGCTGGAACAGCGT	769
Db		909	CAAGGAGACGCTGTGTGGCAACGCTTCCACAGGCTTTTCTGTGATGACACAGCT	968
OY		770	GCGTCATGATCTTCA CCGGTGAGTACTCTGCGGCTCTTTCGCGGCTCCAGCCGCTAC	829
Db		969	GTTACTCATATTTCA CAGGTAAATACCTCTGCGGCTGTTTGCCGCCCCCAAGCCTTGCC	1028
OY		830	GCTTCATCCGCA GCGTCA TGAACA TCA TGCACGTGTGGCATCATGCCCTACTACATCG	889
Db		1029	GCTTCCGCGGAGTGTCA TAGGCTCATGACGTGTGGCATCTGCCCTACTACATTG	1088
OY		890	GTCTGTCATGACCA CAACGAGGAGCTGTCCGGGCTTGCTACGCTCGGGTCTTCC	949
Db		1089	GACTTTTGTGCCCA GAACGACGATGTCTGTGGGCTTTGTCA CCGTGTGTCTCC	1148
OY		950	GCGTCTTCAGGATCTTCA AGTTTTTCCCGCACTCCACGAGGCGCTGCGATCTGGGCTACA	1009
Db		1149	GGGTGTTTCGCA TCTTCAAGTTCTTCCAGGCACTCACAGGGCTTGAGGATTTGGGCTTACA	1208
OY		1010	CAC TGAAGAGCTGTGCTTCCGA ACTGGGCTTCTTCTCTTCCCTCA CCAATGGCCATCA	1069
Db		1209	CAC TGAAGAGCTGTGCTTGA GCTGGGCTTCTCTTTCCTTA ACATGGCCATCA	1268
OY		1070	TCATCTTTGCCA CTGTGATGTTTTATGCGAGAGGGGCTCTCGGCCAGCA GTTCAA	1129
Db		1269	TCATCTTTGGCA CTGTCA TGTTTTATGTGAGAAAGGGCACAAACAAGACCACTTTACAA	1328
OY		1130	GCATCCCTGCGCTGTTTTGGTACA CCA TTGTCA CCA TGAACCA CACTGGGATACGAGACA	1189
Db		1329	GCATCCCTGCGGCTTCTGTGTATACCATGTGTCA CCA TGAACCA CGCTTGGCTACGAGACA	1388
OY		1190	TGTTGCTTAAGACGATTG CAGGGAA GATCTTCCGCTTCATCTGCTCTTGA GTGGCTCC	1249
Db		1389	TGTTGCTTAAGACCA TTTGTG CAGGATTTTCCGGGTCCATCTGCTCACTCA GTGGCGCTCT	1448
OY		1250	TGTTCA TTTGCCCGCAGTCCCTGTG ATTTTCCA ACTTTAGCCGGA TTTACCA CCGA	1309
Db		1449	TGTTCA TTTGCCCGCTGTG CAGTCA TTTGTCCA ACTTTAGCCGGA TTTACCA CCGA	1508
OY		1310	ATCAGAGAGCTGATAAA CGCAGGGCA CAAAAAGAGCCGCTTGCCA GATTCGTGTGG	1369
Db		1509	ACCAGCGGGCTGACAAGCGCCGAGACAGAGAAAGGTGCGCTTGGCAAGATCCGATTGG	1568
OY		1370	CCAAAACAGGCA GTTCCA TGCATACCTGCA CAGCAAGCGCAACGGGCTCTTCAACGAG	1429

Db	1569	C A A A G A G T G T A C C A C C A A T G C T T C C T G C A G T A C A A G C A G A A T G G G G C C T T G A	1623
Qy	1430	C G C T G A G C T G A C G G G C A C C C C A G A A G A G A G C A C A T G G G C A A G A C C A C T C A C T A T C G	1489
Db	1624	---G S A C A G C G G C A G T G G C G A G A A C A G G C T T T G T G C A G A A C G T T C T G C C T T G	1679
Qy	1490	A G A G C C A G C A T C A T C A C C T G C T G C A C T G C C T T G A A A A A A C C A C	1532
Db	1680	A A C A G C A C A T C A C C A C T T G C T G C A C T G T C T A G A G A G A C A A C	1722

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RESULT 13
US-10-296-115-373
; Sequence 373, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hysq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-296-115-373

```

Query Match	37.5%;	Score 795.4;	DB 17;	Length 2578;
Best Local Similarity	72.9%;	Pred. No. 1.5e-209;		
Matches 1075; Conservative	0;	Mismatches 376;	Indels 24;	Gaps 3;

QY	73	ATGCGGCGCCGAGTGGCGGCTTGCTGCTTTTGGCCGGGCTGCGGCATCGGGTGAATG	132
Db	1	ATGGCGGCAGGCGCTGGCCACGTGGCTGCTTTTGGTCGGGGACGACAGTGGGCTGGCTG	60
QY	133	CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCGACAGAAACAAGCGGCAGATGAG	192
Db	61	CCCCGTGGCCCAACCCCTGCCCCCGGACACCGGGGGTGAAGGCATCTCGAGAGATGAG	120
QY	193	CTGATGTCCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACACCGCTGGAAGCGC	252
Db	121	GTTCTGGTGTGAACGTGAGCGGACGCGCTTTGAGACTTGGAAATACGCTGGACCGC	180
QY	253	TACCCGGACACCCTGTGGGCGAGCAGCAGAAAGAGTTCTTCTTCAACGAGACACCAAG	312
Db	181	TACCCAGACACCTTGCTGGGCGAGCTCGGAGAAAGGAATTTCTTACGATGCTGACTCAGGC	240
QY	313	GAGTACTTCTTGACACCGGGGACCCCGAGGTTGTCGGTGGCGTGCTCAACTTCTACCGCACG	372
Db	241	GAGTACTTCTTGAGTCGGACCCCTGACACATGTTCCGCGCATGTGCTGAACTTCTTACCGAACG	300
QY	373	GGGAAGTGCACTACCCGCGCTACGAGTCATCTTGCTTACGACGACGAGCTGGCTTTC	432
Db	301	GGGCGGCTGCATTGGCCCACGGCGAGAGTGCATCCAGGCTTTCGACGAAAGCTGGCTTTC	360
QY	433	TACGGCATCTCCCGGAGATCATCGGGGACTGCTGCTACGAGAGTCAAGAACCGCACG	492
Db	361	TACGCGCTGTCTCCGAGCTAGTCGGTGACTGTGCTTGAAGAGTATCGGGACCGAAAG	420
QY	493	AGGGAGAACCGCAGCGGCTCATGAGACGACACGACTCGGAGAACACGAGACTCCATG	552
Db	421	AAGGAGATGCGAGCGCTTGGCAGAGAGATGAGAGGCGACGAGCGGGACCGGCCA	480
QY	553	CCCTGGCT-----CAGTTTCGCGCAGAACCATGTGGCGGGCTTCGAGAACCCCCAC	603
Db	481	GCCCTGCGACGAGCGAGCTCCCTGCGGCGACGCGCTCTTGGCGGGCTTTCGAGATCCACAC	540

QY 604 ACCAGCAGCTGGCCCTGCTCTTCTAAGTACTGCTGCTTCTTCATCGCTGTGCTC 663
 Db 541 ACAGACACCGAGCCCTGCTTTCTAATATGACCGGCTTCTTCATCGCGTGTGCTC 600
 QY 664 ATACCAACGCTGAGAGCGGTGCGGCTGCGGCTCCCGGAG-----CAAGAG 717
 Db 601 ATGCCAATGTGTGAGACCATCCATGCGGCTGTGACAGGAGTCTCAAGGAG 660
 QY 718 CTGCGGTGGGGAGCGCTACTCGGTGCTTCTTCTGCTTCTGAGACAGCGGTGCTCATG 777
 Db 661 CAGCCCTGTGGGAGCGCTTCCACAGGCTTCTTCTGATGAGACAGCGCTGTGATCTC 720
 QY 778 ATCTTACCGTGGAGTACTCTGCGGCTCTTCCGCGCTCCAGCGCTACCGCTTCATC 837
 Db 721 ATATTCACAGGTGATATCTCTGCGGCTGTTGCGGCCCGAGCGGTGCGCTTCTCCTG 780
 QY 838 CGAGCGTATGAGCATCATGACGTGTGCGCATCATGCTTCTTCTGATGAGTGTGCTGTC 897
 Db 781 CGAGTGTATGAGCTCATGACGTGTGCGCATCTGCGCTTCTTCTGATGAGTGTGCTG 840
 QY 898 ATGACCAACAGAGAGAGTGTGCGGCTTCTGATGAGTGTGCTTCTGCGGTCTTC 957
 Db 841 GTGCCAAGAGAGAGAGTGTGCGGCTTCTGATGAGTGTGCTTCTGCGGTCTTC 900
 QY 958 AGATCTTCAAGTCTTCCGCGCATCTCCAGGCGCTGCGGATCTGCGGTCTACACAGAG 1017
 Db 901 CGATCTTCAAGTCTTCCAGGCGCATCTCCAGGCGCTGAGGATCTGCGGTCTACACAGAG 960
 QY 1018 AGCTGTGCTTCCGAGCTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1077
 Db 961 AGCTGTGCTTCCGAGCTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
 QY 1078 GCCACTGTGATGTTTATGCGGAGAGAGGCTCTCGGCGAGCAAGTCTCAAGAGATCTCCT 1137
 Db 1021 GCCACTGTGATGTTTATGCGGAGAGAGGCTCTCGGCGAGCAAGTCTTCAAGAGATCTCCT 1080
 QY 1138 GCGTGTGTTGTTACACCATGTTGTTCAACCATGACACACCTGAGATCGAGACATGTGCT 1197
 Db 1081 GCGGCTTCTGTTATACCATGTTGTTCAACCATGACACACCTGAGATCGAGACATGTGCT 1140
 QY 1198 AAGACATTTGCGAGGAGAGATCTTGGGCTCCATCTGCTTCTTGAAGTGGCTGCTGCTAT 1257
 Db 1141 AGCACCATTTGCTGGCAAGATTTTGGGCTCCATCTGCTTCTTGAAGTGGCTGCTGCTAT 1200
 QY 1258 GCGTGTGTTGTTACACCATGTTGTTCAACCATGACACACCTGAGATCGAGACATGTGCT 1317
 Db 1201 GCGGCTTCTGTTATACCATGTTGTTCAACCATGACACACCTGAGATCGAGACATGTGCT 1260
 QY 1318 GCTGATTAACGAGAGGCACAAAAGAGGCGGCTTGGCGAGATCCGTGTGCGCAAAACA 1377
 Db 1261 GCTGATTAACGAGAGGCACAAAAGAGGCGGCTTGGCGAGATCCGTGTGCGCAAAACA 1320
 QY 1378 GCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
 Db 1321 GGTACCAACCATGCTTCTGCAAGTATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 1371
 QY 1438 CTGACGGGCAAGGAG 1497
 Db 1372 AGCGGAGTGGGAG 1431
 QY 1498 CATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1532
 Db 1432 CATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466

RESULT 14
 US-10-212-677-255
 ; Sequence 255, Application US/10212677
 ; Publication No. US20030129192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenault, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Fanger, Gary R.

; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: AND DIAGNOSIS OF OVARIAN CANCER
 ; CURRENT APPLICATION NUMBER: US/10/212,677
 ; CURRENT FILING DATE: 2002-08-02
 ; NUMBER OF SEQ ID NOS: 288
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 255
 ; LENGTH: 5404
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-212-677-255

Query Match 32.0%; Score 679; DB 15; Length 5404;
 Best Local Similarity 77.0%; Pred. No. 3.1e-177;
 Matches 868; Conservative 0; Mismatches 250; Indels 9; Gaps 3;

QY 66 AGTACCATGAGCGGCGGAGTGGCGCTGCTGCTTCTTGGCCCGGCTGCGGCGCATCGG 125
 Db 1362 AGTAATCATGCGCGCGGCGGAGCGTGGCTGCTTCTTGGCAAGGCGGCGTATCGG 1421
 QY 126 GTGATGCGCGGCGGCACTGCGGCGGCTGCGGCTTCTTGGCGGCGGCGGCGGCGG 182
 Db 1422 GTGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1481
 QY 183 GCAGATGAGTGTGATGCTTCTCAAGTGTGAGTGGCGGAGGTTCCAGACTGAGAGCAC 242
 Db 1482 CCAAGATGCTCATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1541
 QY 243 GCTGAGCGCTTACCGCGGCAAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 302
 Db 1542 CCGTGAAGCTTACCGCGGCAAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1601
 QY 303 GGACACCAAGAGTACTTCTTCAAGTGTGAGTGGCGGAGGTTCCGCTGCTGCTCACTT 362
 Db 1602 AGAATCTAGAGATTTCTTGAAGTGTGAGTGGCGGAGGCGGCGGCGGCGGCGGCGG 1661
 QY 363 CTACCGCAGCGGAGAGTGTGCTTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422
 Db 1662 CTACCGCAGCGGAGAGTGTGCTTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1721
 QY 423 GCTGCGCTTCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 482
 Db 1722 ACTGCGCTTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1781
 QY 483 GGACCGCAAGAGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 542
 Db 1782 GGATCGAGAGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1841
 QY 543 GGAG---TCCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599
 Db 1842 GGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1901
 QY 600 CCACACCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659
 Db 1902 CCACACCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1961
 QY 660 GGTATCATCAAGAGTGTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 716
 Db 1962 TGTATCGCGAATGTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2021
 QY 717 GCTGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 776
 Db 2022 ACTGCGGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2081
 QY 777 GATCTTACCGTGAAGTACTCTGCGGCGGCTTCTGCGGCGGCGGCGGCGGCGGCGGCT 836
 Db 2082 GATCTTACCGTGAAGTACTCTGCGGCGGCTTCTGCGGCGGCGGCGGCGGCGGCGGCT 2141
 QY 837 CCGAGCGTATGAGATCATGAGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 896

Db 2142 GCGTAGTGTATGATATCATCGACGTGGTGGCCATCCCTTATATCATTTGGGCTGCT 2201
QY 897 CATGACCAACAACGAGAGCTGTCCGGCCTTGTACAGCTCCGGGCTTCCGGCTCT 956
Db 2202 GATGACAGACAAATGAGAGACGTACGCGGACCTTTGTCACTCCGAGTCTTCCGGGCTCT 2261
QY 957 CAGGATCTTCAAGTTTCCCGCCTCCAGGGCCTGGCATCTTGGGCTACACACTGAA 1016
Db 2262 CAGGATCTTAAAGTTTCCCGCCTCAAGGCTGGCATCTTGGGCTACACACTGAA 2321
QY 1017 GAGCTGTGCTCCGAATGCGCTTCTCTCTCCCTCAACATGCGCATCATCTT 1076
Db 2322 GAGTTGTGCTCAGAAATGGGCTTCTTCTCTCTCAACATGCGCATCATCTT 2381
QY 1077 TGCCACTGTGATGTTTATGCGGAGAGGGCTCTCGGCCAGCAAGTTCAACAAGCATCCC 1136
Db 2382 CGGTACAGTTATGTTCTACGAGAGAGGGGCTTTCGGCTAGCAAGTTCAACGACATCCC 2441
QY 1137 TGCCCTGTTTGTGTACACCAATGTACACCATGACACATGCGATACG 1183
Db 2442 TGCAGCCTTCTGTGTATACCATGTGTACCATGACACACTAGGGTAGG 2488

RESULT 15

US-10-361-811-255
; Sequence 255, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361, 811
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 5404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-255

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hic:*
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7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1761.4	83.0	1911	9	AY419308 Pan trogl
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6	904.6	42.6	1893	9	AY406812 Homo sapi
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9	759.8	35.8	1956	9	AY408065 Mus muscu
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ALIGNMENTS

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DEFINITION	Homo sapiens KCND3 gene, VIRUTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY419307				
VERSION	AY419307.1	GI:39775264			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.				
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VERSION AY419308.1 GI:39775265
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civelio, D.R., Lu, F., Murphy, B.,
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Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D., and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
AUTHORS
2 (bases 1 to 1911)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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Adams, M.D., and Cargill, M.
TITLE
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
These sequences were made by sequencing genomic exons and ordering
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Db 1504 ATGAGAGTTCAATGAGAACTAATCCATCCACAAAGAGTCCCTACCTGACGACCA 1563
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QY	1813	AGTGAACAGCCCTCCCTCCACCAACCAAGTCCGCTCCAGCCTTAATTGTAAGCAGACGACGGGA	1872
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QY	1933	CCAGCGCTAACCCACAGAGGGGGAAGTCCGCGCACCCCTGCGAGCCCGCAGCCGCCCAACAG	1992
Db	1804	CCAGCGCTAACCCACAGAGGGGGAAGTCCGCGCACCCCTGCGAGCCCGCAGCCGCCCAACAG	1863
QY	1993	AACATTCCTTCATTAACCAAGCAATGTGTCAAGGTCTCTGTTCTGTAA	2040
Db	1864	AACATTCCTTCATTAAGCCAGCAATGTGTCAAGGTCTCTCGCTTGTAA	1911

RESULT 3	AY419309	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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			Mus musculus KCND3 gene, VIRTUAL TRANSCRIPT, partial sequence,					
			genomic survey sequence.					
				AY419309				
				AY419309.1	GI:39775266			
				GSS.				
				Mus musculus (house mouse)				
				Mus musculus				

REFERENCE	AUTHORS
1 (bases 1 to 1911)	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1911)
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.

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    gene       <1..>1911
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Best Local Similarity	88.6%	Pred. No. 0;		
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Db 1 ATGGCGGCGAGAGTTGCAGCGCTGGCGCTTTTGGCCGGGCTGGGCCCATTTGATGATG 60

QY 133 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCCGCAAGAACAAGCGGCAGATGAG 192

Db 61 CCAGTGGCCAACTGCCCCCATGCCCCCTAGCTCCAGCGGCAAGAACAAGCGGCAGAG 120

QY 193 CTGATTGTCCTCAACGTGAGTGGGCGGAGTTCCAGACCTGAGAGACCAAGCTGAGCGC 252

Db 121 CTGATCGTCCTCAACGTAAAGTGCACACGAGTTCAGACCTGAGAGACCACTTGGAGCGC 180

QY	253	TACCCGGACACCCCTGCTGGGACGACGGAGGAAGATTCTTCTTCAACGAGGACACCAAG	312
Db	181	TATCCCGACACCTTGCTGGGTAGACACAGAAAGAGTTCTTCTTCAATGAGACACGAAG	240
QY	313	GAGTACTTCTTGACCCGGGACCCCGAGGTGTTCCGCTGCGTCTCACTTCTACCGCACG	372
Db	241	GAGTACTTCTTGACCGTGACCCGGAGTGTTCCGTTGTTGTCTTAACTTTACCGCACCC	300
QY	373	GGGAAGCTGCACTACCCCGCGCTACGAGTGCACTCTGTGCTTACGACGACGAGCTGGCTTC	432
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QY	433	TACGCGATCTCCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAGACCGCAAG	492
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QY	493	AGGAGAAACCCGAGCGGCTCATGACGACAACAGCTGGAGAACACCGGAGTCCATG	552
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QY	553	CCCTGCTCAGCTTCCGCCAGAACCATGTGCGGGCCCTTCGAGAAACCCCAACGACG	612
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QY	613	CTGGCCCGGTCTTCTACTACGTGACTGCTTCTTCATCGCTGTCTCGCTCATCAAC	672
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QY	673	GTCGTGAGACCGGTGCGGTGCGGCACCGTCCCGGGCAGCAAGGACTGCCGTGCGGGAG	732
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QY	733	CGCTACTCGGTGCGCTTCTCTGCGCTGGAACAACGCGTGTGATGATCTTCAACCGTGGAG	792
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QY 1933 CCAGCGCTAACCCAGAGGGGAAAGTCCGCCACCCCTGCCAGCCCAAGCCCAACAG 1992
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Db 1864 AACATTCTTCATTAACGAGCAATGTTGTCAAGGTCTCTGCTTGTAA 1911
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RESULT 4

AK033962

LOCUS 3730 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330129C02 product:potassium voltage-gated channel, Shal-related family, member 3, full insert sequence.

ACCESSION AK033962

VERSION AK033962.1 GI:26329580

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carninci, P. and Hayashizaki, Y.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORSGenome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

6 (bases 1 to 3730)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akehira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

JOURNAL

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES

SOURCE

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ORIGIN

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Qy 1210 GGGAGAGTCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1269
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RESULT 5
AK032268
LOCUS 2997 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430513P12 product:potassium channel Kv4.2
mRNA, full insert sequence.
ACCESSION AK032268
VERSION AK032268.1 GI:26328092
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
```

TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	11042159		3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res. 10 (11), 1757-1771 (2000)	20530913	11076861		4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.					
Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)				5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.					
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)				6 (bases 1 to 2997)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.					
Direct Submission					
Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)					
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.					
Please visit our web site for further details.					
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AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
	Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652),	1960-1963 (2003)
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1893)		
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
	Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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genomic survey sequence.
ACCESSION AY406814
VERSION AY406814.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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REFERENCE AUTHORS	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1956)
TITLE	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL PUBMED REFERENCE AUTHORS	Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 1956)
TITLE JOURNAL	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submision Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
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QY	1138	GCCTCGTTTGGTACACCATTTGTACACATGACACACTGGGATACGAGACATGTCCT	1197
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QY	1318	GCTGATTAACGACAGGGACAAAGAAAGGCCGCTTGGCCAGATCCGTGTGGCCAAACA	1377
Db	1261	GCTGACAAAGCCCGGACAGCAGAAAGTGGCGCTGGCAAGATCCGTTTGGCAAGAGT	1320
QY	1378	GGCAGTTCGAATGATACCTGTCACAGCAAGCGCAAGGGCTCTCAACGAGGCGCTGGAG	1437
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Db	1432	CATCACCATCTGCTGCACTGCTGAGAGAAAGACTAC	1466

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 DEFINITION Pan troglodytes KCND1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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 ACCESSION AY408064
 VERSION AY408064.1 GI:39764035
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 1939)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1939)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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ORIGIN
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 Matches 864; Conservative 0; Mismatches 587; Indels 24; Gaps 2;

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RESULT 12
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DEFINITION Tetraodon nigroviridis genome survey sequence T3 end of clone 051G22 of library A from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL327691 GI:8221280
VERSION AL327691
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 993)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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ORIGIN
Genoscope sequence ID : COA051BD1A1-end : T3"

Query Match 27.2%; Score 576.8; DB 9; Length 993;
Best Local Similarity 79.7%; Pred. No. 2.7e-124;
Matches 723; Conservative 0; Mismatches 178; Indels 6; Gaps 4;
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Db 992 GNAGAAAGANTTTTTTNNACGAGAGGAGGCAAGNGTACTTTTGGACGGGATCCGA 933
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Db 932 TGCCTTCAGAGCATCTTCACTTNTACCGGAGCGGNAAGCTCCANTACCTCCGCCAGA 873
QY 399 GTGCATCTCTGCTACGACGAGAGCTGCGCTTCTACGGCATCTCCCGAGATCATCGG 458
Db 872 GTGCATCTCAGCTTATGATGACGAGNTGACATTTCTTCGCAATCATCCAGAGCTCATCG 813
QY 459 GGAAGTCTGCTACGAGAGTACAGAGACCGCAAGAGGAAAGCCGAGCGGCTCATGA 518
Db 812 CGACTGCTGCTACGAGAGTACAGAGACGAGAAAGAGGAAATTTAGAGCGGCTGACAGA 753
QY 519 CGACACGACTGCGAGAACACCAAGAGTCCATGCCCTCGCTCAGCTTCCGCCAGCAT 578
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QY 1179 ATACGGA 1185
Db 98 GTAGATA 92

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LOCUS BI033106
DEFINITION MR4-NN0205-310101-201-e10 NN0205 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI033106
VERSION BI033106.1 GI:14439732
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 567)
AUTHORS Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&e2=MR4-NN0205-310101-201-e10&t3=2001-01-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 567.

FEATURES
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ORIGIN

Query Match 26.1%; Score 552.8; DB 4; Length 567;
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QY 1272 TGTGATTTGTTCCAACTTTAGCCGGATTACCAAGAAATCAGAGAGCTGATAACGCAG 1331
DB 507 TGTGATTTGTTCCAACTTTAGCCGGATTACCAAGAAATCAGAGAGCTGATAACGCAG 448
QY 1332 GGCAAAAGAGAGCGCCGCTTGCAGAGATCCGTGTGGCCAAAGACAGAGTTCGAATGC 1391
DB 447 GGCAAAAGAGAGCGCCGCTTGCAGAGATCCGTGTGGCCAAAGACAGAGTTCGAATGC 388
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DB 27 TAACCTG-CAGCTACTCGCTGGCGCAGC 1

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LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 070F19 of library G from Tetraodon nigroviridis, genomic survey sequence.
AL267651.1 GI:7989467
KEYWORDS GSS: genome survey sequence.
VERSION Tetraodon nigroviridis
SOURCE Tetraodon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS

1 Roest Crolius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizanes, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
2 Roest Crolius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Fizanes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissbach, J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers

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source

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QY 604 ACCAGCAGCTGCGCCCTGCTCTTCTACTAGCTGACTGCTTCTCATCGCTGCTGCTC 663
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RESULT 15
 AK033805
 LOCUS AK033805 3302 bp mRNA linear HTC 03-APR-2004

DEFINITION

Mus musculus adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230112B12 product:potassium voltage-gated channel, Shal-related family, member 1, full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK033805.1 GI:26329482
 AK033805
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE

1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

REFERENCE

6 (bases 1 to 3302)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.
Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

source

location/Qualifiers

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ORIGIN

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Matches 719; Conservative 0; Mismatches 241; Indels 15; Gaps 2;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 11:39:55 ; Search time 10711.6 Seconds
(without alignments)
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Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1912.2	92.6	2722	9	AF120491	AF120491 Homo sapi
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ALIGNMENTS

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DEFINITION	AR371347				
ACCESSION	AR371347				
VERSION	AR371347.1	GI:34608279			
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TITLE	Human potassium channel polynucleotide and polypeptides and uses thereof				
JOURNAL	Patent: US 6395477-A 3 28-MAY-2002;				
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DEFINITION Sequence 1 from patent US 6395477.
ACCESSION AR371346
VERSION AR371346.1 GI:34608278
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1. Unclassified.
AUTHORS Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.
TITLE Human potassium channel polynucleotide and polypeptides and uses thereof
JOURNAL Patent: US 6395477-A 1 28-MAY-2002;
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Query Match 96.8%; Score 1997; DB 6; Length 2121;
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Best Local Similarity 97.3%; Pred. No. 1.1e-297;
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RESULT 3
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LOCUS AF187964 1984 bp mRNA linear PRI 04-OCT-1999
DEFINITION Homo sapiens voltage gated potassium channel Kv4.3 short splice
variant (Kv4.3) mRNA, complete cds.
ACCESSION AF187964
VERSION AF187964.1 GI:6007796
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Buthyria; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1984)
AUTHORS Dilke, D., Ling, H.-P., Cockett, M., Sokol, P. and Numann, R.
TITLE Cloning and expression of the human Kv4.3 potassium channel
JOURNAL J. Neurophysiol. 81 (4), 1974-1977 (1999)
MEDLINE 99218223
PUBMED 10200233
REFERENCE 2 (bases 1 to 1984)
AUTHORS Dilke, D.W., Ling, H.-P., Cockett, M., Sokol, P. and Numann, R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN
8000, Room 1119A, Princeton, NJ 08543-8000, USA
LOCATION/Qualifiers
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DEFINITION		long splice variant, complete cds.	
ACCESSION	AF120491		
VERSION	AF120491.1	GI:5059059	
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AUTHORS		Homo sapiens	
TITLE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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PUBMED		Isbrandt,D., Leicher,T., Waldschutz,R., Zhu,X., Luhmann,U.,	
REFERENCE		Michel,U., Sauter,K. and Pongs,O.	
AUTHORS		Gene structures and expression profiles of three human KCND (Kv4)	
TITLE		potassium channels mediating A-type currents I(TO) and I(SA)	
JOURNAL		Genomics 64 (2), 144-154 (2000)	
MEDLINE		20195625	
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REFERENCE		2 (bases 1 to 2722)	
AUTHORS		Zhu,X.R., Waldschutz,R., Isbrandt,D., Sauter,K. and Pongs,O.	
TITLE		Direct Submission	
JOURNAL		Submitted (15-JAN-1999) ZMNH, Institut fuer Neurale	

Signalverarbeitung, Martinistrasse 52, Hamburg 20246, Germany

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ORIGIN

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VERSION AF048712.1 GI:2935433
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1911)
AUTHORS Kong,W. and Tomassell,J.G.F.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA
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DEFINITION Sequence 1 from Patent WO9842833.

ACCESSION A85164
VERSION A85164.1 GI:6733867
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SOURCE unidentified
ORGANISM unidentified
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AUTHORS Bril,A.M. and Calmels,T.P.
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AUTHORS	1 (bases 1 to 2104)			
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JOURNAL	Faivre, J.-P. Simon, Pierre., Javre, J.-L. and Rouanet, S.			
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LOCUS	1911 bp mRNA linear PRI 29-DEC-1999
DEFINITION	Homo sapiens potassium ion channel Kv4.3 short isoform mRNA, complete cds.

ACCESSION	AF205856
VERSION	AF205856.1
	GI:6644149

KEYWORDS	SOURCE	ORGANISM
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Homo sapiens		

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1911)

TITLE	Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,
AUTHORS	Calmels, T. P. G., Falvire, J. - F., Javre, J. - L., Cheval, B., Rouanet, S. and Brill, A.

Expression, Electrophysiology, Pharmacology and Phosphorylation by Protein Kinase C

REFERENCE
AUTHORS
TITLE
2 (bases 1 to 1911)
Calmels, T. P. G., Faivre, J.-F., Javre, J.-L. and Brill, A.
Direct Submission

FEATURES
Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline Beecham, 4 Rue du Chesnay Beaugrenet, Saint Gregoire 35760, France
Location/Qualifiers

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Matches 1906; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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ACCESSION	AF187963		
VERSION	AF187963.1	GI:6007794	
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SOURCE	Homo sapiens (human)		
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REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2041)		
AUTHORS	Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.		

TITLE	Cloning and expression of the human kv4.3 potassium channel		
JOURNAL	J. Neurophysiol. 81 (4), 1974-1977 (1999)		
MEDLINE	99218223		
PUBMED	10200233		
REFERENCE	2 (bases 1 to 2041)		
AUTHORS	Dilks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN 8000, Room 1119A, Princeton, NJ 08543-8000, USA		
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VERSION A85168.1 GI:6733869
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AUTHORS Bril,A.M. and Caimels,T.P.
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VERSION AR204886.1 GI:21502326
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SOURCE
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AUTHORS Bril,A.Michel,Alain., Calmels,T.Paul, Gerard.,
FAIVRE,J.-F.Simon,Pierre., Jayve,J.-L. and Rouanet,S.
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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1968)
AUTHORS Kong, W. and Tomasselli, G.F.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA

FEATURES Location/Qualifiers

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Db 1921 AACATTCTTCCATTAACCAAGCATGTTGTCAAGTCTCTGTCTTGTAA 1968

RESULT 13

LOCUS A85166 2072 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 3 from Patent WO9842833.
ACCESSION A85166
VERSION A85166.1 GI:6733868

KEYWORDS
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2072)
AUTHORS Bril,A.M. and Calmels,T.P.
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES
JOURNAL Patent: WO 9842833-A 3 01-OCT-1998;
BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)
FEATURES
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Location/Qualifiers
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Query Match 89.1%; Score 1838; DB 6; Length 2072;
Best Local Similarity 96.9%; Pred. No. 3.2e-273;
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;
Qy 73 ATGGCGGCGGAGTTGCGGCTGCTGCTTTTGCCCGGCTGCGGCATCGGCTGATG 132
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Qy 733 CGCTACTGGGTGGCTTCTTCTGCGTGACACGGCGGTGCTATGATCTTCAACCGTGGAG 792
Db 661 CGCTACTGGGTGGCTTCTTCTGCGTGACACGGCGGTGCTATGATCTTCAACCGTGGAG 720
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Qy 1213 AAGATCTTCCGCTCATCTGCTTGAAGTGGGCTGTGTCATTTGCCCTGAGTCCCT 1272
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QY 1876 CCAGCGCTAACCCAGAGGGGAAAGTCCGCCAATCCCTGCGAGCCAGGCCCAACAGCG 1935
Db 1861 CCAGCGCTAACCCAGAGGGGAAAGTCCGCCAATCCCTGCGAGCCAGGCCCAACAGCG 1920
QY 1936 AACATTCCTTCCATACCAAGCAATGTTGTCAAGGTCTCTGTCTTGTAAAA 1985
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LOCUS AR204885 Sequence 3 from patent US 6368823.
DEFINITION AR204885
ACCESSION AR204885
VERSION AR204885.1 GI:21502325
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 2072)
AUTHORS
Bril,A.,Michel,Alain., Calmels,T.,Paul.Gerard.,
Faivre,J.-F.,Simon,Pierre., Javre,J.-L. and Rouanet,S.
TITLE
kv potassium channel polypeptides and polynucleotides
JOURNAL
Patent: US 6368823-A 3 09-APR-2002;
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Query Match 89.1%; Score 1838; DB 6; Length 2072;
Best Local Similarity 96.9%; Pred. No. 3.2e-273;
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

QY 73 ATGCGCGCGAGTTGCGCGCTGCTGCTTTTGCCCGGGCTGGGGCCATCGGGTGTATG 132
Db 1 ATGCGCGCGAGAGTTGAGCTTGGCTGCTTTTGCCCGGGCTGGGGCCATCGGGTGTATG 60
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DEFINITION	Sequence 4 from Patent W003097682.			
ACCESSION	AX956786			
VERSION	AX956786.1	GI:40785267		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	1			
TITLE	Kaletta,T.J., Dewulf,N.E. and Plaetnick,G.K.			
JOURNAL	Methods for identifying and developing compounds that interact with voltage-gated potassium channels of the kv4 family			
FEATURES	Patent: WO 03097682-A 4 27-NOV-2003,			
source	Devgen NV (BE)			
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Query Match 89.0%; Score 1836; DB 6; Length 1968;
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 Matches 1906; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

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QY	253	TACCCGGACACCTCTGCTGGGACAGACGGAGAGAGTTCTTTCTTCAACGAGACACCAAG	312
DB	181	TACCCGGACACCTCTGCTGGGACAGACGGAGAGAGTTCTTTCTTCAACGAGACACCAAG	240
QY	313	GAGTACTTCTTCGACCGGGGACCCCGAGGTTCCGCTGCGTCTCACTTCTACCGGACG	372
DB	241	GAGTACTTCTTCGACCGGGGACCCCGAGGTTCCGCTGCGTCTCACTTCTACCGGACG	300
QY	373	GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCTTACGACGACGAGCTGGCCTTC	432
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QY	433	TACGGCATCTTCCCGAGATCATCTGGGACCTGCTCTACGAGAGTACAAAGACCGCAAG	492
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DB	781	ATCATGACGCTGTGGCCATCATGCCCTTACTACATCGGTCTGTCTGTATGACCAACAGAG	840
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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36	338	16.4	612	4	ABA40984	Abat40984 Probe #19
37	338	16.4	612	4	AAK51097	Aak51097 Human bon
38	338	16.4	612	4	AAK25090	Aak25090 Human bra
39	338	16.4	612	4	ABS50654	Abs50654 Human liv
40	338	16.4	612	6	ABS24615	Abs24615 Human gen
41	324.6	15.7	3254	11	ADM10920	Adm10920 Human O64
42	324.6	15.7	3254	12	ADJ11250	Adj11250 Human ova
43	324.6	15.7	3254	12	ADM43511	Adm43511 Human ova
44	266	12.9	2882	13	ADS16307	Adsl6307 Rabbit vo
45	240	11.6	3004	13	ABD33130	Abd33130 Human can

ALIGNMENTS

RESULT 1	
ABN84401	
ID	ABN84401 standard; cDNA; 2064 BP.
XX	
AC	ABN84401;
XX	
DT	01-OCT-2002 (first entry)
XX	
DE	Human Kv4.3 potassium channel (short form) cDNA.
XX	
KW	Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KM	neotrophic; neuroprotective; cardiant; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "Kv4.3"
XX	
PN	US6395477-B1.
XX	
PD	28-MAY-2002.
XX	
PF	23-OCT-1998; 98US-00178109.
XX	
PR	23-OCT-1998; 98US-00178109.
XX	
PA	(AMHP) AMERICAN HOME PROD CORP.
XX	
PI	Cockett MI, Dilks DW, Ling HC, Sokol PT;
XX	
DR	WPI; 2002-556093/59.
DR	P-PSDB; ABB79585.
XX	
PT	New isolated polynucleotide encoding human Kv4.3 potassium channel
PT	polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT	acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT	diseases.
PS	Claim 7; Col 21-22; 19pp; English.
XX	
CC	The present sequence is that of cDNA encoding the short isoform of novel

CC human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been identified. One form is full-length (hKv4.3 long) while the second form CC has a deletion of 19 amino acids in the carboxy domain after the CC predicted sixth transmembrane domain (hKv4.3 short). Human heart CC primarily expresses hKv4.3 long, whereas human brain contains both forms. CC To obtain the present hKv4.3 short cDNA, PCR amplification was performed using primers that flanked the 57 bp insert in hKv4.3 long. The invention CC provides Kv4.3 polypeptides, polynucleotides, and methods for producing CC these polynucleotides. The Kv4.3 polypeptides and polynucleotides are CC useful in the diagnosis, treatment and screening of human diseases CC relating to an excess or deficiency of hKv4.3 activity, including CC Alzheimer's disease and heart disease

XX Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;

Query Match 100.0%; Score 2064; DB 6; Length 2064;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTTGCTGAACCTAATCCAGCTGTGTGCTTACGCTCCGCGCGCTGCGGCCCAAGA 60
DB 1 GATTTGCTGAACCTAATCCAGCTGTGTGCTTACGCTCCGCGCGCTGCGGCCCAAGA 60
QY 61 GCTGAGTCAACATGCGCGCGAGTTGCGGCTGCTGCTTTTGGCCGGCTGCGGC 120
DB 61 GCTGAGTCAACATGCGCGCGAGTTGCGGCTGCTGCTTTTGGCCGGCTGCGGC 120
QY 121 ATCGGCTGATGCGGCTGCGCACTGCCCCATGCCCCCTGGCCCCCGGCAAGAACAG 180
DB 121 ATCGGCTGATGCGGCTGCGCACTGCCCCATGCCCCCTGGCCCCCGGCAAGAACAG 180
QY 121 ATCGGCTGATGCGGCTGCGCACTGCCCCATGCCCCCTGGCCCCCGGCAAGAACAG 180
DB 121 ATCGGCTGATGCGGCTGCGCACTGCCCCATGCCCCCTGGCCCCCGGCAAGAACAG 180
QY 181 CCGCAGATGAGCTGATTTCTCTCAACGTGAGTGGCGGAGTTCCAGACTGGAGAGC 240
DB 181 CCGCAGATGAGCTGATTTCTCTCAACGTGAGTGGCGGAGTTCCAGACTGGAGAGC 240
QY 241 ACCGTGAGCGCTACCCGGAACCTCTGCTGGGAGCAACGAGAGAGTTCTTCTTCAAC 300
DB 241 ACCGTGAGCGCTACCCGGAACCTCTGCTGGGAGCAACGAGAGAGTTCTTCTTCAAC 300
QY 241 ACCGTGAGCGCTACCCGGAACCTCTGCTGGGAGCAACGAGAGAGTTCTTCTTCAAC 300
DB 241 ACCGTGAGCGCTACCCGGAACCTCTGCTGGGAGCAACGAGAGAGTTCTTCTTCAAC 300
QY 301 GAGGACACCAAGAGTACTTCTTCCAGCCGGGACCCCGAGGTTCCGCTGCGTCAAC 360
DB 301 GAGGACACCAAGAGTACTTCTTCCAGCCGGGACCCCGAGGTTCCGCTGCGTCAAC 360
QY 361 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTCACTCTGCTTCAACGAC 420
DB 361 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTCACTCTGCTTCAACGAC 420
QY 421 GAGCTGCGCTTCTACGCGCATCTCTCCGAGATCATCGGGACTGCTGCTACGAGAGTAC 480
DB 421 GAGCTGCGCTTCTACGCGCATCTCTCCGAGATCATCGGGACTGCTGCTACGAGAGTAC 480
QY 481 AAGGACCGCAGAGAGAGACGCGCGAGCTCATGAGCAGCAACGACTCGAGAACAC 540
DB 481 AAGGACCGCAGAGAGAGACGCGCGAGCTCATGAGCAGCAACGACTCGAGAACAC 540
QY 541 CAGGAGTCCATGCGCTGCTCACTTCCGCGCAGACCATGTGGCGGCTTCCGAGAACCC 600
DB 541 CAGGAGTCCATGCGCTGCTCACTTCCGCGCAGACCATGTGGCGGCTTCCGAGAACCC 600
QY 601 CACACCAAGCAGTGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
DB 601 CACACCAAGCAGTGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
QY 661 GTTCATCAACCAAGTGTGAGACGCTGCGGCAAGTCCCGGCAAGCAAGAGCTG 720
DB 661 GTTCATCAACCAAGTGTGAGACGCTGCGGCAAGTCCCGGCAAGCAAGAGCTG 720
QY 721 CCGTGGGAGGAGCGCTACTCGTGGCTTCTTCTGCTGAGACAGGCGTGCATGATC 780
DB 721 CCGTGGGAGGAGCGCTACTCGTGGCTTCTTCTGCTGAGACAGGCGTGCATGATC 780
QY 781 TTCAACGAGTACCTCTGCGGCTCTTGGCGCTCCAGCGCTACCGCTTCTATCCGC 840
DB 781 TTCAACGAGTACCTCTGCGGCTCTTGGCGCTCCAGCGCTACCGCTTCTATCCGC 840

DB 781 TTCAACGAGTACCTCTGCGGCTCTTGGCGCTCCAGCGCTACCGCTTCTATCCGC 840
QY 841 AGCGTATGAGCATCATGAGCGTGTGGCCATCATGCGCTTACTACTGCGTGTGATG 900
DB 841 AGCGTATGAGCATCATGAGCGTGTGGCCATCATGCGCTTACTACTGCGTGTGATG 900
QY 901 ACCAACAAGAGACGTGTCCGCGCTTCTGACGCTCCGGGTCTTCCGGCTTTCAGG 960
DB 901 ACCAACAAGAGACGTGTCCGCGCTTCTGACGCTCCGGGTCTTCCGGCTTTCAGG 960
QY 961 ATCTTCAAGTTTCCCGCACTCCAGGCGCTGCGATCTCGGCTACACATGAAAGC 1020
DB 961 ATCTTCAAGTTTCCCGCACTCCAGGCGCTGCGATCTCGGCTACACATGAAAGC 1020
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DB 1021 TGTGCTCCGAACCTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
QY 1081 ACTGTGATGTTTATGCGGAGAGGCTCTCGGCAAGATTCAACAGATCCCTGACC 1140
DB 1081 ACTGTGATGTTTATGCGGAGAGGCTCTCGGCAAGATTCAACAGATCCCTGACC 1140
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DB 1141 TCGTTTGTGACACCATTTGTCACCATGACACACACTGGGATACGAGACATGTCCTAAG 1200
QY 1201 ACGATTGAGGAGGATCTTCCGCTCATCTGCTTCTGAGTGGCGTCTGCTATTCGC 1260
DB 1201 ACGATTGAGGAGGATCTTCCGCTCATCTGCTTCTGAGTGGCGTCTGCTATTCGC 1260
QY 1261 CTGCGATGCTCTGATGATTTGTTCCAACTTACCGGATTTACCAAGATCAGAGACT 1320
DB 1261 CTGCGATGCTCTGATGATTTGTTCCAACTTACCGGATTTACCAAGATCAGAGACT 1320
QY 1321 GATTAACGAGGAGCAAAAGAGGCGCTTCCAGGATCCGCTGCGCAAAACAGGC 1380
DB 1321 GATTAACGAGGAGCAAAAGAGGCGCTTCCAGGATCCGCTGCGCAAAACAGGC 1380
QY 1381 AGTTGGAATGATATCTGCAACAGAGCGCAACGCGCTCTTCAACGAGCGCTGAGCTG 1440
DB 1381 AGTTGGAATGATATCTGCAACAGAGCGCAACGCGCTCTTCAACGAGCGCTGAGCTG 1440
QY 1441 ACGGCGACCCCAAGAGAGACACATGGGAGAACCACTCATCTATCGAAGCCAGAT 1500
DB 1441 ACGGCGACCCCAAGAGAGACACATGGGAGAACCACTCATCTATCGAAGCCAGAT 1500
QY 1501 CATCACCTGCTGACTGCTGGAAGAAACCACTAACACAGAGTTTATGATGAGCAGATG 1560
DB 1501 CATCACCTGCTGACTGCTGGAAGAAACCACTAACACAGAGTTTATGATGAGCAGATG 1560
QY 1561 TTTGAGCAGAACTGATGAGAGTTCAATGCAAGTACCATCCACAGAAAGTCCCTCA 1620
DB 1561 TTTGAGCAGAACTGATGAGAGTTCAATGCAAGTACCATCCACAGAAAGTCCCTCA 1620
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DB 1621 CTGTCCAGCCACCAAGGCTCACTACCACTGCTGCTCCGCTCGTATGAAAGACCA 1680
QY 1681 CACCTGCGCAATTTCACTGCTGAGCTACTGCGCTGCGGAGCATGCAAGAGCTCAGCAG 1740
DB 1681 CACCTGCGCAATTTCACTGCTGAGCTACTGCGCTGCGGAGCATGCAAGAGCTCAGCAG 1740
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DB 1741 ATCCACATCCAGGAGTGAAGAGCCCTCCCTTCAACCAAGTCCGCTTCAATTG 1800
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DB 1801 AAAGCAGACGAGGAGTGAAGCCAACTGCAAAACATCCAGATCAACACAGCATCATC 1860
QY 1861 AGCATCCCACTCCCGCAGGCTAAACCCAGAGGGGAGAAAGTCCGCCACCCCTGCGAGC 1920
DB 1861 AGCATCCCACTCCCGCAGGCTAAACCCAGAGGGGAGAAAGTCCGCCACCCCTGCGAGC 1920

QY 1921 CCAGCCCCAACAGAACTTCCTTCATTAACGAGCAATGTTGTCAGGTCCTGTG 1980
 |||||||
 Db 1921 CCAGCCCCAACAGAACTTCCTTCATTAACGAGCAATGTTGTCAGGTCCTGTG 1980
 |||||||
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 |||||||
 Db 1981 TAAAAATCCCGCGCCATGCGCGCGGAGCATGCGAGCTCGGGCCCAATTCGCCCTATA 2040
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 QY 2041 GTGAGTCGTATTAAAGCCGAATTC 2064
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 Db 2041 GTGAGTCGTATTAAAGCCGAATTC 2064
 |||||||
 RESULT 2
 ABN84400
 ID ABN84400 standard; cDNA; 2121 BP.
 XX
 AC ABN84400;
 XX
 DT 01-OCT-2002 (first entry)
 XX
 DE Human Kv4.3 potassium channel (long form) cDNA.
 XX
 KW Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
 KW nootropic; neuroprotective; cardiact; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 73..2040
 FT /*tag= a
 FT /product= "Kv4.3"
 FT
 PN US6395477-B1.
 XX
 PD 28-MAY-2002.
 XX
 PF 23-OCT-1998; 98US-00178109.
 XX
 PR 23-OCT-1998; 98US-00178109.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PI Cockett MI, Dilks DW, Ling HC, Sokol PT;
 XX
 DR WPI; 2002-556093/59.
 DR P-PSDB; ABB79584.
 XX
 PT New isolated polynucleotide encoding human Kv4.3 potassium channel
 PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
 PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
 PT diseases.
 PS
 XX Claim 5; Col 15-18; 19pp; English.
 XX
 CC The present sequence is that of cDNA encoding the long isoform of novel
 CC human potassium channel Kv4.3. To obtain the cDNA, oligonucleotides based
 CC on the published rat sequence were used to screen a whole heart cDNA
 CC library. A 511 bp fragment was obtained and used as a probe to rescreen
 CC the library. The resulting clones lacked the extreme 5' and 3' coding
 CC regions, and 5' and 3' RACE was therefore used to amplify these sequences
 CC from a human brainstem cDNA library. 2 Isoforms of human Kv4.3 were
 CC identified. One form is full-length (hKv4.3 long) while the second form
 CC has a deletion of 19 amino acids in the carboxy domain after the
 CC predicted sixth transmembrane domain (hKv4.3 short). Human heart
 CC primarily expresses hKv4.3 long, whereas human brain contains both forms.
 CC The invention provides Kv4.3 polypeptides, polynucleotides, and methods
 CC for producing these polynucleotides. The Kv4.3 polypeptides and
 CC polynucleotides are useful in the diagnosis, treatment and screening of
 CC human diseases relating to an excess or deficiency of hKv4.3 activity,
 CC including Alzheimer's disease and heart disease
 XX

SQ Sequence 2121 BP; 457 A; 694 C; 557 G; 413 T; 0 U; 0 Other;
 Query Match 96.8%; Score 1997; DB 6; Length 2121;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;
 QY 1 GATTGCTGAACCTAATCCAAAGCTGTGTGCTTAGCGTCCGCGGCTGCGGCCCAAGA 60
 |||||||
 Db 1 GATTGCTGAACCTAATCCAAAGCTGTGTGCTTAGCGTCCGCGGCTGCGGCCCAAGA 60
 |||||||
 QY 61 GCTGAGTCAACATGCGCGCCGAGATTGCGGCTGCTGCTTTTGGCCCGGCTGCGGCC 120
 |||||||
 Db 61 GCTGAGTCAACATGCGCGCCGAGATTGCGGCTGCTGCTTTTGGCCCGGCTGCGGCC 120
 |||||||
 QY 121 ATCGGCTGATGCGCGTGCCTCAATGCCCCCATGCCCCCTGCGCCCGGCGCAAGAA 180
 |||||||
 Db 121 ATCGGCTGATGCGCGTGCCTCAATGCCCCCATGCCCCCTGCGCCCGGCGCAAGAA 180
 |||||||
 QY 181 CGGACGATGAGCTGATTGTCTCAACGTGAGTGCGCGAGGTTCCAGACCTGAGAGACC 240
 |||||||
 Db 181 CGGACGATGAGCTGATTGTCTCAACGTGAGTGCGCGAGGTTCCAGACCTGAGAGACC 240
 |||||||
 QY 241 ACGCTGAGACGCTAACCCCGGACACCCCTGCTGGGACAGCAGGAGAGAGATTCTTCAAC 300
 |||||||
 Db 241 ACGCTGAGACGCTAACCCCGGACACCCCTGCTGGGACAGCAGGAGAGAGATTCTTCAAC 300
 |||||||
 QY 301 GAGACACCAAGAGTACTTCTTCGACCCGGAACCCCGAGGTGTTCCGCTGCGTCTCAAC 360
 |||||||
 Db 301 GAGACACCAAGAGTACTTCTTCGACCCGGAACCCCGAGGTGTTCCGCTGCGTCTCAAC 360
 |||||||
 QY 361 TTCTACCGCAGCGGGGAAGTGTGACTTACCCGCTACAGAGTGATCTTGCTTACGAGAC 420
 |||||||
 Db 361 TTCTACCGCAGCGGGGAAGTGTGACTTACCCGCTACAGAGTGATCTTGCTTACGAGAC 420
 |||||||
 QY 421 GAGCTGGCTTCTACGGCATCTCCCGGAGATCATCGGGGACTGCTGTACGAGAGTAC 480
 |||||||
 Db 421 GAGCTGGCTTCTACGGCATCTCCCGGAGATCATCGGGGACTGCTGTACGAGAGTAC 480
 |||||||
 QY 481 AAGGACCGCAAGAGGAGAAACCGGAGCGGCTCATGAGCAACGACTGCGAGAACAC 540
 |||||||
 Db 481 AAGGACCGCAAGAGGAGAAACCGGAGCGGCTCATGAGCAACGACTGCGAGAACAC 540
 |||||||
 QY 541 CAGAGTCCATGCGCTCGTCAAGCTCCGACAGACCATGTGCGGGGCTTCGAGAACCCC 600
 |||||||
 Db 541 CAGAGTCCATGCGCTCGTCAAGCTCCGACAGACCATGTGCGGGGCTTCGAGAACCCC 600
 |||||||
 QY 601 CACACGACACGCTGCGCTGTCTTCTACTACGTGACTGCTTCTTCATGCTGTCTCG 660
 |||||||
 Db 601 CACACGACACGCTGCGCTGTCTTCTACTACGTGACTGCTTCTTCATGCTGTCTCG 660
 |||||||
 QY 661 GTCATACCAACGCTGTGTGAGACGCGTCCGCGGACGCTGCCGGGCGAGCAAGAGCTG 720
 |||||||
 Db 661 GTCATACCAACGCTGTGTGAGACGCGTCCGCGGACGCTGCCGGGCGAGCAAGAGCTG 720
 |||||||
 QY 721 CCGTGGCGGAGCGCTACTCGGTGCGCTTCTGCTGGAACAGCGGCTGCTATGATC 780
 |||||||
 Db 721 CCGTGGCGGAGCGCTACTCGGTGCGCTTCTGCTGGAACAGCGGCTGCTATGATC 780
 |||||||
 QY 781 TTCACCGTGAAGTACTCTCTGCGGCTCTTGCGGCTTCCAGCGCTTATCTCCG 840
 |||||||
 Db 781 TTCACCGTGAAGTACTCTCTGCGGCTCTTGCGGCTTCCAGCGCTTATCTCCG 840
 |||||||
 QY 841 AGCGTATGAGCATCATGAGCGTGTGCGCATCATGCGCTTACTATCGGCTGTGATG 900
 |||||||
 Db 841 AGCGTATGAGCATCATGAGCGTGTGCGCATCATGCGCTTACTATCGGCTGTGATG 900
 |||||||
 QY 901 ACCAACAAGAGAGAGTGTGCGGCGCTTGTGACGCTCCGGGCTTTCGCGCTTTCAGG 960
 |||||||
 Db 901 ACCAACAAGAGAGAGTGTGCGGCGCTTGTGACGCTCCGGGCTTTCGCGCTTTCAGG 960
 |||||||
 QY 961 ATCTTAAGTTTCCCGCACTCCAGGGCGCTGCGGATCTTGCGCTACACTGAAGAGC 1020
 |||||||
 Db 961 ATCTTAAGTTTCCCGCACTCCAGGGCGCTGCGGATCTTGCGCTACACTGAAGAGC 1020
 |||||||

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QY 1021 TGTGCTCCGAACTGGGCTTCTTCTCTCTCCCTCACCATGGCCATCATCTTTGCC 1080
DB 1021 TGTGCTCCGAACTGGGCTTCTTCTCTCTCCCTCACCATGGCCATCATCTTTGCC 1080
QY 1081 ACTGTGATGTTTTTATGCGGAGAGGGCTCTCGGCAGCAAGTTCAAGCATCCCTGCC 1140
DB 1081 ACTGTGATGTTTTTATGCGGAGAGGGCTCTCGGCAGCAAGTTCAAGCATCCCTGCC 1140
QY 1141 TCGTTTGGTACACCAATTGTACCATGACCACTGGGATACGAGACATGGCTTAAG 1200
DB 1141 TCGTTTGGTACACCAATTGTACCATGACCACTGGGATACGAGACATGGCTTAAG 1200
QY 1201 ACGATTGCAAGGAAGATCTTGGGCTCCATCTGCTCTTGAGTGGCGCTGGTCAATTGCC 1260
DB 1201 ACGATTGCAAGGAAGATCTTGGGCTCCATCTGCTCTTGAGTGGCGCTGGTCAATTGCC 1260
QY 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACCAACAGATCAGAGAGCT 1320
DB 1261 CTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACCAACAGATCAGAGAGCT 1320
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DB 1321 GATTAACGAGGGGCAAAAAAGAGGGCGGCTTGCAGAGATCCGTGCGCCAAACAGGC 1380
QY 1381 AGTTGGAATGCATACCTCTGACAGCAAGGCGACCGGCTCTCAACGAGGCGCTGAGCTG 1440
DB 1381 AGTTGGAATGCATACCTCTGACAGCAAGGCGACCGGCTCTCTCAACGAGGCGCTGAGCTG 1440
QY 1441 ACGGGGCAACCCAGAGAGAGAGACATGGGCAAGACCACTCACTCATCGAGAGCCAGCAT 1500
DB 1441 ACGGGGCAACCCAGAGAGAGAGACATGGGCAAGACCACTCACTCATCGAGAGCCAGCAT 1500
QY 1501 CATCACTCTGCTGACCTGCTGGAAGAAACCACT----- 1533
DB 1501 CATCACTCTGCTGACCTGCTGGAAGAAACCACTGCGTGTCTATCTTGATGATGCC 1560
QY 1534 -----AACACGAGTTTATTGATGAGCAGATGTTT 1563
DB 1561 CTGTATCTGTACGAACCTCCACCATCAAGAACCAAGATTATTGATGAGCAGATGTTT 1620
QY 1624 TCCAGCCACCCAGGCTCTCACTACCACTGCTGCTCCGCTGCTAGTAAAGACACACAC 1683
DB 1681 TCCAGCCACCCAGGCTCTCACTACCACTGCTGCTCCGCTGCTAGTAAAGACACACAC 1740
QY 1684 CTGCCCCAATTCTAACCCTGCGAGTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGATC 1743
DB 1741 CTGCCCCAATTCTAACCCTGCGAGTACTGCGCTGCGCAGCATGCAAGAGCTCAGCAGATC 1800
QY 1744 CACATCCAGGCGAGTGAAGCAGCCCTCCCTCAACAACAGTCCCTCCAGCCTTAATTGAAA 1803
DB 1801 CACATCCAGGCGAGTGAAGCAGCCCTCCCTCCCTCAACAACAGTCCCTCCAGCCTTAATTGAAA 1860
QY 1804 GCGAGCAGGAGGAGTGAAGCAGCAAACTGCAAAACATCCAGATCACCACAGCCATCATCAGC 1863
DB 1861 GCGAGCAGGAGGAGTGAAGCAGCAAACTGCAAAACATCCAGATCACCACAGCCATCATCAGC 1920
QY 1864 ATCCCACTCCCGCAGCGCTAAACCCAGAGGGGAGAAAGTGGGCGACACCCCTGCGAGCCCA 1923
DB 1921 ATCCCACTCCCGCAGCGCTAAACCCAGAGGGGAGAAAGTGGGCGACACCCCTGCGAGCCCA 1980
QY 1924 GGGCCCAACAGAACTTCTTCCATAACAGCAATGTTGTCAAGGCTCTGTCTTGTAA 1983
DB 1981 GGGCCCAACAGAACTTCTTCCATAACAGCAATGTTGTCAAGGCTCTGTCTTGTAA 2040
QY 1984 AATATCCCGGGCCATGCGCGGAGAGCATGCGAGCTGGGCGCAATTGCGCTATAGTG 2043
DB 2041 AATATCCCGGGCCATGCGCGGAGAGCATGCGAGCTGGGCGCAATTGCGCTATAGTG 2100
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QY 2044 AGTCGATTAAGCCGAATTC 2064
DB 2101 AGTCGATTAAGCCGAATTC 2121

RESULT 3
AAV61571
ID AAV61571 standard; cDNA; 2104 BP.
XX
AC AAV61571;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.
XX
KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
XX therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1908
FT /tag= a
FT
PN W09842833-A2.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-EP001901.
XX
PR 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
PA (SMIK ) SMITHKLINE BEECHAM LAB PHARM.
XX
PI Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
XX
DR WPI; 1998-542277/46.
XX
DR P-PSDB; AAW79589.
XX
PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
PS Claim 2; Page 24; 47pp; English.
XX
CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3.
CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated
CC from human heart cDNA by PCR amplification (see AAV61574-77). Another
CC claimed polynucleotide (see AAV61572) encodes an isoform (see AAW79590)
CC of hKv4.3 having an additional 19 amino acids. The invention relates to
CC these hKv4.3 polynucleotides and polypeptides and to methods for
CC producing such polypeptides by recombinant techniques. Also claimed are
CC methods for utilising the hKv4.3 polynucleotides for the treatment of
CC subjects in need of enhanced or reduced activity or expression of hKv4.3
CC polypeptide. These include the treatment of cardiac arrhythmias and
CC Alzheimer's disease. The invention can also be used to identify agonists
CC and antagonists of hKv4.3, and to detect disease associated with
CC inappropriate hKv4.3 expression or activity
XX
SQ Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other;

Query Match 92.3%; Score 1905; DB 2; Length 2104;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 73 ATGGCGGCGGAGTTGCGGCTGCTGCTTTTGGCCCGGCTGCGGCATCGGGTGATG 132
DB 1 ATGGCGGCGGAGTTGCAAGCTGCTGCTTTTGGCCCGGCTGCGGCATCGGGTGATG 60
QY 133 CCGGTGGCAACTGCCCATGCCCTTGGCCCGGCGGACAAAGAAAGCGGAGATGAG 192
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Db      61  ||||| CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGCCGACAAAGAACAGCGGACAGATGAG 120
Qy      193  ||||| CTGATGTCTCTCAACGTGAGTGGGGGAGGTTCCAGACCTTGAGAGCCACGCTGAGCGC 252
Db      121  ||||| CTGATGTCTCTCAACGTGAGTGGGGGAGGTTCCAGACCTTGAGAGCCACGCTGAGCGC 180
Qy      253  ||||| TACCCGAGACCCCTGCTGGGACGACGAGAGAGTCTTCTTCAACGAGGACACCAAG 312
Db      181  ||||| TACCCGAGACCCCTGCTGGGACGACGAGAGAGAGTCTTCTTCAACGAGGACACCAAG 240
Qy      313  ||||| GAGTACTCTTTCGACCCGGGACCCCGAGGTGTTCCGCTGCGTCTCAACTTCTACCCGACG 372
Db      241  ||||| GAGTACTCTTTCGACCCGGGACCCCGAGGTGTTCCGCTGCGTCTCAACTTCTACCCGACG 300
Qy      373  ||||| GGGAGCTGCACTACCCCGGCTACGAGTGCATCTCTGCTTACGACGAGCTGGCTTC 432
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Qy      493  ||||| AGGAGAACCCCGGAGCGGCTCATGACGACAACTTCGAGAACCAACGAGATCTCATG 552
Db      421  ||||| AGGAGAACCCCGGAGCGGCTCATGACGACAACTTCGAGAACCAACGAGATCTCATG 480
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Db      481  ||||| CCTCGCTCAGCTTCCGCGACAGCATGTGGGGGCTTTCGAGAACCCCGACACCGACAGC 540
Qy      613  ||||| CTGSCCTGTCTTCTTACTACGTGACTGGCTTCTTCAATCGCTGTCTCGTCTATCAAC 672
Db      541  ||||| CTGSCCTGTCTTCTTACTACGTGACTGGCTTCTTCAATCGCTGTCTCGTCTATCAAC 600
Qy      673  ||||| GTGTGTGAGACCGGTCCGCTGCGGACCGTCCCGGGACAGAGAGCTGCCGTGGGGAG 732
Db      601  ||||| GTGTGTGAGACCGGTCCGCTGCGGACCGTCCCGGGACAGAGAGCTGCCGTGGGGAG 660
Qy      733  ||||| CGCTACTCGGTGGCTTCTTCTGCTGGAACAAGGCTGCTCAATGATCTTCAACGCTGAG 792
Db      661  ||||| CGCTACTCGGTGGCTTCTTCTGCTGGAACAAGGCTGCTCAATGATCTTCAACGCTGAG 720
Qy      793  ||||| TACCTTCTGGGCTCTTTCGCGGCTTCCAGCGCTACCGCTTCAATCGGACGCTATGAGC 852
Db      721  ||||| TACCTTCTGGGCTCTTTCGCGGCTTCCAGCGCTACCGCTTCAATCGGACGCTATGAGC 780
Qy      853  ||||| ATCATTCGACGTGTGGCTCATCATGCTTACTACATCGGTCTGGTCTATGACCAACAGAG 912
Db      781  ||||| ATCATTCGACGTGTGGCTCATCATGCTTACTACATCGGTCTGGTCTATGACCAACAGAG 840
Qy      913  ||||| GACGTGTCCGGGCTTTCGTCACGCTCCGGGTCTTCCGCTTTCAGAGTCTTCAAGTTT 972
Db      841  ||||| GACGTGTCCGGGCTTTCGTCACGCTCCGGGTCTTCCGCTTTCAGAGTCTTCAAGTTT 900
Qy      973  ||||| TCCCGCCACTCCCAAGGCTGCGGATCTTGAGGCTACACACTGAAGAGCTGTGCTCCGAA 1032
Db      901  ||||| TCCCGCCACTCCCAAGGCTGCGGATCTTGAGGCTACACACTGAAGAGCTGTGCTCCGAA 960
Qy      1033  ||||| CTGGGCTTCTTCTCTTCTCCCTCAACCATGAGCATCATCTTGGCACTGTGATGTTT 1092
Db      961  ||||| CTGGGCTTCTTCTCTTCTCCCTCAACCATGAGCATCATCTTGGCACTGTGATGTTT 1020
Qy      1093  ||||| TATGCCGAGAAAGGCTCTCGGCAAGTTTCAACAGCATCTGCTGCTGTTTGGTAC 1152
Db      1021  ||||| TATGCCGAGAAAGGCTCTCGGCAAGTTTCAACAGCATCTGCTGCTGTTTGGTAC 1080
Qy      1153  ||||| ACCATGTACCATGACCACTGGGATACGAGAGCATGTGCTTAAGAAGATTGAGAGG 1212
Db      1081  ||||| ACCATGTACCATGACCACTGGGATACGAGAGCATGTGCTTAAGAAGATTGAGAGG 1140
Qy      1213  ||||| AAGATCTTGGGCTCCATCTGCTTGTAGTGGGCTCTGTGATGTGCTGCGCTGCTCCT 1272
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Db      1141  ||||| AAGATCTTGGGCTCCATCTGCTCTTGAATGGGCTCTGTGATTTGCCCTGCCAGTCCCT 1200
Qy      1273  ||||| GTGATGTCTTCCAACTTTAGCCGGATTTTACACAGATCAGAGCTGATTAACGAGG 1332
Db      1201  ||||| GTGATGTCTTCCAACTTTAGCCGGATTTTACACAGATCAGAGCTGATTAACGAGG 1260
Qy      1333  ||||| GCACAAAAGAAAGCCCGCTTGCAGATCCGTGTGGCCAAAACAGGAGTTGAAATGCA 1392
Db      1261  ||||| GCACAAAAGAAAGCCCGCTTGCAGATCCGTGTGGCCAAAACAGGAGTTGAAATGCA 1320
Qy      1393  ||||| TACCTGCACAGAAAGCGCAACGGGCTCTTCAACGAGCGCTGAGCTGACGGGCACTCCA 1452
Db      1321  ||||| TACCTGCACAGAAAGCGCAACGGGCTCTTCAACGAGCGCTGAGCTGACGGGCACTCCA 1380
Qy      1453  ||||| GAAGAGGACATGGGCAAGACCACTCACTCATGAGAGCCAGCATCACTGCTGCTG 1512
Db      1381  ||||| GAAGAGGACATGGGCAAGACCACTCACTCATGAGAGCCAGCATCACTGCTGCTG 1440
Qy      1513  ||||| CACTGCTTGAAAAAACCACTAACCAAGATTATTGATGAGAGATGTTTGAAGCAAG 1572
Db      1441  ||||| CACTGCTTGAAAAAACCACTAACCAAGATTATTGATGAGAGATGTTTGAAGCAAG 1500
Qy      1573  ||||| TGCAATGAGAGATTCAATGCAAGAACTAACCCATCCACAGAAAGTCCCTACTGTCCAGCCAC 1632
Db      1501  ||||| TGCAATGAGAGATTCAATGCAAGAACTAACCCATCCACAGAAAGTCCCTACTGTCCAGCCAC 1560
Qy      1633  ||||| CCAGGCTCACTAACCACTGCTGCTCCCGTGTGTAAGAAAGCAACACCTGCCCCAAT 1692
Db      1561  ||||| CCAGGCTCACTAACCACTGCTGCTCCCGTGTGTAAGAAAGCAACACCTGCCCCAAT 1620
Qy      1693  ||||| TCTAACCTGCCAGCTACTGCGCTGCGGACAGATGCAAGAGCTGAGCAAGATCCACATCCAG 1752
Db      1621  ||||| TCTAACCTGCCAGCTACTGCGCTGCGGACAGATGCAAGAGCTGAGCAAGATCCACATCCAG 1680
Qy      1753  ||||| GGCAGTGAGAGCCCTCCCTCAACCAACAGTGGCTCCAGCTTAATTGAAAGCAGACGAC 1812
Db      1681  ||||| GGCAGTGAGAGCCCTCCCTCAACCAACAGTGGCTCCAGCTTAATTGAAAGCAGACGAC 1740
Qy      1813  ||||| GGCAGTGAGAGCCAACTGCAAAACATCCAGATCACCAAGCATCATGACATCCCACT 1872
Db      1741  ||||| GGCAGTGAGAGCCAACTGCAAAACATCCAGATCACCAAGCATCATGACATCCCACT 1800
Qy      1873  ||||| CCCCAGCGCTAAACCCAGAGAGGGGAAAGTCCGCGCAACCCCTGCCAGGCCAGGCCCAAC 1932
Db      1801  ||||| CCCCAGCGCTAAACCCAGAGAGGGGAAAGTCCGCGCAACCCCTGCCAGGCCAGGCCCAAC 1860
Qy      1933  ||||| ACGAATTCCTTCCATTAACAGCAATGTGTCAAGTCTCTGTCTTGTAAATAATCCCGC 1992
Db      1861  ||||| ACGAATTCCTTCCATTAAGCCAGCAATGTGTCAAGTCTCTGTCTTGTAAATAATCCCGC 1920
Qy      1993  ||||| GGCCATGGC 2001
Db      1921  ||||| ACAAGAGGC 1929

RESULT 4
AAV61573 standard; cDNA; 2104 BP.
ID      AAV61573;
XX      AAV61573;
AC      11-JAN-1999 (first entry)
DT      Human Kv potassium channel hKv4.3 cDNA.
XX      Human Kv potassium channel hKv4.3; human; Alzheimer's disease; arrhythmia;
KW      Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
OS      therapy; diagnosis; ss.
XX      Homo sapiens.
XX      Homo sapiens.
FH      key      Location/Qualifiers
FT      CDS      1..1911
FT      FT      /*tag= a
```


XX W09842833-A2.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-EP001901.
 XX 27-MAR-1997; 97GB-00006377.
 XX 09-DEC-1997; 97EP-00402971.
 XX 11-DEC-1997; 97EP-00403007.
 XX (SMIK) SMITHKLINE BEECHAM LAB PHARM.
 XX Bril AWA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
 XX WPI; 1998-542277/46.
 XX P-PSDB; AAW79591.
 XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
 PT polynucleotide(s) useful in the treatment of disorders including cardiac
 PT arrhythmias and Alzheimer's disease.
 XX Claim 18; Page 27; 47pp; English.
 CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
 CC AAW79591). It was isolated using expressed sequence tag analysis. The
 CC sequence has about 91% identity in 1914 nucleotide residues with rat
 CC Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAW61571-72)
 CC are also claimed. The invention relates to hKv4.3 polynucleotides and
 CC polypeptides and to methods for producing such polypeptides by
 CC recombinant techniques. Also claimed are methods for utilizing hKv4.3
 CC polynucleotides for the treatment of subjects in need of enhanced or
 CC reduced activity or expression of hKv4.3 polypeptide. These include the
 CC treatment of cardiac arrhythmias and Alzheimer's disease. The invention
 CC can also be used to identify agonists and antagonists of hKv4.3, and to
 CC detect disease associated with inappropriate hKv4.3 expression or
 CC activity
 XX Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;
 SQ
 Query Match 91.9%; Score 1897; DB 2; Length 2104;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1909; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

DB 421 AGGAGAACCGCCGAGCGGCTCATGACGACAACTCGGAGAACACAGAGTCCATG 480
 QY 553 CCTCGCTCAGCTTCCGCGACCATGTGCGCGCTTGCAGAAACCCACACGACG 612
 DB 481 CCTCGCTCAGCTTCCGCGACCATGTGCGCGCTTGCAGAAACCCACACGACG 540
 QY 613 CTGGCCCTGCTCTTACTACTGACTGAGCTTCTTCACTGCTGTCTCGGTATCA 672
 DB 541 CTGGCCCTGCTCTTACTACTGACTGAGCTTCTTCACTGCTGTCTCGGTATCA 600
 QY 673 GGTGTGAGACGGTCCGCGGACGAGTCCGCGGACGAAAGAGCTGCGGCGGAG 732
 DB 601 GTGTGAGACGGTCCGCGGACGAGTCCGCGGACGAAAGAGCTGCGGCGGAG 660
 QY 733 CGCTACTCGGTGCGCTTCTTCTGCTGACACGCGGTGCTCATGATCTTCA 792
 DB 661 CGCTACTCGGTGCGCTTCTTCTGCTGACACGCGGTGCTCATGATCTTCA 720
 QY 793 TACCTCTGCGGCTCTTCTGCGGCTCCGACGCGCTTCACTGCGGCTCATGAGC 852
 DB 721 TACCTCTGCGGCTCTTCTGCGGCTCCGACGCGCTTCACTGCGGCTCATGAGC 780
 QY 853 ATCATCGACGTGTGCGCATCATGCGCTTACTACTGCTGTGCTATGACCAACGAG 912
 DB 781 ATCATCGACGTGTGCGCATCATGCGCTTACTACTGCTGTGCTATGACCAACGAG 840
 QY 913 GACGTGTGCGGCTCTTCTGACGCTTCCGCTTCCGCTTCAAGATCTTCAAGTT 972
 DB 841 GACGTGTGCGGCTCTTCTGACGCTTCCGCTTCCGCTTCAAGATCTTCAAGTT 900
 QY 973 TCCGCGCACTCCGAGGCGCTGCGGATCTGCGCTACACACTGAAGAGCTGCTCCGA 1032
 DB 901 TCCGCGCACTCCGAGGCGCTGCGGATCTGCGCTACACACTGAAGAGCTGCTCCGA 960
 QY 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092
 DB 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
 QY 1093 TATGCCGAGAGGCTCCTCGGCGGACGAGTTCACAGCATCCCTGCTTGTGATC 1152
 DB 1021 TATGCCGAGAGGCTCCTCGGCGGACGAGTTCACAGCATCCCTGCTTGTGATC 1080
 QY 1153 ACCATTGTCAACATGACCACTGCGGATTAACGAGATGAGAGCTGCTTAAGACGAG 1212
 DB 1081 ACCATTGTCAACATGACCACTGCGGATTAACGAGATGAGAGCTGCTTAAGACGAG 1140
 QY 1213 AAGATCTTGGCTCATGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1272
 DB 1141 AAGATCTTGGCTCATGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
 QY 1273 GTGATTGTTTCACTTTAGCCGAGTTTACACAGAAATCAGAGAGCTGATTAACGAG 1332
 DB 1201 GTGATTGTTTCACTTTAGCCGAGTTTACACAGAAATCAGAGAGCTGATTAACGAG 1260
 QY 1333 GCACAAAAGAGGCGCTTTCAGAGATCCGTGTGCCAAACAGGAGTTGAAATGCA 1392
 DB 1261 GCACAAAAGAGGCGCTTTCAGAGATCCGTGTGCCAAACAGGAGTTGAAATGCA 1320
 QY 1393 TACCTGACAGCAAGCGGCTTCAAGAGCGCTTCAAGAGCGCTGAGAGCGGACCCCA 1452
 DB 1321 TACCTGACAGCAAGCGGCTTCAAGAGCGCTTCAAGAGCGCTGAGAGCGGACCCCA 1380
 QY 1453 GAAAGAGACACATGGGCAAGACCACTCATCTATGAGAGCCAGATCATCCTGCTG 1512
 DB 1381 GAAAGAGACACATGGGCAAGACCACTCATCTATGAGAGCCAGATCATCCTGCTG 1440
 QY 1513 CACTGCTGGAAGAAACCACTTAACAGAGATTATGATGAGCAAGATGTTGAGCAAGAC 1572
 DB 1441 CACTGCTGGAAGAAACCACTTAACAGAGATTATGATGAGCAAGATGTTGAGCAAGAC 1500
 QY 1573 TGCATGAGAGTTCAATGACAACTTACCATCCACAAGAGTCCCTCACTGTCCAGCCAC 1632

Db 1501 TGCATGAGAGTTCATGACGAGACTACCCATCCACAAAGTCCCTCACTGTCCAGCCAC 1560
QY 1633 CCAGGCTCACTACCACTGCTGCTCCGCTAGTAGTAAGAGACACACACTGCCCAAT 1692
Db 1561 CCAGGCTCACTACCACTGCTGCTCCGCTAGTAGTAAGAGACACACACTGCCCAAT 1620
QY 1693 TCTAACCTGACGCTACTGCTGCTGCGAGCATGCAAGAGCTCAGACGATCCACATCCAG 1752
Db 1621 TCTAACCTGACGCTACTGCTGCTGCGAGCATGCAAGAGCTCAGACGATCCACATCCAG 1680
QY 1753 GGCAGTGAGCAGCCCTCCCTCACAACAGTGCTGCCAGCTTAATTTGAAGCAGACGAC 1812
Db 1681 GGCAGTGAGCAGCCCTCCCTCACAACAGTGCTGCCAGCTTAATTTGAAGCAGACGAC 1740
QY 1813 GGCAGTGAGCAGCCCTCCCTCACAACAGTGCTGCCAGCATCATCAGCATCCCACT 1872
Db 1741 GGCAGTGAGCAGCCCTCCCTCACAACAGTGCTGCCAGCATCATCAGCATCCCACT 1800
QY 1873 CCCCCAGCGCTAACCCCGAGAGGGGAAAGTGGCCACCCCTGCGCAGCCCGCCCAAC 1932
Db 1801 CCCCCAGCGCTAACCCCGAGAGGGGAAAGTGGCCACCCCTGCGCAGCCCGCCCAAC 1860
QY 1933 ACGAACATTCCTTCATTAACAGCATGTTGTCAGAGTCTCTGTTGTAATAATCCCGC 1992
Db 1861 ACGAACATTCCTTCATTAACAGCATGTTGTCAGAGTCTCTGTTGTAATAACCATCG 1920
QY 1993 GGCCATGCG 2001
Db 1921 ACAGAGGGC 1929

RESULT 5
AAV61572
ID AAV61572 standard; cDNA; 2072 BP.
AC AAV61572;
XX

DT 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hKv4.3 (longer isoform) cDNA.
XX

KM Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
XX therapy; diagnosis; ss.
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1.1965
FT /*tag= a

XX W09842833-A2.

XX PD 01-OCT-1998.

XX PF 23-MAR-1998; 98WO-EP001901.

XX PR 27-MAR-1997; 97GB-00006377.

XX PR 09-DEC-1997; 97EP-00402971.

XX PR 11-DEC-1997; 97EP-00403007.

XX PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.

XX PI Bril AMA, Calmels TPG, Falvre JSP, Javre J, Rouanet S;
XX DR WPI; 1998-542277/46.
XX DR P-PSDB; AAW79590.

XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
PS Claim 2; Page 26; 47BP; English.
XX

CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.
CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated
CC from human heart cDNA by PCR amplification (see AAV61574-77). Another
CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589)
CC of hKv4.3 having 19 fewer amino acid residues. The invention relates to
CC these hKv4.3 polynucleotides and polypeptides and to methods for
CC producing such polypeptides by recombinant techniques. Also claimed are
CC methods for utilizing the hKv4.3 polynucleotides for the treatment of
CC subjects in need of enhanced or reduced activity or expression of hKv4.3
CC polypeptide. These include the treatment of cardiac arrhythmias and
CC Alzheimer's disease. The invention can also be used to identify agonists
CC and antagonists of hKv4.3, and to detect disease associated with
CC inappropriate hKv4.3 expression or activity
XX
SQ Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;

Query Match 89.1%; Score 1838; DB 2; Length 2072;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

QY 73 ATGGCGCGGAGTTCGCGCTGCTGCTTTTCCCGGGCTGCGCCATCGGGTGATG 132
Db 1 ATGGCGCGGAGTTCGCGCTGCTGCTTTTCCCGGGCTGCGCCATCGGGTGATG 60
QY 133 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCCGGCGCAACAAGCGGCAAGATGAG 192
Db 61 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCCGGCGCAACAAGCGGCAAGATGAG 120
QY 193 CTGATTGCTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGGACCGCTGAGCGC 252
Db 121 CTGATTGCTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGGACCGCTGAGCGC 180
QY 253 TACCCGACACCCCTGCTGGGACAGCAGGAAAGAGTCTTTCTTCAACGAGACCAAG 312
Db 181 TACCCGACACCCCTGCTGGGACAGCAGGAAAGAGTCTTTCTTCAACGAGACCAAG 240
QY 313 GAGTACTTCTTCGACCGGGACCCCGAGGTTCCTGCTGCTGCTCACTTACCGCAGC 372
Db 241 GAGTACTTCTTCGACCGGGACCCCGAGGTTCCTGCTGCTGCTCACTTACCGCAGC 300
QY 373 GGAAGCTGCACTACCCGCGCTACGAGTGCATCTGCTTACGACGAGCTGCGCTTC 432
Db 301 GGAAGCTGCACTACCCGCGCTACGAGTGCATCTGCTTACGACGAGCTGCGCTTC 360
QY 433 TACGGCATCTCCCGGAGATCATGGGAGCTGCTGCTTACGAGAGTACAAGACCGCAAG 492
Db 361 TACGGCATCTCCCGGAGATCATGGGAGCTGCTGCTTACGAGAGTACAAGACCGCAAG 420
QY 493 AGGAGAACCGCGAGCGGCTCATGAGCAGCAAGACTCGAAGAACCAAGAGATCCATG 552
Db 421 AGGAGAACCGCGAGCGGCTCATGAGCAGCAAGACTCGAAGAACCAAGAGATCCATG 480
QY 553 CCTGCTCAGCTTCGCCAGACCATGTGGCGGGCTTCGAGAACCCCAACACGACGACG 612
Db 481 CCTGCTCAGCTTCGCCAGACCATGTGGCGGGCTTCGAGAACCCCAACACGACGACG 540
QY 613 CTGGCCCTGCTTCTTACTACGTAAGTGGCTTCTTATGCTGCTGGTATACCAAC 672
Db 541 CTGGCCCTGCTTCTTACTACGTAAGTGGCTTCTTATGCTGCTGGTATACCAAC 600
QY 673 GTGATGAGACGGTCCGTGCGGACAGGTCCCGGCGAAGAGAGTCCGTGCGGGAG 732
Db 601 GTGATGAGACGGTCCGTGCGGACAGGTCCCGGCGAAGAGAGTCCGTGCGGGAG 660
QY 733 CGCTACTCGGTGGCTTCTTCTGCTGACACAGGCGTGCATGATCTTACCGGTGAG 792
Db 661 CGCTACTCGGTGGCTTCTTCTGCTGACACAGGCGTGCATGATCTTACCGGTGAG 720
QY 793 TACTCTCTGCGGCTCTTTCGCGGCTCCACCGCTTACCGCTTATCCGAGCGTATGAGC 852
Db 721 TACTCTCTGCGGCTCTTTCGCGGCTCCACCGCTTACCGCTTATCCGAGCGTATGAGC 780

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QY 853 ATCATCGACGTGTGGCCATCATGCCCCCTACTATCGGTCTGTGTATGACCAACAACGAG 912
DB 781 ATCATCGACGTGTGGCCATCATGCCCCCTACTATCGGTCTGTGTATGACCAACAACGAG 840
QY 913 GACGTGTCCGGCCCTTGTGTACAGCTCCGGGTCTTCCGGCTCTTCAAGATCTTCAAGTTT 972
DB 841 GACGTGTCCGGCCCTTGTGTACAGCTCCGGGTCTTCCGGCTCTTCAAGATCTTCAAGTTT 900
QY 973 TCCCGCCACTCCCAAGGGCCCTGCGATCCTGGGCTACACACTGMAAGAGCTGTCGCGAA 1032
DB 901 TCCCGCCACTCCCAAGGGCCCTGCGATCCTGGGCTACACACTGMAAGAGCTGTCGCGAA 960
QY 1033 CTGGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092
DB 961 CTGGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
QY 1093 TATGCCGGAAGGGCTCTCGGCCAGCAAGTTGACCAAGCATCCCTGCTCTTGTGTAC 1152
DB 1021 TATGCCGGAAGGGCTCTCGGCCAGCAAGTTGACCAAGCATCCCTGCTCTTGTGTAC 1080
QY 1153 ACCATTGTACCATGACCACTGGAATACGAGACATGTGCTTAAGACGATTCAGAGG 1212
DB 1081 ACCATTGTACCATGACCACTGGAATACGAGACATGTGCTTAAGACGATTCAGAGG 1140
QY 1213 AAGATCTTGGGCTCATCTGTCTCTTGAATGTGGCTCTGCTCATTTGCCCTGCACTCCT 1272
DB 1141 AAGATCTTGGGCTCATCTGTCTCTTGAATGTGGCTCTGCTCATTTGCCCTGCACTCCT 1200
QY 1273 GTGATTGTTTCCAACTTAAAGCGGATTTACCAAGAAATCAGAGAGCTGATTAACGACAG 1332
DB 1201 GTGATTGTTTCCAACTTAAAGCGGATTTACCAAGAAATCAGAGAGCTGATTAACGACAG 1260
QY 1333 GCACAAAAGAGGGCCCTTGGCCAGGATCCGTGTGGCCAAAACAGGCAATTGGAATGCA 1392
DB 1261 GCACAAAAGAGGGCCCTTGGCCAGGATCCGTGTGGCCAAAACAGGCAATTGGAATGCA 1320
QY 1393 TACCTGACAGCAAGCGGCTCTTCAACGAGCGCTGGAGCTGACGGGCAACCCCA 1452
DB 1321 TACCTGACAGCAAGCGGCTCTTCAACGAGCGCTGGAGCTGACGGGCAACCCCA 1380
QY 1453 GAAGAGGAGCATGTGGCCAAAGACCACTCTCTGAGAGCCAGCATCATCACTGTCTG 1512
DB 1381 GAAGAGGAGCATGTGGCCAAAGACCACTCTCTGAGAGCCAGCATCATCACTGTCTG 1440
QY 1513 CACTGCCGTGAAAAAACCACT----- 1533
DB 1441 CACTGCCGTGAAAAAACCACTGGTGTCTATCTTGTGATGATCCCTGTATCTGTA 1500
QY 1534 -----AACCAAGATTATGATGAGCAGATGTTGAGCAAGAACTGC 1575
DB 1501 CGAACCCTCCACATCAAGAACCAAGATTATGATGAGCAGATGTTGAGCAAGAACTGC 1560
QY 1576 ATGAGAGATTCAATGCAAACTAACCCATCCCAAGAAGTCCCTCACTGTCCAGCCACCA 1635
DB 1561 ATGAGAGATTCAATGCAAACTAACCCATCCCAAGAAGTCCCTCACTGTCCAGCCACCA 1620
QY 1636 GGCCTCACTAACCACTGCTCTCCGTGTAGTAAGAAGACCAACACTGCTCCCAATTCT 1695
DB 1621 GGCCTCACTAACCACTGCTCTCCGTGTAGTAAGAAGACCAACACTGCTCCCAATTCT 1680
QY 1696 AACCTGCAGCTACTCGCTGGCGAGCATGCAAGAGCTCAGCAGCATCCATCCAGGGC 1755
DB 1681 AACCTGCAGCTACTCGCTGGCGAGCATGCAAGAGCTCAGCAGCATCCATCCAGGGC 1740
QY 1756 AGTGAAGAGCCCTCTCTCAACAACAGTGCCTCCAGCTTAATTGAAAGACAGACGGA 1815
DB 1741 AGTGAAGAGCCCTCTCTCAACAACAGTGCCTCCAGCTTAATTGAAAGACAGACGGA 1800
QY 1816 CTGAGAGCAAACTGCAAAACATCCAGATCACCACAGCCATCATCAGCATCCCACTCC 1875
DB 1801 CTGAGAGCAAACTGCAAAACATCCAGATCACCACAGCCATCATCAGCATCCCACTCC 1860
QY 1876 CCAAGCGCTAACCCCAAGGGGGAAGTGGCCACCCCTGCGACGACCAAGGCCCAACAGC 1935

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DB 1861 CCAGCGCTAACCCAGAGGGGGAAGTGGCCACCCCTGCGACGACCCCAACAGC 1920
QY 1936 AACATTCCTTCATTAACCAAGCATGTGTCAAGGTCTGTCTGTGTAATA 1985
DB 1921 AACATTCCTTCATTAACCAAGCATGTGTCAAGGTCTGTCTGTGTAATA 1970

RESULT 6
ADF91397
ID ADF91397 standard; cDNA; 1968 BP.
XX
AC ADF91397;
XX
DT 26-FEB-2004 (first entry)
XX
DE Wild-type hKv4.3 cDNA #SEQ ID 4.
XX
KW Antiarhythmic; cardiovascular; anticonvulsant; cerebroprotective;
KW tranquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;
KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;
KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;
KW tachycardia; congestive heart failure; epilepsy; stroke;
KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;
KW Parkinson's disease; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1968
FT FT /*tag= a
FT FT /product= "hKv4.3"

WO2003097682-A1.
XX
PD 27-NOV-2003.
XX
PF 14-MAY-2003; 2003WO-IB002453.
XX
PR 15-MAY-2002; 2002GB-00011123.
PR 15-MAY-2002; 2002US-0378076P.
PR 15-MAY-2002; 2002US-0378131P.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Kaletta TJ, Dewulf NE, Plaetinck GK;
XX
DR WPI, 2004-061981/06.
DR P-PSDB; ADF91398.
XX
PT New nematode worm expressing a heterologous nucleotide sequence encoding
PT a functional voltage-gated potassium channel of the Kv4 family, useful
PT for determining compounds that interact with the voltage-gated potassium
channel.
XX
PS Example 1; SEQ ID NO 4; 82pp; English.
XX
CC The invention relates to a nematode worm that expresses a heterologous
CC nucleotide sequence encoding a functional voltage-gated potassium channel
CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,
CC part or fragment. The nematode worm is useful in determining whether a
CC compound interacts with the voltage-gated potassium channel of the Kv4
CC family or whether a compound is an agonist, antagonist, opener and/or
CC blocker of the voltage-gated potassium channel expressed by the nematode
CC worm. The methods are used for identifying and developing compounds that
CC interact with voltage-gated potassium channels of the Kv4 family. The
CC compounds may be used in the development and/or preparation of
CC compositions for pharmaceutical, agrochemical and/or veterinary use.
CC These may be used in preparing compositions for preventing or treating
CC diseases or conditions such as arrhythmia, tachycardia, congestive heart
CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,
CC Alzheimer's disease or Parkinson's disease. The current sequence
CC represents wild-type hKv4.3 cDNA.

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XX	Sequence	1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;	
5Q	Query Match	89.0%; Score 1836; DB 12; Length 1968;	
	Best Local Similarity	96.8%; Pred. No. 0;	
	Matches 1906; Conservative	0; Mismatches 5; Indels 57; Gaps 1;	
QY	73	ATGGCGGCGGAGTTGGCGGCTGGGCTTTTGGCCGGGCTGGCCCATGGGTGATG	132
Db	1	ATGGCGGCGGAGTTGGCGGCTGGGCTTTTGGCCGGGCTGGCCCATGGGTGATG	60
QY	133	CCGGTGGCAACTGCCCCCATGCCCCCTGGCCCCCGGCGACAAGAACAGCGGAGATGAG	192
Db	61	CCGGTGGCAACTGCCCCCATGCCCCCTGGCCCCCGGCGACAAGAACAGCGGAGATGAG	120
QY	193	CTGATTGTCTCAACGTGAGTGGGGGAGGTTCCAGACCTGGAGGACCAAGCTGAGCGC	252
Db	121	CTGATTGTCTCAACGTGAGTGGGGGAGGTTCCAGACCTGGAGGACCAAGCTGAGCGC	180
QY	253	TACCCGAGACCCCTGTGGGCGAGCAGAGAGAGATTCTTCAACGAGACCAAG	312
Db	181	TACCCGAGACCCCTGTGGGCGAGCAGAGAGAGATTCTTCAACGAGACCAAG	240
QY	313	GAGTACTTCTTGACCCGGGACCCCGAGGTGTTCCGCTGCTCAACTTTTACCGCAG	372
Db	241	GAGTACTTCTTGACCCGGGACCCCGAGGTGTTCCGCTGCTCAACTTTTACCGCAG	300
QY	373	GGGAGCTGCACTACCCGGGCTACGAGTGACTCTGCTTACGACGAGCTGGCTTC	432
Db	301	GGGAGCTGCACTACCCGGGCTACGAGTGACTCTGCTTACGACGAGCTGGCTTC	360
QY	433	TACGCGATCTCTCCGAGATCATCGGGGACTGTGCTACGAGAGTACAGACCGCAG	492
Db	361	TACGCGATCTCTCCGAGATCATCGGGGACTGTGCTACGAGAGTACAGACCGCAG	420
QY	493	AGGAGAACCGCGGAGCGGCTCATGAGCAGACAAAGACTTCGAGAGAGTCCATG	552
Db	421	AGGAGAACCGCGGAGCGGCTCATGAGCAGACAAAGACTTCGAGAGAGTCCATG	480
QY	553	CCCTGCTCAGCTTCCGCGAGACCATGTGGCGGCTTGGAGAACCCCAACACGACAG	612
Db	481	CCCTGCTCAGCTTCCGCGAGACCATGTGGCGGCTTGGAGAACCCCAACACGACAG	540
QY	613	CTGGCCCTGTGTTCTTACTAGTGACTGGCTTCTTCAATGCTGCTGCTATCAAC	672
Db	541	CTGGCCCTGTGTTCTTACTAGTGACTGGCTTCTTCAATGCTGCTGCTATCAAC	600
QY	673	GTGTGGAGAGCGGTGCGGTGGCGGACCGTCCCGGGGAGAGAGCTGCGGGGAG	732
Db	601	GTGTGGAGAGCGGTGCGGTGGCGGACCGTCCCGGGGAGAGAGCTGCGGGGAG	660
QY	733	CGTACTCGGTGGCTTCTTCTGCTGAGACAGGCGTGCATGATCTTCAACGTGAG	792
Db	661	CGTACTCGGTGGCTTCTTCTGCTGAGACAGGCGTGCATGATCTTCAACGTGAG	720
QY	793	TACCTTCCTGGGCTCTTGGCGGCTTCCAGCGCTTACCGCTTATCCGAGCGTATGAG	852
Db	721	TACCTTCCTGGGCTCTTGGCGGCTTCCAGCGCTTACCGCTTATCCGAGCGTATGAG	780
QY	853	ATCATGACGTGGTGGCCATCATGCGCTTACTACATGCGTCTGTCATGACCAACAGAG	912
Db	781	ATCATGACGTGGTGGCCATCATGCGCTTACTACATGCGTCTGTCATGACCAACAGAG	840
QY	913	GACGTGTCCGGGCTTGTGACAGCTCCGGGCTTTCGCGCTTTCAGAGTCTTCAAGTTT	972
Db	841	GACGTGTCCGGGCTTGTGACAGCTCCGGGCTTTCGCGCTTTCAGAGTCTTCAAGTTT	900
QY	973	TCCGCGCACTCCAGGCGCTGCGGATCTGGGCTACACTGAGAGAGCTGCTCCGAA	1032
Db	901	TCCGCGCACTCCAGGCGCTGCGGATCTGGGCTACACTGAGAGAGCTGCTCCGAA	960
QY	1033	CTGGGCTTCTTCTTCTTCTCCCTCAACGAGCATCATCTTTGCACTGTGATGTTT	1092

Db	961	CTGGGCTTCTTCTTCTTCTCCCTCAACCATGGCCATCATCTTTGGCCACTGTGATGTTT	1020
QY	1093	TATGCCGAGAGGGCTCCTCGGCGAGCAAGTTACAGAGCATCCCTGCTTGGTATC	1152
Db	1021	TATGCCGAGAGGGCTCCTCGGCGAGCAAGTTACAGAGCATCCCTGCTTGGTATC	1080
QY	1153	ACCATGTCAACATGACCAACATGGGATACGAGACATGTGCTTAAGACGATTGAGGG	1212
Db	1081	ACCATGTCAACATGACCAACATGGGATACGAGACATGTGCTTAAGACGATTGAGGG	1140
QY	1213	AAGATTTTGGCTTCAATCTGCTCTTGAAGTGGCTGCTGTGATTTGCTGCTGCTT	1272
Db	1141	AAGATTTTGGCTTCAATCTGCTCTTGAAGTGGCTGCTGTGATTTGCTGCTGCTT	1200
QY	1273	GTGATTGTTTCCAACTTTAGCCGGAATTTACCAACAGAAATCAGAGCTGATTAACG	1332
Db	1201	GTGATTGTTTCCAACTTTAGCCGGAATTTACCAACAGAAATCAGAGCTGATTAACG	1260
QY	1333	GCACAAAAGAGGCCCGCTTGGCAGATCGTGTGGCCAAAACAGGAGTTGAAATGCA	1392
Db	1261	GCACAAAAGAGGCCCGCTTGGCAGATCGTGTGGCCAAAACAGGAGTTGAAATGCA	1320
QY	1393	TACCTGACAGAGCGGCAACGGGCTCTTCAACGAGCGCTGAGAGTGAACGGGACCC	1452
Db	1321	TACCTGACAGAGCGGCAACGGGCTCTTCAACGAGCGCTGAGAGTGAACGGGACCC	1380
QY	1453	GAAGAGAGCAGATGGGCAAGACCACTCACTCATGAGAGCGCAGATCATCACTGCTG	1512
Db	1381	GAAGAGAGCAGATGGGCAAGACCACTCACTCATGAGAGCGCAGATCATCACTGCTG	1440
QY	1513	CACCTGCTGAAAAAACCACT-----	1533
Db	1441	CACCTGCTGAAAAAACCACTGGGTTGCTTATCTTGATGATATCCCTGTTATCTGTA	1500
QY	1534	-----AACCAAGATTATTGATGAGCAGATGTTTGAGCAGAACTGC	1575
Db	1501	CGAAGCTCCACCATCAAGAAACCAAGATTATTGATGAGCAGATGTTTGAGCAGAACTGC	1560
QY	1576	ATGAGAGTTCAATGACAGAACTAACCATCAACAGAAAGTCCCTCACTGTCCAGCCCA	1635
Db	1561	ATGAGAGTTCAATGACAGAACTAACCATCAACAGAAAGTCCCTCACTGTCCAGCCCA	1620
QY	1636	GGCTTCACTACCACTGTGCTCCGCTGCTAGTAAGAAGACCAACACTGCGCCAAATTCT	1695
Db	1621	GGCTTCACTACCACTGTGCTCCGCTGCTAGTAAGAAGACCAACACTGCGCCAAATTCT	1680
QY	1696	AACCTGCACTACTGCGCTGCGGAGCATGCAAGAGCTCAGACGATCCATCCAGGGC	1755
Db	1681	AACCTGCACTACTGCGCTGCGGAGCATGCAAGAGCTCAGACGATCCATCCAGGGC	1740
QY	1756	AGTGAAGAGCCCTCCCTCAACACAGTGGCTCCAGCTTAATTGAAAAGACAGACGGA	1815
Db	1741	AGTGAAGAGCCCTCCCTCAACACAGTGGCTCCAGCTTAATTGAAAAGACAGACGGA	1800
QY	1816	CTGAGAACCAACTGCAAAACATCCAGATACCAAGCCATCATGAGATCCCACTCCC	1875
Db	1801	CTGAGAACCAACTGCAAAACATCCAGATACCAAGCCATCATGAGATCCCACTCCC	1860
QY	1876	CCAGGCTAAACCCAGAGGGGGAAGTCCGCCACCCCTGCGAGCCCGGCGCCCAACAG	1935
Db	1861	CCAGGCTAAACCCAGAGGGGGAAGTCCGCCACCCCTGCGAGCCCGGCGCCCAACAG	1920
QY	1936	AACATTCCTTCATACCAAGCAATGTTGTCAAGGTCTGTGTTGTA 1983	
Db	1921	AACATTCCTTCATACCAAGCAATGTTGTCAAGGTCTGTGTTGTA 1968	

RESULT 7
AAH21247
ID AAH21247 standard; cDNA; 2351 BP.
XX
AC
XX
AAH21247;
XX

DT 13-SEP-2001 (first entry)
 XX Human Kv4.2 cDNA.
 DE Human Kv4.2 cDNA.
 XX Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;
 KM neurodegenerative disease; ischemia; stroke; Alzheimer's disease;
 KM Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;
 KM learning capacity; protein kinase activator; anti-arrhythmic; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 433..2322
 FT /*tag= a
 FT /product= "Kv4.2 alpha subunit"
 XX DE19963612-A1.
 XX PD 12-JUL-2001.
 XX 29-DEC-1999; 99DE-01063612.
 XX 29-DEC-1999; 99DE-01063612.
 XX 29-DEC-1999; 99DE-01063612.
 XX (GENT-) FORSCHUNGSEBELLSCHAFT GENTON MBH.
 XX MPI; 2001-426637/46.
 XX P-PSDB; AAB86319.
 DR New potassium channel subunit proteins, useful for identifying and
 PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological
 PT agents.
 XX Claim 11; Page 18-21; 50pp; German.
 XX This invention describes a novel potassium channel protein (I) that is
 CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium
 CC channels containing (I) are used to identify and test: (i) compounds for
 CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,
 CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac
 CC arrhythmia, or those that improve learning capacity and memory; and (ii)
 CC activators of protein kinases. Host cells that express (I) can identify
 CC agents that do not interact significantly with channels and control I_t_o
 CC (a quickly activated transient current), so lack the side effects of
 CC known anti-arrhythmic agents. They also eliminate, or reduce, the need
 CC for testing on organ cultures
 CC
 XX Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
 SO
 Query Match 48.5%; Score 1000.8; DB 4; Length 2351;
 Best Local Similarity 72.8%; Pred. No. 1.3e-188;
 Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 363 CTACCGACGGGGAAGCTGCACTACCGCGCTACGAGTGCATCTCTGCTTACGACGACGA 422
 DB 723 CTACCGACCTGGGAAGCTCCACTATCTCTGCGACGAGTGCATCTCTGCTTACGATGAAGA 782
 QY 423 GCTGGCCTTCTACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTCA 482
 DB 783 ACTGGCTTCTTGGCCTCATCCCGAATCATCGGCACTGCTGTTATGAGAGTACAA 842
 QY 483 GGACCGCAAGAGGGAAGACCGCGGCTCATGACGACCAACGACTCGGAACAACA 542
 DB 843 GATCGCAGGCGAGAGAACCGCGGCTGACGACGACGCGGATACCGACCGCTGG 902
 QY 543 GGAG--TTCATGCGCTCGCTCAGCTTCCGCAACCATGTGGGGGCTTGAAGACC 599
 DB 903 GGAAGCGCCTTGGCCACCATGACTGCAAGGAGGCTGGAAGGCTTGAAGACC 962
 QY 600 CCACACGACGCGCTGCGCTGCTTCTACTAGTGAAGTGGCTTCTCATCGCTGCTC 659
 DB 963 CCACACGACGACGATGCGCTGCTGCTTCTACTATGTCACGGGCTTTCATGCGCTGC 1022
 QY 660 GGTCAATCAACACGCTGTGAGACCGGTGCGGCGACGCTCCCGG--CAGCAAGA 716
 DB 1023 TGTCACTCGCAATGTGTGGAACAGTCCGTCGGATCAAGCCAGGTCACTTAAGA 1082
 QY 717 GCTGCCGTGCGGAGCGCTACTCGGTGCTTCTGCTGCTGACACGCGGCTGCTCAT 776
 DB 1083 ACTGCCCTGTGAGAGCGGTATGCTGTGCTTCTGCTTGTGACACGCGCTGCTCAT 1142
 QY 777 GATCTTCAACGCTGATGCTCTGCGGCTTCTGCGGCTCCAGCGCTTACCGCTTCT 836
 DB 1143 GATCTTCAAGTGAATGATTTGCTTCTGCTGCTGCTGACGCGCTTACTGCTTGT 1202
 QY 837 CCGCAGCGCTATGACATATCGACGTGTGCGCATATGCCCTTACTACATGCTGTGT 896
 DB 1203 GCGTAGTGCATGATGATATCGACGTGTGCGCATATGCCCTTACTACATGCGCTGT 1262
 QY 897 CATGACCAACAAGAGAGCTGTGCGGCTTCTGTCACGCTCCGCTTCCGCTTCT 956
 DB 1263 GATGACAGCAATAGAGACGTCAGCGAGCTTGTGTCACACTCGAGTCTTCCGCTT 1322
 QY 957 CAGGATCTTCAAGTTTCCCGGCACTCCAGGCGCTGCGGATCTGCGGTACACACTGA 1016
 DB 1323 CAGGATCTTCAAGTTTCCCGGCACTCCAGGCGCTGCGGATCTGCGGTACACACTGA 1382
 QY 1017 GAGCTGTGCTCCGACACTGCGCTTCTTCTTCTCCCTCACCATGGCCATCATCTT 1076
 DB 1383 GAGTGTGCTCCGACACTGCGCTTCTTCTTCTCCCTCACCATGGCCATCATCTT 1442
 QY 1077 TGCACATGATGATTTTATGCGGAGAGGCTCTCGGCGCAAGTTTACAGCATCTCC 1136
 DB 1443 CGTACAGTATGTTCTACGAGAGAGGCTTCTGCTTCTGCTGCTGAGGCGCTTGTGAT 1502
 QY 1137 TGCCTGTTTGTACACCATGTGTACCATGACCACTGCGGATACGAGACATGTGCT 1196
 DB 1503 TGCAGCTTCTGTATACCATGTGTACCATGACCACTGCGGATACGAGACATGTGCT 1562
 QY 1197 TAAGACGATTCAGGGAAGATCTTCCGCTCATCTGCTTCTGAGTGGCGCTGTGAT 1256
 DB 1563 AAAAACAATAGCAGGGAAGATTTTGGTTCTATCTGCTGCTGAGGCGCTTGTGAT 1622
 QY 1257 TGCCTGCGAGTCCCTGTGATTTTCCACTTACCGGATTTACACAGATCAAG 1316
 DB 1623 TGTCTTACTGTTCCGCTGATGTTATTCACCTTCAAGTGCATTTACACAGATCAAG 1682
 QY 1317 AGCTGATAAGCGAGGCAAAAGAGGCGCGCTTGCACAGATCCGTGTGCGCAAAAC 1376
 DB 1683 AGCAGACAAAGAGGCAAAAGAGGCTGACACTGCGCAGATCGCGGCGCAAAAG 1742
 QY 1377 AGCAGTTGCAATGATACCTGACACAGCAAGCAACGCGCTCTCAACGAGCGCTGA 1436
 DB 1743 CGAAGCGCAATGCTTACATGACAGACCAACGGAATGTTTACTACATCAAGTGA 1802
 QY 1437 GCTGACGGGCAACCAAGAGAGGACATGGGCAAGACCACTCACTCATGAGAGCA 1496

QY	83	CCGACAGCGTCA	TGAGCATCAT	CGACGCTG	TGCGCATCAT	TCCCTCACTACAT	CGGTCTG	896				
Db	1203	GCGTGTGTCA	TGAGTATCAT	CGACGCTG	TGCGCATCAT	TCCCTCACTACAT	CGGTCTG	1262				
QY	897	CATGACCAACA	CGAGCAGT	GTCCGGCGCTT	CGTCA	CGCTCCGGGCTT	CCGCGCTT	956				
Db	1263	GATGACAGACA	TAGAGACGT	CAGCGGAGCCTT	TGTCA	CACTCCGAGCTT	CCGGGCTT	1322				
QY	957	CAGATCTTCAA	AGTTTTT	CCGCCACT	CCCAAGGGCCT	GGCATCT	TGGGCTTACAC	CTGAA	1016			
Db	1323	CAGATCTTAA	AGTTTTT	CCGCCACT	CTCAAGGGCCT	GGCATCT	CTGGGCTTACAC	CTGAA	1382			
QY	1017	GAGCTGTGCT	CCGAAC	TGGGCTTCT	CTCTCTCC	TCAACAT	GGCCATCATCTT	1076				
Db	1383	GAGTGTGCT	CCGAAT	TGGGCTTCT	CTCTCTCC	TCAACAT	GGCCATCATCTT	1442				
QY	1077	TGCCACTGT	GATGTTTT	TATGCGAG	AAGGGCTCCT	CGCGCA	CAAGTTTCA	CAAGCATCC	1136			
Db	1443	CGCTACAGT	TATGTTTT	CTACGAG	AAGGGGCTCTT	CGGCTT	AGCAAGTTCA	CAAGCATCC	1502			
QY	1137	TGCCGTGTTT	TGTAACA	CCATTGT	CAACCATG	ACCACT	TGGGATAT	GGAGACATGTGCC	1196			
Db	1503	TGCAGCCTT	CTGTGTAT	ACCATCGT	CAACATGACA	CACTAG	GGTATGTG	ATGATGTGCC	1562			
QY	1197	TAAGCATTG	CAGGGAAG	ATCTTCG	CTCCATCTG	CTCTG	ATGTGCGTCTGT	CTAT	1256			
Db	1563	AAAAACAT	AGCAGGGA	AGATTTT	TGTTCTAT	CTGTCTG	CTAGTGGGCTT	TGTCTAT	1622			
QY	1257	TGCCCTGCC	AGTCTCT	GTGATTT	TTTCCAACTT	TAACCG	GAATTTAC	CAACATCAG	1316			
Db	1623	TGCTCTAC	CTGTTC	CGGTGAT	TGTATC	CACTTCA	GTGCGATCT	ACACCAATCA	CG	1682		
QY	1317	AGCTGAT	TAAACG	CAGGGA	CAAAAGG	CCGCTT	GCACAG	ATCCGTGT	GGCAAAAC	1376		
Db	1683	AGCAGACA	AAAGGGA	CGCACAA	AAAGCTAG	ACTGGCC	AGATCC	GGGCA	CCCAAAAG	1742		
QY	1377	AGGCAGT	TGGAAT	GAATCACT	TGCACAG	CAAGCG	CAACGGGCT	CTCAACG	AGCGCTGGA	1436		
Db	1743	CGGAAGCG	CAATGCTT	ATCATG	CAAGCAACG	AAATGTTT	ACTCA	GTATCA	CGCTGCA	1802		
QY	1437	GCTGACGGG	CACCCCA	GAAGAG	ACACAT	TGGCAAG	ACCACTCA	CTCATG	AGAGCA	1496		
Db	1803	GTCTCAG	AGAGA--	TGACAG	GGCTTT	TGTAG	CAAAATCC	GGCTT	CAAGCTT	GAAACCA	1859	
QY	1497	GCATCAT	CACTGCTG	CACTGCT	CGAAAAA	AAACCACT	AAACCA	CGAGATTT	ATGATG	AGCA	1556	
Db	1860	GCACCA	CACTGCTT	CACTGCT	CGAAAAA	AAACCA	CGAATCA	CGAGATTT	GTGAG	CGAACA	1919	
QY	1557	GATGTTG	AGCAGAA	CTGATG	AGAGTT	CAATGCA	GAACCTA	CCCATCC	ACAAGATCC	1616		
Db	1920	AGCTTTG	AAGAAAG	CTGATG	AGAGTT	GCAACT	GTAAAT	GTCTT	CAAGTCA	CAAGTCC	1979	
QY	1617	CTCATGT	CCAGCC	ACCGAG	CCCTCACT	ACACCT	GTGCTCC	CGGTAG	TAAAG	AGAC	1676	
Db	1980	TTCACTG	TCCTTCA	CAACA	GAGATCA	CCAGCA	CTGCTGTT	CAACG	AGACAC	AAAAAAC	2039	
QY	1677	CACACAC	CTGCCCA	ATTCTTA	ACTG	CCAGCT	ACTGCG	CGAGCAT	GCAAG	CTCAG	1736	
Db	2040	TTTTGCA	TCCCAAT	GTGAT	TCAGGA	AGCCATCA	AGGTAT	GTATCA	AGAACT	CAG	2099	
QY	1737	CACGAT	CCACAT	CCAGG	CAGTGA	GCAGCC	CTCC	CAACA	CCAGT	GGCTCC	AGCCTTAA	1796
Db	2100	CACGAT	CCACAT	CCAGT	GTGTGA	GAACA	CACTGT	GTCTA	ACAG	CGATCC	AGTTTAA	2159
QY	1797	TTTGAAG	CAGACG	AGCTG	AGACCA	AAATG	CAAAA	CATCTC	CAAGAT	CAACCA	CAGCCAT	1856
Db	2160	TGCCAA	ATGGA	AGTGT	GTAACT	TAAC	TGTGA	CAACCTT	ATGTG	ACTA	CAGCAAT	2219
QY	1857	CATCAG	ATCCCA	CTCCCC	CAAGCG	CTAAC	CCCA	GAGGGG	GAAGT	CGGCCA	1908	
Db	2220	AATA	AGATCC	CAAC	CTCC	AGTAA	CCACCA	CCGAAG	GAAG	CGATAG	GGCCA	2271

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RESULT 9
ADJ11252
ID ADJ11252 standard; DNA, 2351 BP.
AC ADJ11252;
XX
XX 15-APR-2004 (first entry)
XX
XX
XX Human ovarian tumour antigen DNA SegID 253.
DE
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
XX cytosstatic; gene.
XX
XX Homo sapiens.
OS
XX
XX US2003232056-A1.
XX
XX 18-DEC-2003.
XX
XX 14-FEB-2003; 2003US-00369186.
XX
XX 10-SEP-1999; 99US-00394374.
XX
XX 01-MAY-2000; 2000US-00561778.
XX
XX 15-AUG-2000; 2000US-00640173.
XX
XX 07-SEP-2000; 2000US-00656668.
XX
XX 14-NOV-2000; 2000US-00713550.
XX
XX 03-APR-2001; 2001US-00825294.
XX
XX 02-OCT-2001; 2001US-00970966.
XX
XX 02-AUG-2002; 2002US-00212677.
XX
XX 05-FEB-2003; 2003US-00361811.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
PI
XX
XX WPI; 2004-178717/17.
XX
XX P-PSDB; ADJ11258.
XX
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes for detecting presence of cancer
XX in a patient.
XX
XX Example 12; SEQ ID NO 253; 222pp; English.
XX
XX This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/ or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide is a human ovarian tumour antigen DNA
CC sequence given in an exemplification of the invention.
XX
XX Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
SQ
Query Match 48.5%; Score 1000.8; DB 12; Length 2351;
Best Local Similarity 72.8%; Pred. No. 1.3e-188;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4
DB
66 AGTCACCATGGCGCGCGAGTTGGCGGCTTGGCTTGGCCCCGCGGCTGCGGCATCG 125
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
423 AGTAATCATGGCGCGCGGCGGTGGCGAGCGTGGCTGCTTTTGCAGGCGCGGCTATCG 482
126 GTGATGCGCGTGGCCCACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAGAACGCG 182
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
483 GTGATGCGCTGTGGCTTCGGGGGCTTATGCGCGCTCCCCCGAGGCAAGAGAAAGGAC 542

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QY	183	GCAAGATGAGCTGATTGTCTCTCAACGTAGTGGGGCGGAGTTCCAGACCTGGAGCAAC	242
Db	543	CCAAGATGCTCTCATTTGTGTGTAATGTAGTGGCACCCGCTTCCAGACGTGGCAGACAC	602
QY	243	GCTGGAGGGCTACCCGGACACCCCTGCTGGGAGCACGGAGAGAGTCTTCTTCAACGA	302
Db	603	CCTGGAACGTTATCCAGACACTCTACTGGGAGTTCTGAGAGGACCTTTTCTACACCC	662
QY	303	GGACACCAAGAGTACTTCTTCCGACCCGGGACCCCGAGGTGTTCGCTGCTCAACTT	362
Db	663	AGAAACTCAGCAGTATTTCTTGAACCGTGACCCAGACATCTTCCGCCACATCTGAATTT	722
QY	363	CTACCCGACGGGGAGCTGECATACCCGCGCTACGAGTGATCTCTGCTACGACGAGA	422
Db	723	CTACCCGACTGGGAGCTCACTATCTCGCCACGAGTGATCTCTGCTTACATGAAGA	782
QY	423	GCTGGCTTCTACGGCATCTCTCCGGAGATCATCGGGGACTGCTGCTACGAGATACA	482
Db	783	ACTGGCTTCTTTGGCTCATCCCGGAATCATCGGCGACTCTGTTATGAGAGTACAA	842
QY	483	GGACCGCAAGGGGAGAACCGCGGCGCTCATGAGCGACACGACTTCGGAGAACCA	542
Db	843	GGATCGAGGCGAGAGAACCGCGCGCTGACAGAGCGACGGGATACCGACCGCTGG	902
QY	543	GGAG--TCCATGCCCTCGCTCAGCTTCCGCAGACCATGTGGCGGCTTCAGAACCC	599
Db	903	GGAGAGCGCTTTCGCCCATGACTGCAGAGCGAGAGGCTTGGAGGGCTTCAGAACCC	962
QY	600	CCACACCAAGCAGCGCTGGGCTGTCTTCTACTACGTGACTGGCTTCTCATGCTGTCTC	659
Db	963	CCACACCAAGCAGATGGGCTGTGTCTTCTACTATGTCACGGGGTTTTCATTGCCGTCTC	1022
QY	660	GCTCATCAACCAAGTGTGGAGACGCTGCCGCGGACCGTCCCGG--CAGCAAGGA	716
Db	1023	TGTCATCGCAATGTGTGGAAACAGTCCGTCCGATCAAGCCAGGTCACATTAAAGA	1082
QY	717	GCTGCCGTGGGGGAGCGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGGCTGCTCAT	776
Db	1083	ACTGCCCTGTGGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACACGGCTGCGTCA	1142
QY	777	GATCTTCAACCGTGAAGTACTCTGCGGCTTCCGGGCTCCAGCGCTACCGCTTCA	836
Db	1143	GATCTTCAAGTGAAGTATTTGCTTCGCTGGCTGACGCGCTAGTGTATCCGTTTGT	1202
QY	837	CCGACGGTCATGAGCATCGACGTGTGGGCCATCATGCCCTACTCATATGSGTCTGGT	896
Db	1203	GCGTAGTGCATGATATCATCGACGTGTGGCCATCTGCTTATTAATATGGGCTGGT	1262
QY	897	CATGACCAACACGAGACGTGTCCGGCGCTTCTGTACGCTCCGGGTCTTCCGCTCTT	956
Db	1263	GATGACAGACAATGAGGAGCTCAGCGGAGCTTTGTACACTCCGAGTCTTCCGGGTCTT	1322
QY	957	CAGGATCTTCAAGTTTCCCGCCACTCCACAGGGCTGCGGATCTGGGCTTACACTGAA	1016
Db	1323	CAGGATCTTAAAGTTTCCCGCCACTTCAAGGCTGCGCATCTTGGGGTACACACTGAA	1382
QY	1017	GAGCTGTGCTCCGAAGTGGGCTTCTTCTTCTCTCCCTACCATGGCCATCATCATTT	1076
Db	1383	GAGTTGTGCTCAGAAATGGGCTTCTGTCTTTCTGCTCAACATGGCTATCATCATTT	1442
QY	1077	TGCCACTGTGATGTTTATGCGGAGAGGGCTCTCGGCCACGAAGTTCACAAGCATCCC	1136
Db	1443	CGCTAACGTTATGTTCTTACGACAGAAAGGGCTTTCGGCTTACGAAGTTTACAGCATCCC	1502
QY	1137	TGCTCGTTTGGTACCAATTGTTCACCATGACCACTGGGATACGAGACATGTGTCC	1196
Db	1503	TGCAGCTTCTGGTATATCATGTCACCAATGACAACTAGGGTATGTGACATGTGTCC	1562
QY	1197	TAAAGCATTTGACGGAAGATCTTCGGCTCATGCTCTCTTGAGTGGCGTCTGTGTCAT	1256
Db	1563	AAAAACATAGCAGGGAAGATTTTGGTTCTATCTGTTCGCTGAGTGGGCTTGTGTGTCAT	1622
QY	1257	TGCCCTGCCAGTCCCTGTGATGTTCACCTTAACTTAAACGCGGATTTAACCAACGATCAGAG	1316

D	b		1623	TGCTCTACCGTGTCCGGTGATGTATCCAATTCAAGTCGATCTTACCACCAAGAATCAACG	1682				
O	y		1317	AGCTGATATAACGACAGGCACAAAAGAAAGGCCCGCCTTGCCAGAGATCCGTTGGCCAAAAAC	1376				
D	b		1683	AGCAGACAACGAAAGGGCACAAAAGAAAGCTAAGACTGGCCAGATCCGGGCAGCCAAAAAG	1742				
O	y		1377	AGCAGATTGCANATGCAATCACTTGCACAGCAAGCGCAA CGGGCTCTCAACGAGGGCGCTGA	1436				
D	b		1743	CGGAAGCGCAATGCTTAATCATGACAGCAACGGAA TGGTTTA CTCAAGTAATCAGCTGCA	1802				
O	y		1437	GCTGACGGGCAACCCGAGAAGAGACACATGGGCAAGAACCACTCCTCATCTGAGAGCCA	1496				
D	b		1803	GTCCTCAGAGGA---TGACAGGCTTTTGTAGCAATCCGGCTCCAGCTTTGAAACCA	1859				
O	y		1497	GCATCATCACTGCTGCTGCACTGCGCTGAAAACCACTAACCAAGAGTTTATTTAGTAGCA	1556				
D	b		1860	GCAACACCACCTGCTTCACTGCTGGAACCAACGAAATCAAGATTGTGACGAAACA	1919				
O	y		1557	GATGTTTGACGAGAACTGCATGAGAGATTCAATGCAAGAACTAACCCATCCACAAGAGTCC	1616				
D	b		1920	AGTCTTTGAAGAAAGCTGCATGAGAGATTGCAACTGTTAATGTCCTTCAAGTCACAGTCC	1979				
O	y		1617	CTCACTGTCCAGCCACCCAGGCTCACTAACCACTGCTGCTCCGTCGTAGTAAGAAAGAC	1676				
D	b		1980	TTCACTGTCTTCACACAAGAGATCACAGCACTGTGTTCACGACACACAAAAAAC	2039				
O	y		1677	CACACACCTGCCCAATTCTTAACCTGACAGCTACTGCGCTGGCAGCATGCAAGAGCTCAG	1736				
D	b		2040	TTTTTCGATCCCAATGCAATGTATCAGAAAGCATCAAGGTAGTAACAAGAACTCAG	2099				
O	y		1737	CACGATCCACATCCAGGGCAGTGAGCAGCCCTCCCTCACAAACAGTGCCTCAGCCTTAA	1796				
D	b		2100	CACGATTCAGATCAGATGTGTGAGAGAAACACCTCTGTCTTAACAGCCGATCCAGTTTAA	2159				
O	y		1797	TTTGAAGACGACGACGAGACTGAGACCAAACTGCAAAACATCCAGATCACCAAGCCAT	1856				
D	b		2160	TGCCAAATGGAAGAGTGTTTAACATACTGTGAACAACCTTATGTGACTACAGCAAT	2219				
O	y		1857	CATCAGATCCCCCACTCCCCCAGCGCTAACCCAGAGGGGGAAGTGGGCCA	1908				
D	b		2220	AATTAAGATCCCAACACTCCAGTAACCA CACCGAAGAGACGATAGGCCA	2271				
RESULT 10									
ADM43513									
ID	ADM43513 standard; DNA; 2351 BP.								
XX	AC ADM43513;								
XX	DT 03-JUN-2004 (first entry)								
DE	Human ovarian cancer cDNA homologous DNA #7.								
XX	ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.								
OS	Homo sapiens.								
PN	US2003129192-A1.								
PD	10-JUL-2003.								
P	F	02-AUG-2002; 2002US-00212677.							
PR	10-SEP-1999; 99US-00394374.								
PR	01-MAY-2000; 2000US-00561778.								
PR	15-AUG-2000; 2000US-00640173.								
PR	07-SEP-2000; 2000US-00656668.								
PR	14-NOV-2000; 2000US-00713550.								
PR	03-APR-2001; 2001US-00825294.								
PR	02-OCT-2001; 2001US-00970966.								
PA	(CORI-) CORIXA CORP.								

XX Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
XX WPI: 2004-051070/05.
DR P-PSDB; ADM43519.
XX
PT New isolated polynucleotide encoding an ovarian tumor protein for use in
PT diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX
PS Claim 1; SEQ ID NO 253; 220pp; English.
XX
CC The invention relates to an isolated polynucleotide. The invention is
CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.
CC The present sequence represents a human ovarian carcinoma cDNA homologous
CC DNA.
XX
SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Query Match 48.5%; Score 1000.8; DB 12; Length 2351;
Best Local Similarity 72.8%; Pred. No. 1.3e-188;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 66 AGTCACCATGGCGGCGGAGTTGCGGCTGCTGCTTTGCCCCGGGCTGCGCCATCGG 125
DB |||||
QY 423 AGTAATCATGGCGGCGGAGTGGAGCGTGGCTGCTTTTGCAAGGCGAGCGCTATCGG 482
DB |||||
QY 126 GTGGATGCGGGTGGCCAACTGCGCCCATGCCCCCTGGCCCC---GGCCGACAAGAACAGCG 182
DB |||||
QY 483 GTGGATGCTGTGGCTCGGGGCTATGCGGCTCCCGAGGAGAGAGAGAAAGAGC 542
DB |||||
QY 183 GAGAGATGAGTGAATGCTCTCAACGTAAGTGGCGGAGGTTCCAGACTGTGAAGACAC 242
DB |||||
QY 543 CCAAGATGCTCTCATTTGCTGTAATGTAAGTGGACCCGCTTCCAGACGTGGAGAGAC 602
DB |||||
QY 243 GCTGGAGCGCTACCGCGACACCCCTGCTGGGAGAGACGAGAGAGAGTCTTTCAACGA 302
DB |||||
QY 603 CTGGGAACGTTACCCAGACACTCTACTGGGAGTCTGAGAGGAGCTTTTCAACACCC 662
DB |||||
QY 303 GGAACCAAGAGTACTTCTTGACCCGAGACCCGAGGTGTTCCGCTGCTCAACTT 362
DB |||||
QY 663 AGAACTCAGCAGTATTTCTTGAACCGTGAACCGACATCTTCCGACATCTGAATTT 722
DB |||||
QY 363 CTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGATGCACTCTGCTTACGACGCA 422
DB |||||
QY 723 CTACCGCAGCTGGGAAGCTCCACTATCTCGCCAGAGTGAATCTGCTTACGATGAAGA 782
DB |||||
QY 423 GCTGGCCTTCTACGCGCATCTCCCGAGATCATCGGAGACTGTGCTACGAGAGTACAA 482
DB |||||
QY 783 ACTGGCCTTCTTTGGCCTCATCCGGAATCATCGGAGCTGCTGTATGAGAGTACAA 842
DB |||||
QY 483 GGAACCGAAGAGGAGAACGCGGAGCGGCTCATGAGACGACGACTCGAGAACAAACA 542
DB |||||
QY 843 GGAATCGAGGCGAGAGAACGCGGAGCGGCTGAGAGACGAGCGGATACCGACACCGCTGG 902
DB |||||
QY 543 GGAG---TCCATGCGCTCGCTCAGCTTCCGCCAGACCATGCGGCGCTTGAAGAACCC 599
DB |||||
QY 903 GGAGAGCGGCTTGGCCACCATGATGCAAGGAGGAGGTCTGGAGGCGCTTGAAGAACCC 962
DB |||||
QY 600 CCAACACGACGAGTGGCGGCTGCTTCTACTAGTGAATGAGCTTCTTCACTGCTGCTC 659
DB |||||
QY 963 CCAACACGACGAGTGGCGGCTGCTTCTACTAGTGAATGAGCTTCTTCACTGCTGCTC 1022
DB |||||
QY 660 GGTTCATCAACCAAGTGGAGAGCGGTGCGGCGGAGCGGTCCCGG---CAGCAAGGA 716
DB |||||
QY 1023 TGTTCATCGCAATGTGTGGAAGAGTGGCGGTGCGGATCAAGCCCGCTACATTAAGA 1082
DB |||||
QY 717 GCTGCGGTGGGAGGAGCGTACTCGGTGCGCTTCTTCTGCGTGAACAGCGGCGTGCAT 776
DB |||||
QY 1083 ACTGCGCTGTGGAGAGCGGTATGCTGTGCTTCTTCTGCTTGAACAGCGGCGTGCAT 1142
DB |||||
QY 777 GATCTTACCGTGAAGTACTCTGCGGCTCTTCTGCGGCTCCAGCGCTACCGCTTCAAT 836
DB |||||
QY 1143 GATCTTACAGTGAATTTGCTTCCGCTGCGTGAACGCGCTAGTGTACCGTATTGT 1202
DB |||||

QY 837 CCGAGCGTCATGAGCATCATGAGGTGGCCATCATGCCCCCTACTACATCGGCTGCT 896
DB |||||
QY 1203 GCGTAGTGCATGAGTATCATCGACGTGGTGGCATCTGCGCTTATTAATGAGGCTGCT 1262
DB |||||
QY 897 CATGACCAACAAGAGAGCGTGTCCGGCGCTTGTGTCACGCTCCGGGTCTTCCGCGTCT 956
DB |||||
QY 1263 GATGACAGACAAATGAGAGCGTCAGCGGAGCTTTGTGACACTCCGAGTCTTCCGGGTCT 1322
DB |||||
QY 957 CAGGATCTTCAAGTTTCCCGCCACTCCAGGCGCTGGGATCCCTGGGCTACACACTGA 1016
DB |||||
QY 1323 CAGGATCTTAAATTTTCCCGCCACTCTCAAGGCGCTGGGATCCCTGGGCTACACACTGA 1382
DB |||||
QY 1017 GAGCTGCGCTCGAAGTGGGCTTCTTCTCTCTCCCTCAGCAATGGCCATCATCTT 1076
DB |||||
QY 1383 GAGTGTGCGCTCAGAAATGGGCTTCTGCTTCTGCTCAGCAATGGCTATCATCTT 1442
DB |||||
QY 1077 TGCCACTGTGATGTTTATGCGGAGAGAGGCTCTCGGCGAGCAATTCAGACATCCC 1136
DB |||||
QY 1443 CGCTACAGTATGTTCTACGAGAGAGAGGCTCTCGGCTAGCAAGTTCACAGCATCCC 1502
DB |||||
QY 1137 TGCCCTGTTTGTGTAACCACTTGTCAACATGACCACTGGGATACGGAATCATGTC 1196
DB |||||
QY 1503 TGCAAGCTTCTGTATACCATCGTCAACATGACCAACTAGGATAGTGAATGTCATGTC 1562
DB |||||
QY 1197 TAAGACGATTCAGAGGAGATCTTGGCTCATCTGCTCTTGAAGTGGCTCTGCTCAT 1256
DB |||||
QY 1563 AAAAACCATAGCAGGAGAGATTTTGGTCTTATCTGTTGCTGAGTGGGCTTGTGTCAT 1622
DB |||||
QY 1257 TGCCCTGCGAGTCCCTGTGATGTTTCCACTTTAGCGGATTTACCAAGATCAGAG 1316
DB |||||
QY 1623 TGCTCTACCTGTTCCGGTGTATGATCCAACTTCAGTGCATCTACCAAGATCCAG 1682
DB |||||
QY 1317 AGCTGATTAACGAGGAGGACAAAAGAGGCGGCTTGGCAGAGATCGTGTGGCCAAAG 1376
DB |||||
QY 1683 AGCAGACAAAGAAAGGACAAAGAAAGCTGAGCTGGCAGAGATCCGGGACCCAAAG 1742
DB |||||
QY 1377 AGCGATTCGATGATCATCTGCAACAGCAAGCGGCTCTTCAACGAGCGCTGCA 1436
DB |||||
QY 1743 CGGAAGCGCAATGCTTACATGACAGAGCAACGGAATGTTTACTCAAGTATCAAGTCA 1802
DB |||||
QY 1437 GCTGACGGGCAACCCAGAGAGAGCATGGGCAAGACCACTCATCTCATCGAGAGCCA 1496
DB |||||
QY 1803 GTCCCTCAGAGAG---TGAGAGAGGCTTTGTTAGCAAAATCCGCTCCAGCTTGAACCCA 1859
DB |||||
QY 1497 GCATCATCACTGCTGCACTGCTGCAAAAAAACCACTAAACAGAGTTTATGATGAGCA 1556
DB |||||
QY 1860 GCAACACCACTGCTTCACTGCTGCAAAAAAACCAAGATCAAGAGTTTGTGAGCAACA 1919
DB |||||
QY 1557 GATGTTGAGCAGAACTGATGAGAGTTCATGACAGACTACCAATCCACAGAGATCC 1616
DB |||||
QY 1920 AGTCTTGAAGAAAGCTGCAATGGAATGCAACTGTAAATGCTTCAAGTCAACAGTCC 1979
DB |||||
QY 1617 CTCACTGTCCAGCCAGGCGCTCACTACCACTGCTGCTCCGCTGTAAGTGAAGAGAC 1676
DB |||||
QY 1980 TTCACTGTCTTCAACAAGAGAGTCAACAGCACTGCTGTTCAAGACAGCAAAAAAAC 2039
DB |||||
QY 1677 CACACACCTGCGCAATTTAACTGCAAGTACTGCTGCGGAGAGTGAAGAGTCAAG 1736
DB |||||
QY 2040 TTTTTCGATCCCAAAATGCCAAATGTAATGAGAGGAGTCAAGTATGTAAGAGTCAAG 2099
DB |||||
QY 1737 CAGGATTCAGTCAAGGAGTGAAGAGCGGCTCCCTCAACAACGAGTCCGAGCTTAA 1796
DB |||||
QY 2100 CAGGATTCAGTCAAGTGTGTGAGAGAGAACACTCTGTCTTAAACGCGATCCAGTTTAA 2159
DB |||||
QY 1797 TTTGAAGAGAGAGCGAGTGAAGACCAAACTGCAAAACATCCAGATCAACAGAGCAT 1856
DB |||||
QY 2160 TGCCAAATGGAAGAGTGTGTTAACTTAACTGTAACAACTTATGTGATCAAGCAAT 2219
DB |||||
QY 1857 CATCAGCATCCCACTCCCGAGCGCTAACCCAGAGGAGGAGAAAGTCCGCCA 1908
DB |||||
QY 2220 AATTAAGCATCCCAACACTCAAGTAAACACACAGAGAGAGAGATAGGCCA 2271
DB |||||

RESULT 11
ADM10923
ID ADM10923 standard; cDNA; 5333 BP.
XX
AC ADM10923;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue cDNA #5.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KV cyostatic; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PE 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR MPI; 2003-901037/82.
DR P-PSDB; ADM10929.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 254; 221pp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cyostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
Query Match 48.5%; Score 1000.8; DB 11; Length 5333;
Best Local Similarity 72.8%; Pred. No. 1.5e-188;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;
QY 66 AGTCACCATGGCGCGGAGTGGCGCTGCTGCTTTTGGCCGGGCTGGCCATCGG 125
DB 959 AGTAATCATGGCGCGGCGGCGGCGTGGCGCTGCTTTTGCAGGGGCGAGCGGTATCGG 1018
QY 126 GTGATGCGCGTGGCCAACTGCGCCCATGCGCCCTTGCGCC--GGCCGACAGAAACAAGCG 182
DB 1019 GTGATGCGCTGTGGCGCTCGGGGCGCTATGCGCGCTCCCGAGGAGAGAGAAAGAC 1078
QY 183 GCAGATGAGCTGATTTGCTCTCAAGTGAGTGGGCGGAGGTTCCAGACTGGAGGACCAAC 242

DB 1079 CCAAGATGCTCTCATTTGTGCTGAATGTGAGTGGCACCCGCTTCCAGACGTGGCAGACAC 1138
QY 243 GCTGAGCGCTACCCGAGACCCCTGCTGGGAGCAGCAGAGAGAGATTCTTCTTCAACGA 302
DB 1139 CTTGAAAGTTACCCAGACACTCTACTGGCAGTTCTAGAGAGGACTTTTCTACACACC 1198
QY 303 GGACACCAAGAGTACTTCTTTCGACCGGAGCCCGAGGTGTTCCGCTGCTGCTCAACTT 362
DB 1199 AGAAACTCAGCAGTATTCTTTGACCGTGACCCAGACATCTTCCGCAACATCTTGAATTT 1258
QY 363 CTACCGCAGCGGGAAGCTGACCTACCCGCGCTACGAGTGCATCTTGCCTTACGACGCA 422
DB 1259 CTACCGCAGCTGGGAAGCTCACTATCTCTGCGCAGAGTGCATCTTGTCTTACGATGAAGA 1318
QY 423 GCTGCGCTTCTACGCGATCTCTCCGAGATCATGCGGAGCTGCTGTACGAGAGTACAA 482
DB 1319 ACTGCGCTTCTTTGGCCCTCATCCCGAAATCATCGGCGACTGTATTAGAGATCAAA 1378
QY 483 GGACCGCAGAGGAGAAAGCCGAGCGCTCATGACGACAAAGCACTCGAGAAACAACA 542
DB 1379 GGATCGCAGCGAGAGAACGCCGAGCGCTGACGAGCAGCGGATACCAACACCGCTGG 1438
QY 543 GGAG---TCCATGCCCTCGCTCAGTTCCGCGCAGACCAATGTGGCGGCGCTTGAAGAACCC 599
DB 1439 GGAAGCGCGCTTGCCACCATGACTGCAAGGAGAGAGGCTGTGAGAGGCGCTTGAAGAACCC 1498
QY 600 CCACACGACGACGCTGCGCTGCTGCTTCTACTACGTAAGTGAAGTCTTCTTCACTGCTCTC 659
DB 1499 CCACACGACGACGATGCGCTGCTGCTTCTACTATGTCACGCGGCTTTTCACTGCGCTCTC 1558
QY 660 GGTCTATCAACCAAGTGTGAGAGAGCGGTGCGGTGCGGACGAGTCCGCG---CAGCAAGA 716
DB 1559 TGTCTATGCGAATGTGTGAGAAACAGTCCGCTGCGGATCAAGCCAGGTACATTAAAGA 1618
QY 717 GCTGCGGTGCGGAGAGCGCTACTGCGGTGCGCTTCTTCTGCTGAGACACGCGTGGCTCAT 776
DB 1619 ACTGCGCTTGTGAGAGCGGTATGCTGTGCGCTTCTTCTGCTTGTGAGACACGCGCTGCTCAT 1678
QY 777 GATCTTACCGTGAAGTACTCTGCGGCTCTTTCGCGGCTCTCCAGCGCTTACCGCTTCTCAT 836
DB 1679 GATCTTCAAGTTGAGTATTGCTTCTGCTGCGCTGCGCTGAGCGCTTATGCTTATCCGTTTGT 1738
QY 837 CCGCAGCGTCAATGAGCATCATGAGCGTGTGCGCATGATGCCCTACTACATCGGTGTGT 896
DB 1739 GCGTAGTGTCAATGAGTATCATGAGCGTGTGCGCATGCTGCTTATTAATTTAGGCTGTGT 1798
QY 897 CATGACCAACAAGAGAGAGTGTGCGGCGCTTCTGCTCAAGCTTCCGCGTCTTCCGCTCTT 956
DB 1799 GATGACAGACATGAGGAGCGTCAAGCGGAGCGCTTGTCAACATCTCGAGTCTTCCGCGTCTT 1858
QY 957 CAGGATCTTCAAGTTTCCCGCACTCCAGGCGCTGCGGATCTTGGGCTTACACACTGAA 1016
DB 1859 CAGGATCTTCAAGTTTCCCGCACTCCAGGCGCTGCGGATCTTGGGCTTACACACTGAA 1918
QY 1017 GAGCTGTGCTCCGAGCTGGGCTTCTTCTTCTTCCCTACCATGCGCATCATATCTT 1076
DB 1919 GAGTGTGCTCAGAAATTTGGGCTTCTTCTTCTGCTCAGCATGCGTATCATATCTT 1978
QY 1077 TGCCACTGTGATTTTATATGCGGAGAGGCTCTCGGCGCAGCAAGTTCAACAAGATCCC 1136
DB 1979 CGCTCAGTTATGTTCTTACGAGAGAGAGGCTTCTGCGCTTACGCAAGTTCAACAAGATCCC 2038
QY 1137 TGCCCTGTTTGTGATACCATATGTCACCATGACCACTGAGATGAGATGAGATGAGTGC 1196
DB 2039 TGCAAGCTTCTGATATCATCATGTCACCATGACCACTAGAGGATATGATGATGATGAGTGC 2098
QY 1197 TAAGACGATGAGGAGAGATCTTCCGCTCATCTGCTCTTGAAGTGGCGTCTGCTCAT 1256
DB 2099 AAAAACCATAGCAGGAGAGATTTTGTCTTATCTATCTGCTGAGTGGGCTTGTGCTCAT 2158
QY 1257 TGCCCTGCGAGTCCCTGATGATTTTCCAACTTATGCGGAGTTTACCAACAGATTCAGAG 1316
DB 2159 TGCTTACCTGTTCCGCTGATGATGATCAACTTCACTGCGCATCTTACCAACAGATTCAGAG 2218


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Db      1559 TGTCAATCGGAATGTGTGGAAACAGTCCGTCGGATCAAGCCAGGTACATTAAAGA 1618
QY      717 GTCGCCGCGGGGAGCGGCTACTCGGTGGCCCTTCTTCGCTGACACAGCGGTCGTCAT 776
Db      1619 ACTGCCCTGTGGAGAGCGGTATGTCTGGCCCTTCTTCTGCTTGACACGCGCTGCTCAT 1678
QY      777 GATCTTCAACCGTGAAGTACTCTCGCGGCTCTTCCGCGCTCCAGCCGCTTACCGCTTCA 836
Db      1679 GATCTTCAAGTGAATTTGCTTGGCTGCGCTGACAGCGCTTACGTTTGT 1738
QY      837 CCGCAGCGTCATGATGATTCGACGCTGTGGCCATCATGCCCCCTACTACATGCTGTGT 896
Db      1739 GCGTAGTGTATGATGATTCGACGCTGTGGCCATCCGCTTATTAATTTAGGCGTGT 1798
QY      897 CATGACCAACAAGAGAGCGTGTCCGCGCTTGTACAGCTCCGCGCTTCCGCGCTT 956
Db      1799 GATGACAGACAATGAGAGAGCGTGTCCGCGCTTGTACACTCCAGTCTTCCGCGCTT 1858
QY      957 CAGATCTTCAAGTTTTCGCGCACTCCAGAGGCTGTGGGATCTGGGCTACACTGAA 1016
Db      1859 CAGATCTTAAAGTTTTCGCGCACTCTCAAGGCTGTGGGATCTGGGCTACACTGAA 1918
QY      1017 GAGCTGTGCTCCGAACTGGGCTTCTTCTCTCTCCCTCACCAATGGCCATCATCTT 1076
Db      1919 GAGTTGTGCTCAGAAATGGGCTTCTTCTCTCTCCCTCACCAATGGCTATCATCTT 1978
QY      1077 TGCCACTGTGATTTTATATGCGAGAGAGGCTCTCGGCGAGCAATTCACAAGCATCC 1136
Db      1979 CGCTACAGTATATTTCTACGAGAGAGGCTCTCGGCTAGCAAGTTTACAGCATCC 2038
QY      1137 TGCCCTGTTTGGTACACCAATGTGTACCATGACCAACTGGGATACGAGACATGTGCT 1196
Db      2039 TGCAGCTTCTGTATACCACTGTGTCACCATGACCAACTAGGATATGTGTACATGTGCT 2098
QY      1197 TAAAGCATTTGAGGAAAGATCTTCCGCTCACTGTGCTTGTAGTGGCGTCTGTGCTAT 1256
Db      2099 AAAAACCATAGCAGGAAAGATTTTGGTCTTATCTGTGCTGTAGTGGGCTTGTGCTAT 2158
QY      1257 TGCCCTGCGAGTCCCTGTGATTTTTCACCTTTAGCCGGATTTACACAGAAATCAGAG 1316
Db      2159 TGCTTAACCTGTTCCGGTGTGTATTCACCTTCAAGTGCATTAACCAACGAATCAACG 2218
QY      1317 AGCTGATAAACGAGGCGCACAAAAGAGGCGCCCTTGCCAGGATCCGTGTGGCCAAAC 1376
Db      2219 AGCAGACAAACGAAAGGCGCACAAAAGAGTGAAGTGCAGATCCGCGAGCCAAAG 2278
QY      1377 AGCAGTTTGAATGATACCTGACACAGCAAGCGGCTCTCAACGAGCGGCTGGA 1436
Db      2279 CGAAGCGCAAAATGCTTACATGACAGCAACGAAATGTTTACTCATTAATCAGCTGCA 2338
QY      1437 GCTGACGGGCACTCCAGAGAGAGACATGGGCAAGCACTGCTACTCATTCAGAGCCA 1496
Db      2339 GTCCTCAGAGGA---TGAGAGGCTTTTGTAGCAAAATCCGGCTCAGCTTTGAACCCA 2395
QY      1497 GCATCATCACCTGCTGACATGCTGGAAGAAACCACTAACCAAGTTTATTTGATGACA 1556
Db      2396 GCACCAACCACTGCTTCACTGCTGGAAGAAACCAAGATCAGAGTTTGTGAGACGACA 2455
QY      1557 GATGTTTGAAGCAAGTGTGAGAGTTCATGACAGACTACCATTCACAGAAAGTCC 1616
Db      2456 AGTCTTTGAAGAAAGCTGATGGAAGTTGCACTGTTAATGCTTCAAGTTCACAGTCC 2515
QY      1617 CTCACGTTCAGGCAAGCAAGGCTCTACTACCACTGCTGCTCCGCTGTAGTAAGAGAC 1676
Db      2516 TTCACGTGCTTCAACAAGAGAGTGCACAGACCTGTGTTACAGACGACCAAAAAAAC 2575
QY      1677 CACACACCTGCGCAATTTCTAAGCTGTGAGTACTGCTGCGCAGCATGCAAGAGCTCAG 1736
Db      2576 TTTTCGATCCCAAAATGCCAATGTATCAAGAAACCATCAAGTATATCAAGAACTCAG 2635
QY      1737 CACGATCCACATCCAGGCGAGTGAAGAGCCCTCCCTCAACACCAATCCGCTCAGCCTTAA 1796
Db      2636 CACGATTCAGATCAGATGTGTGAGAGAAACACCTCTGTCTAAACAGCCGATCAGTTTAA 2695

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QY      1797 TTTGAAGCAGACGAGCGACTGAGACCAAACTGCAAAACATCCAGATCACACAGCCAT 1856
Db      2696 TCCCAAAATGAAAGAGTGTGTTAACTAAACTGTGAACAACCTTATGTGACTACAGCAAT 2755
QY      1857 CATCAGATCCCACTCCCAAGCGCTAACCCCAAGAGGGGAAAGTCCGCCA 1908
Db      2756 AATAAGCATCCCAACACCTCCAGTAAACCAACAGAGAGAGCATAGGCCA 2807

RESULT 13
ADJ11253
ID ADJ11253 standard; DNA; 5333 BP.
XX
AC ADJ11253;
XX
XX
DT 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SeqID 254.
XX
KW human; ds; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
KW cyostatic; gene.
XX
OS Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
XX
PF 14-FEB-2003; 2003US-00369186.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIXA CORP.
XX
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2004-178717/17.
XX
XX
PT P-PSDB; ADJ11259.
XX
PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
XX
PS Example 12; SEQ ID NO 254; 222pp; English.
XX
CC This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cyostatic
CC activity. This polynucleotide is a human ovarian tumour antigen DNA
CC sequence given in an exemplification of the invention.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;

```

Query Match 48.5%; Score 1000.8; DB 12; Length 5333;
 Best Local Similarity 72.8%; Pred. No. 1.5e-188;

Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

```
QY 66 AGTCACCATGGCGCGCGGAGTTCGGGCTGCTGCTTTTGGCCCGGCGTGGCCATCGG 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 959 AGTAATCATGGCGCGCGGAGTTCGGGCTGCTGCTTTTGGCCCGGCGTGGCCATCGG 1018

QY 126 GTGGATGCGGCTGCGCAACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAAGAACGCG 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1019 GTGGATGCTGTGGCTTCGGGGCTTATGCGGCTCCCGCCGAGCAGAGAGAGAAAAGAC 1078

QY 183 GCAAGATGAGCTGATTGCTCTCAACGTAGTGGCGGAGGTTCCAGACTTGAGAGACCA 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1079 CCAAGATGCTCTCATTTGTGCTGAATGTAGTGGACCCCGCTTCCAGACTGAGAGAGAC 1138

QY 243 GCTGAGCGCTACCCGAGCACCCCTGCTGGGAGAGACGAGAGAGAGAGTTCTTCAACGA 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1139 CCTGGAACGTTTACCCAGACACTCTACTGCGGCAAGTTCTGAGAGGACTTTTCTAACACCC 1198

QY 303 GGAACCAAGAGTACTTCTTTCGACCGGAGCCCGAGGTGTTCGCTGCTGCTCAACTT 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1199 AGAAACTCAGCAGTATTTCTTTGACCGGTGACCCAGACATCTTCCGCCACATCTGAATTT 1258

QY 363 CTACCGCAGCGGGAGCTGCACTACCCCGCTAGCAGTGTCTCTGCTTACGACGCA 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1259 CTACCGCAGCTGGGAGCTCCACATCTCTGCGCAAGAGTGCATCTCTGCTTACGATGAAGA 1318

QY 423 GCTGGCTTCTACGCACTCTCCCGAGATCATCGGGAGCTGCTGCTACGAGAGTACAA 482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1319 ACTGGCTTCTTTGGCTCTATCCCGGAATCATGGCGGACTGCTGTATGAGAGATACAA 1378

QY 483 GGAACCGAAGAGGAGAACGCCGAGCGCTCATGACGACAAACGACTCGGAGAACCA 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1379 GGAATCGAGGAGAGAACGCCGAGCGCTGCAAGACGACCGGATACCGACACCGCTGG 1438

QY 543 GGAG--TCCATGCGCTCGCTGAGCTTCCGCCAGACCATGTGGCGGGCTTCAGAAACC 599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1439 GGAAGCGCTTGGCCCAACATGACTGCAAGGAGGAGGTGAGAGGCTTCCAGAACCC 1498

QY 600 CCACACCAAGACGCTGGCGCTGTCTTCTACTAGTGTGCTTCTTCACTGCTGTCTC 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1499 CCACACCAAGACGATGGCGCTGTGTTCTTACTATGTCAACGGGGTTTTCATTGCGCTTC 1558

QY 660 GGTATCAACCAAGTGTGGAACGCTGCGCTGCGGACCGGTCCCGG--CAGCAAGGA 716
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1559 TGTATCGCGAATGTGTGGAACAGTGCCTGCGGATCAAGCCAGGTCACTTAAAGA 1618

QY 717 GCTGCGGTGGGAGCGCTACTCTGCTGCTTCTTCTGCTGAGACAGCGGTGCTCAT 776
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1619 ACTGCGCTGTGAGAGAGGGTATGCTGTGCTTCTTCTGCTGAGACAGCGCTGCTCAT 1678

QY 777 GATCTTCAACGCTGAGTACTCTCTGCGCTCTTCTGCGGCTCCAGCGCTACCGCTTCA 836
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1679 GATCTTCAACGTTGAGTATTTGCTTCTGCTGCTGAGCGCTAGTCTTACCGTTTGT 1738

QY 837 CCGCAGCGTATGAGCATCATGACGTGGTGGCAATCATGCCCTACTACTACGCTTGGT 896
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1739 GCGTATGTATGATGATCATCATGACGTGGTGGCAATCATGCCCTTATTAATTTGGGCTGT 1798

QY 897 CATGACCAACAGAGAGAGTGTCCGGCGCTTCTGCTACGCTCCGGGTCTTCCGCTCTT 956
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1799 GATGACAGACATGAGAGAGTGTGAGCGGAGCTTGTTCACACTCCGAGTCTTCCGGGTCTT 1858

QY 957 CAGGATCTTCAAGTTTCCCGCACTCCAGAGGCGCTGGCGGATCTTGGGCTACACACTGAA 1016
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1859 CAGGATCTTAAAGTTTCCCGCACTCTCAAGCGCTGCGCATCTCTGGGGTACACACTGAA 1918

QY 1017 GAGCTGTGCTCCGAACTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1076
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1919 GAGTTGTGCTCAGAAATGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1978

QY 1077 TGCCACTGTGATGTTTATGCGGAGAGAGGCTCTTGGCGCAAGATTCACAAAGCATCCC 1136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1979 CGCTACAGTATGTTCTTACGCAAGAGAGGGGTCTTGGCTTACGAACTTCAACGACATCCC 2038
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QY 1137 TGCCCTGTTTGGTACACCATGTGTCAACCATGACCACTGGGATACGAGACATGTGCC 1196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2039 TGCAAGCTTCTGTGATATACCATGTGTCAACCATGACCAACATGAGGATGTGTGACATGTGCC 2098

QY 1197 TAAGCAGTTGACGGGAAGATCTTGGCTCCATCTGCTCTTGAAGTGGCGTCTGTCTAT 1256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2099 AAAAACCATGACGAGGAGAGATTTTGGTTCTATCTGTTCGTGAGTGGGTCTTGGTCTAT 2158

QY 1257 TGCCCTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTTACCAAGATACGAG 1316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2159 TGCTCTACTGTTCCGGTGTGATGTATCCAACTTCACTGATGATACCAAGATACGAG 2218

QY 1317 AGCTGATTAACGACGGGACAAAAGAGCCCGCTTCCAGAGATCCGTGTGGCCAAAC 1376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2219 AGCAGACAAACGAAAGGACAAAAGAAAGCTAGACTGGCCAGATCCGGGACGCAAAAG 2278

QY 1377 AGGCAAGTTGCAATGATATCTGCAACGCAAGGCAACGGGCTCTTCAACGAGCGCTGGA 1436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2279 CGGAAGCGCAATGCTTACATGCAAGACCAACGGAATGGTTTACTCAGTATCAGCTGCA 2338

QY 1437 GCTGACGGGCAACCCAGAAAGAGACACATGGGCAAGACCACTCACTCATTCGAGAGCA 1496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2339 GTCTCTCAGAGGA--TGAGCAGGCTTTTGTGTAACAAATCCGCTCCAGCTTGAACCCA 2395

QY 1497 GCATCATACCTGCTGCACTGCTGTGAAAAAACCACTTAACCAAGATTATGTATGAGCA 1556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2396 GCAACCAACACCTGCTTCACTGCTGTGAAAAAACCAAGAAATCAAGAGTTGTGAGACGA 2455

QY 1557 GATGTTGACAGAACTGCACTGAGAGTTCAATGACAGAACTAACCATCAACAAGATCC 1616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2456 AGTCTTTGAAGAAAGCTGACATGAAAGTTGCAACTGTAAATCGTCTTCAAGTCAACAGTCC 2515

QY 1617 CTCACCTGTCAGCCACCCAGCGCTCACTACCACTGCTGCTCCGCTGCTAGTAAAGAAAC 1676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2516 TTCACTGCTTTCACACAAAGAGTCAACAGACCTGCTGTTCAAGACGACAAAAAAAC 2575

QY 1677 CACACACCTGCCCAATTCTTAACCTGCCAGCTACTCGCTGCGGACGATGCAAGAGCTCAG 1736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2576 TTTTCGATCCCAATGCGAATGTATATCAAGAGCCATCAAGTATATCAAGAACTCAG 2635

QY 1737 CACGATCCACATCCAGGGGAGTGAAGACCCCTCCCTCAACAACAGTCCGCTCAGGCTTAA 1796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2636 CACGATTCAGATCAGATGTGTGAGAGAAACACCTCTGTCTTAACGCCGATCAAGTTTAA 2695

QY 1797 TTTGAAGCAGACGACGACTGAGACCAACCTGCAAAACATCCAGATCACCACAGCCAT 1856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2696 TGCCAAATGGAAGAGTGTGTTAACTTAACTGTGAACAACCTTATGTGACTACAGCAAT 2755

QY 1857 CATCAGCATCCCACTCCCGCAGCGCTTAACCCAGAGGGGAAAGTCCGCCA 1908
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2756 AATTAAGCATCCCAACACCTCCAGTAAACACACAGAGAGAGACGATAGGCCA 2807

RESULT 14
ADJ11251
ID ADJ11251 standard; DNA; 5333 BP.
XX
XX ADJ11251;
XX
DT 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SegID 252.
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
XX antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
XX cytostratic; gene.
XX
XX Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
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XX	PF	14-FEB-2003; 2003US-00369186.
XX	PR	10-SEP-1999; 99US-00394374.
XX	PR	01-MAY-2000; 2000US-00561778.
XX	PR	15-AUG-2000; 2000US-00640173.
XX	PR	07-SEP-2000; 2000US-00656668.
XX	PR	14-NOV-2000; 2000US-00713550.
XX	PR	03-APR-2001; 2001US-00825294.
XX	PR	02-OCT-2001; 2001US-00970966.
XX	PR	02-AUG-2002; 2002US-00212677.
XX	PR	05-FEB-2003; 2003US-00361811.
XX	PA	(CORI-) CORIXA CORP.
XX	PI	Fanger GR, Fling SP;
XX	DR	WPI; 2004-178717/17.
XX	PT	P-PsDB; ADJ11257.
XX	PT	Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
XX	PT	polypeptide, useful as probes of primers for detecting presence of cancer
XX	PS	in a patient.
XX	SS	Example 12; SEQ ID NO 252; 222pp; English.
XX	CC	This invention relates to novel isolated polynucleotides and methods for
XX	CC	the therapy and diagnosis of cancer, particularly ovarian cancer.
XX	CC	Specifically, it refers to these polynucleotides and the encoded
XX	CC	polypeptides thereof, as well as immunogenic peptides, antibodies,
XX	CC	antigen presenting cells (APCs) and immune system cells (e.g. T cells)
XX	CC	that are targeted to those cells expressing the proteins of interest. The
XX	CC	present invention describes methods that are useful for stimulating and/or
XX	CC	expanding T cells specific for a tumourigenic protein (i.e. T cell
XX	CC	therapy). Furthermore, compositions for a tumourigenic protein (i.e. T cell
XX	CC	treatment and/or prevention of ovarian cancer by stimulating an immune
XX	CC	response in a patient. Accordingly, these compositions exhibit cytostatic
XX	CC	activity. This polynucleotide is a human ovarian tumour antigen DNA
XX	CC	sequence given in an exemplification of the invention.
XX	SQ	Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
XX	Query Match	48.5%; Score 1000.8; DB 12; Length 5333;
XX	Best Local Similarity	72.8%; Pred. No. 1.5e-188;
XX	Matches 1348; Conservative	0; Mismatches 492; Indels 12; Gaps 4; ;
OY	66	AGTACCATGGCGGCGGAGTGCGGCCCTGGCTGCTTTGCCCGGGGTGGCCATCGG 125
Db	959	AGTAATCATGGCGCGGGGTGGCAAGCTGCTGCTTTTGAAGGCAGCGGCTATCGG 1018
OY	126	GTGGATCCGGTGGCCAACTGCCCATGCCCTTGCCCC---GGCCGCAAAACAACGG 182
Db	1019	GTCGATGCCGTGGCCTCGGGGCTTATGCGCGCTCCCCGAGGCAAGAAAAGAC 1078
OY	183	GCAGGATGAGCTGATTGTCTCAACGTAGTGGGCGGAGTTCCAGACTTGAAGACCAC 242
Db	1079	CCAAGATGCTCTCATTTGTGCTGAATGTAGTGGCACCCGCTTCCAAGCTGGCAGAACAC 1138
OY	243	GCTGAGCGCTACCCCGACACCTGCTGGCGACACGAGAAGAGTTCTTTCAACGA 302
Db	1139	CCTGGAACGTTACCCAGACACTTACTGCGCAGTTGTGAGAGGACCTTTTCAACACCC 1198
OY	303	GGACACCAAGAGTACTTCTTTCGACCGGGAACCCCGAGGTTCCTCGCTCAACTT 362
Db	1199	AGAACTCAGCAGTATTCTTTGACCGTGAACCCAGACATCTTCCGACACATCCTGAATTT 1258
OY	363	CTACCGCAGCGGGAAGCTGCATACCCCGCTACGAGTGCATCTTGCTTACGACAGCA 422
Db	1259	TACCGCACTGGGAAGCTCCACTATCTCTGCGCAGAGTGCATCTTGCTTACGATGAAGA 1318
OY	423	GCTGACCTTCTACGGCATCTCCCGAGATCATCGGGAAGTCTGCTTACGAGAGTACAA 482
Db	1319	ACTGGCTTCTTGGCTCTATCCGGAATCATCGGCACTGCTGTTATGAGAGTACAA 1378

QY	483	GGACCCGAAGAGGAGAAACGCCAGCGGCTCATGACGACAAACGACTCGGAGAAACA	542
Db	1379	GGATCGAGCGGAGAGAACGCCAGCGCTGCAGAGACGACCGGATTACGACACCGCTGG	1438
QY	543	GGAG--TTCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCTTCGAGAACCC	599
Db	1439	GGAGAGCGGCTTGGCCACCATGACTGCAGAGGAGAGGGGTGTGAAGGGCTTCGAGAACCC	1498
QY	600	CCACACGAGCAGCTGGCCCTGGTCTTCTACTACGHTAGCTGGCTTCTTCATCGCTGTCTC	659
Db	1499	CCACACGAGCAGATGGCCCTGGTGTCTTACTATGTACCGGGGTTTTTCATTTGCCGTCTC	1558
QY	660	GGTCATCACCAACGTGGTGGAGACGGTGGCTGGCGGACCGGTCCCGG--CAGCAAGGA	716
Db	1559	TGTTCATCGCGAATGTGGTGGAAACAGTGGCTGGCGGATCAAGCCCAAGTTCATTTAAGA	1618
QY	717	GCTGGCGTGGGGGAGCGGCTACTCGGTGGCTTCTTCTGCTGGACAGGGCGTGGCTCAT	776
Db	1619	ACTGGCCCTGTGGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACAGGCGCTGGCTCAT	1678
QY	777	GATCTTCAACCGTGAAGTACCTCTCGCGGCTCTTGGCGGCTCCAGCCGCTACCGCTTCAT	836
Db	1679	GATCTTCAACAGTTGAGTATTGTCTTGGCTGGCTGCAGCGGCTAGTGTGCTTACCTTTGT	1738
QY	837	CCGAGCGTTCATGAGCATCATGACGTGGTGGCCATCATGGCTTACTTACATCGCTGTGT	896
Db	1739	GCGTAGTGTTCATGAGTATCATGACGTGGTGGCCATCTGCTTATTATTCATTGGGCTGGT	1798
QY	897	CATGACCAACAAGAGGAGCGTGGCGGCGCTTGGTCAACGCTCCGGGTCTTCGGGCTT	956
Db	1799	GATGACAGACAATGAGGAGCGTCAAGCGGAGCTTGTTCACACATCCGAGTCTTCCGGTCTT	1858
QY	957	CAGATCTTCAAGTTTCCCGGCACTCCAGGGGCTGGCGGATCTGGGCTACACACTGAA	1016
Db	1859	CAGATCTTAAAGTTTCCCGCACTCTCAAGGCTTGGCGATCTGGGGTACACACTGAA	1918
QY	1017	GAGTGTGGCTCCGAACCTGGGCTTCTTCTTCTTCCCTCAACCATGGCCATCATCATCTT	1076
Db	1919	GAGTGTGGCTCAGATTGGGCTTCTTGGCTTCTTCTTCTTCCGCTCAACCATGGCTATCATCTT	1978
QY	1077	TGCCACTGTGATGTTTATATGCGGAGAAAGGGCTCTCGGCCAGCAAGTTCACAAAGCATCCC	1136
Db	1979	CGCTACAGTATATGTTCTACGCAAGAAAGGGGTCTTCGGTTAGCAAGTTCACAGCATCCC	2038
QY	1137	TGCTCGTTTGGTACACCATGTGTCAACATGACCACTGGGATACGAGACATGTGCC	1196
Db	2039	TGCAAGCTTCTGGTATACCATGTGTCAACATGACCAACTAGGATATGTGACATGTGCC	2098
QY	1197	TAAAGCATTTGAGGGAAGATCTTGGCTCCATCTGCTCTTGTAGTGGCGTCTGGTTCAT	1256
Db	2099	AAAAACCATAGCAGGGAAGATTTTGGTCTATCTGTTCGCTGAGTGGGCTCTTGGTTCAT	2158
QY	1257	TGCCCTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGGAATTTACCAACGAAATCAGAG	1316
Db	2159	TGCTCTACTGTTCGGGTGATGTTATCCAACTTCAGTGGCATCTTACCAACGAAATCAACG	2218
QY	1317	AGCTGATTAACGAGGGGCAAAAGAAAGGCCCGCTTGGCAGGATCCGTGTGGCCAAAC	1376
Db	2219	AGCAGACAAACGAAGGGCAAAAGAAAGCTAGACTGGCAGGATCCGGGCGAGCCAAAAG	2278
QY	1377	AGGCAAGTTGCAATGCACTACGACAGCAAGCGCAACGGGCTCTCAACGAGGCGCTGGA	1436
Db	2279	CGGAAGCGCAATGTTCATATGACAGAGCAAAACGGAATGTTTAACTCAGTATCAGCTGCA	2338
QY	1437	GCTGACGGGCAACCCAGAGAGGAGACATGGGCAAGACCACTACTCATTCGAGACCA	1496
Db	2339	GTCCTCAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCGGGCTCCAGCTTTGAAACCA	2395
QY	1497	GCATCATCACTGTGCACCTGCTGAAAAAAACCACTAACCAAGATTTATTGTATGAGCA	1556
Db	2396	GCACCAACCACTGTTCACCTGCTGAAAAAAACCAAGATCAAGATTTGTGAGCAACA	2455

Oy	1557	GATGTTTGAGCAGAACTGCATGGAGAGTTCATGTGACGAAGTAACCAATCCATCCACAAGAAGTCC 	1616
Dd	2456	AGTCTTTGAGAAAAGCTGCATGGAAAGTTGCACACTGTTAATCGTCCCTTCAAGTCACAGTCC 	2515
Oy	1617	CTCATGTTCCAGCCACCAGGCCCTCACACTACCACTGCTGCTCCCCGTCGTAGTAAGAGAAC 	1676
Dd	2516	TTCACGTCTTTCACAACAAGAGTCACCCAGCACCTGCTGTTTTCACGACGACACAAAAAAG 	2575
Oy	1677	CACACACCTGCCCAATTCTAACCTGCAGCTACTGCGCTGGCGAGCATGCAAGAAGCTCAG 	1736
Dd	2576	TTTTGCGATCCCAAATGCCAATGTATCAGGAAGCATCAAGGTAGTATACAAAGACTCAG 	2635
Oy	1737	CACGATCCACATTCAGGAGGAGTGAGCAGCCCTCCCTACAACAGTTCGCTCCAGCCTTAA 	1796
Dd	2636	CACGATTCAGATTCAGATGTGTGGAGAAACACCTCTGTCTTAACAGCCGATCCAATTAAA 	2695
Oy	1797	TTTGAAGCAGACGACGAGCTGAGACCAACTGCAAAAACATCCAGATCACCACAGCCAT 	1856
Dd	2696	TGCCAAATGGAAGAGTGTGTTAACTTAACTGTGAACAACTTATGTGACTACAGCAAT 	2755
Oy	1857	CATCAGATCCCACCTCCCCCAGCGCTAACCCACAGAGGGGGAAGTCGGCCA 	1908
Dd	2756	AATAAGATCCCAACCTTCAGTAAACCAACCAAGAGAGACGATAGGCCA 	2807

RESULT 15
ID ADM43512
AC ADM43512 standard; DNA; 5333 BP.
XX
XX ADM43512;
AC
XX
XX 03-JUN-2004 (first entry)
XX
XX Human ovarian cancer cDNA homologous DNA #6.
DE
XX
XX ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.
XX
XX Homo sapiens.
OS
XX US2003129192-A1.
PN
XX 10-JUL-2003.
PD
XX 02-AUG-2002; 2002US-00212677.
PF
XX
XX 10-SEP-1999; 99US-00394374.
PR
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
PI
XX
XX WPI; 2004-051070/05.
DR
XX P-PSDB; ADM43518.
DR
XX
XX New isolated polynucleotide encoding an ovarian tumor protein for use in
PT
PT diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX
XX
XX Claim 1; SEQ ID NO 252; 220pp; English.
PS
XX
XX The invention relates to an isolated polynucleotide. The invention is
CC
CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.
CC The present sequence represents a human ovarian carcinoma cDNA homologous
CC DNA.
XX
XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
SQ

Query Match 48.5%; Score 1000.8; DB 12; Length 5333;

	Best Local Similarity	72.8%	Pred. No. 1.5e-188;	
	Matches 1348;	Conservative	0;	Mismatches 492; Indels 12; Gaps 4;
QY	66	AGTCAACATGCGCGCGAGTTGCGGCTGCTGCTTTTGCCCGGCGTGGCCATCGG	125	
Db	959	AGTAATCATGGCGCGGGGTGGCAGCTGTGCTTTTGCAAGGGCAGCGGCTATCGG	1018	
QY	126	GTGATGCGCGGTGGCCAACTGCCCCCATATGCCCCCGGCCCC--GGCCGACAAGACAAGCG	182	
Db	1019	GTGATGCGCTGTGGCTCGGGGCTATATCCCGGCTCCCCCGAAGGAGAGGAAAGGAC	1078	
QY	183	GCAGATGAGCTGATGTGCTCTCAACGTGAGTGGGCGAGGTTCCAGACTGAGAGCAC	242	
Db	1079	CCAAATGCTCTCATTTGTCTGAATGTGAGTGACCCGCTTCCAGACGTGGCAGACAC	1138	
QY	243	GCTGGAGCGCTAACCCGACACCCCTGTGGGACAGACGAGAAAGATTCTTTCAACGA	302	
Db	1139	CCTGGAAAGTTACCCAGACACTCTACTGGGCAAGTTCTGAGAGGCACTTTTCTACCAACC	1198	
QY	303	GGACACCAAGAGTACTTCTTGTGACCGGGACCCCGAGGTGTCCGCTGCGTCAACTT	362	
Db	1199	AGAACTCAGCAATATTCTTTGACCGGTGACCCAGACATCTTCCGCAACATCTGAATTT	1258	
QY	363	CTACCGCACGGGGAAGCTGACTAACCCGCGCTACGAGTGCACTCTGCTTACGACAGCA	422	
Db	1259	CTACCGCACTGGGAAGCTCCACTATCTCTGCGCAAGTGCACTCTGCTTACATGAAGA	1318	
QY	423	GCTGGCTTCTACGCACTCTCCGAGATCATCTGGGCACTGTCTGCTACGAGAGTACAA	482	
Db	1319	ACTGGCTTCTTTGGCTCTATCCGGAATCATCTGGCGACTGCTGTATGAGAGTACAA	1378	
QY	483	GGACCGCAAGAGGAGAAAGCCGCAAGCGGCTCATGTGACGACAAACGACTCGGAGAACACCA	542	
Db	1379	GGATGCAAGGAGAAAGCCGCAAGCGGCTGACGAGACGACGCGGATACCGACACCGCTGG	1438	
QY	543	GGAG---TCCATGCGCTCGCTCAGCTTCCGCGACAGACCATGTGGCGGGCTTGGAAACC	599	
Db	1439	GGAGAGCGCTTGCCCAACATGACTGCAAGGAGGAGGTGTGAGGGGCTTGGAAACC	1498	
QY	600	CCACAACGACAGCGCTGCGCTGTCTTACTAGTGACTGCTTCTTATCTGCTGTCTC	659	
Db	1499	CCACAACGACAGCTGCGCTGTGTCTTACTAGTCAAGGAGGTTTTCATGCGGCTCTC	1558	
QY	660	GGTCATCACCAACGTGTGAGAGCGGTGCGGCGGACCGTCCCGGG--CAGCAAGGA	716	
Db	1559	TGTCACTCGCAATGTGTGTGAACAGTGCCTGCGGATCAAGCCAGGTACATTAAAGA	1618	
QY	717	GCTGCGGTGCGGGAGGCTACTCGGTGCGCTTCTTGTGCTGACACGGCGTGCCTCAT	776	
Db	1619	ACTGCGCTGTGAGAGCGGTATCTGTGCGCTTCTTGTGCTTGACACGGCGTGCCTCAT	1678	
QY	777	GATCTTACCGGTGAGTAACTCTCTGCGGCTCTTGGCGGCTTCCAGCGGCTAACCGTTCAT	836	
Db	1679	GATCTTACAGTGTGATTAATTGCTTCCGCTGCTGACGCGCTAGTGTGACCGTTTGT	1738	
QY	837	CCGACGCTCATGAGCATCATGACAGTGTGCGCATCATATGCCCTACTACATGCTGTGT	896	
Db	1739	GCGTAGTGTATGATATCATGACAGTGTGCGCATCTTGTGCTTATTAATTGGGCTGTGT	1798	
QY	897	CATGACCAACAAGAGACGTGTCCGGCGGCTTGTGTCACGCTCCGGGTCTTCCGGTCTT	956	
Db	1799	GATGACAGACATGAGAGCGTCAAGCGGAGCTTGTGTCACACTCCGAGTCTTCCGGGTCTT	1858	
QY	957	CAGATCTTCAAGTTTCCCGCACTCCAGAGGCGTGGCGATCTTGGGCTTACACTGAA	1016	
Db	1859	CAGATCTTAAAGTTTCCCGCACTTCAAGGCGTGGCGATCTTGGGGTACACACTGAA	1918	
QY	1017	GAGCTGTGCTTCGAAGTGGGCTTCTTCTCTTCTCCCTCAACATGGCCATCATCATCTT	1076	
Db	1919	GAGTTGTGCTTCAAGATTTGGGCTTCTTCTTCTTCTGCTCAACATGGCTATCATCATCTT	1978	
QY	1077	TGCCACTGTGATGTTTATGCCGAGAGGGGCTCTCGGCCAGCAATTCAACAGATCCC	1136	

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OY	1	GATTTCGTGAACTAACCTCAAGCGTGGTGTGGCTAGCGTCGCGGGCGGCGCCACA	60
Db	1	GATTTCGTGAACTAACCTCAAGCGTGGTGTGGCTAGCGTCGCGGGCGGCGCCACA	60
OY	61	GCTGGAATCACCATGGCGGCGCGGAGTTGCGGCTTGCTCTTTGGCCGCGCTGGGCC	120
Db	61	GCTGGAATCACCATGGCGGCGCGGAGTTGCGGCTTGCTCTTTGGCCGCGCTGGGCC	120
OY	121	ATCGGGTGGATGCCGGTGGCCAACTGCCCAATGCCCTTGCCCCGGCCGCAAGAACAAG	180
Db	121	ATCGGGTGGATGCCGGTGGCCAACTGCCCAATGCCCTTGCCCCGGCCGCAAGAACAAG	180
OY	181	CGGACGATGACCTGATTGCTCTCAACGTGAGTGGCGGAGTTCCAGACTTGAGGACCC	240
Db	181	CGGACGATGACCTGATTGCTCTCAACGTGAGTGGCGGAGTTCCAGACTTGAGGACCC	240
OY	241	ACGCTGAGAGCGCTAACCCGGAACCCCTGCTGGGAGACACGGAAGAAGATTCTTCTTCAAC	300
Db	241	ACGCTGAGAGCGCTAACCCGGAACCCCTGCTGGGAGACACGGAAGAAGATTCTTCTTCAAC	300
OY	301	GAGACACCAAGAGTACTTCTTTCGACCGGACCCGAGGTGTTCCGCTGCGTGTCTAAC	360
Db	301	GAGACACCAAGAGTACTTCTTTCGACCGGACCCGAGGTGTTCCGCTGCGTGTCTAAC	360

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QY 361 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTTGCCCTACGACGAC 420
DB 361 TTCTACCGCAGCGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTTGCCCTACGACGAC 420
QY 421 GAGCTGGCTTTCTAGGCGATCTCTCCGAGATCATCGGGGACTGCTGCTACGAGAGTAC 480
DB 421 GAGCTGGCTTTCTAGGCGATCTCTCCGAGATCATCGGGGACTGCTGCTACGAGAGTAC 480
QY 481 AAGGACCGCAAGAGGGAAGAAAGCGCGGCGCTCATGGAAGCAACGACTCGGAGAACAC 540
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DB 1021 TGTGCTCCGCACTGGGCTTCTTCTCTTCTCCCTCAACCATGCGCATCATCTTGGC 1080
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DB 1621 CTGTCCAGCCACCAAGGCTCTCACTAACCACTGCTGCTCCGCTGAGTAAAGACCA 1680
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DB 1741 ATCCACATCCAGGAGAGTGAAGAGGCTTCCCTCAACCAAGTGGCTCAGCTTAATTG 1800
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QY 1861 AGCATCCCCACTCCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGCCACCCCTGCCAGC 1920
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QY 2041 GTGAGTGTGATTAAGCCGAATTC 2064
DB 2041 GTGAGTGTGATTAAGCCGAATTC 2064

RESULT 2
US-09-178-109-1
; Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Diks, Daniel W.
; APPLICANT: Chang Ling, Hui-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-09-178-109-1

Query Match 96.8%; Score 1997; DB 3; Length 2121;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;
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RESULT 3
 US-09-142-791A-1
 ; Sequence 1, Application US/09142791A
 ; Patent No. 6368823


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/ GENERAL INFORMATION:
/ APPLICANT: Antoine Michel Alain Bril
/ APPLICANT: Thierry Paul Gerard Calmejs
/ APPLICANT: Jean-Francois Simon Pierre Faivre
/ APPLICANT: Jean-Luc Javre
/ APPLICANT: Sabine Rouanet
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GH-30012
/ CURRENT APPLICATION NUMBER: US/09/142,791A
/ PRIOR FILING DATE: 1999-02-02
/ PRIOR APPLICATION NUMBER: PCT/EP98/01901
/ PRIOR FILING DATE: 1998-03-23
/ PRIOR APPLICATION NUMBER: UK 9706377.0
/ PRIOR FILING DATE: 1997-03-27
/ PRIOR APPLICATION NUMBER: EP 97402971.2
/ PRIOR FILING DATE: 1997-12-09
/ PRIOR APPLICATION NUMBER: EP 97403007.4
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 2104
/ TYPE: DNA
/ ORGANISM: HOMO SAPIENS
US-09-142-791A-1
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Query Match      92.3%; Score 1905; DB 3; Length 2104;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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QY 133 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCGCAAGAAAGAGCGGAGATG 192
DB 61 CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCGCAAGAAAGAGCGGAGATG 120
QY 193 CTGATTGTCTTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGACCAAGCTGAGCGC 252
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 Db 1921 ACAGAGGGC 1929

RESULT 4
 US-09-142-791A-5
 ; Sequence 5, Application US/09142791A
 ; Patent No. 6368823
 ; GENERAL INFORMATION:
 ; APPLICANT: Antoine Michel Alain Bril
 ; APPLICANT: Thierry Paul Gerard Calmels
 ; APPLICANT: Jean-Francois Simon Pierre Falvre
 ; APPLICANT: Jean-Luc Javre
 ; APPLICANT: Sabine Rouanet
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GH-30012
 ; CURRENT APPLICATION NUMBER: US/09/142, 791A
 ; PRIOR FILING DATE: 1999-02-02
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01901
 ; PRIOR FILING DATE: 1998-03-23
 ; PRIOR APPLICATION NUMBER: UK 9706377.0
 ; PRIOR FILING DATE: 1997-03-27
 ; PRIOR APPLICATION NUMBER: EP 97402971.2
 ; PRIOR FILING DATE: 1997-12-09
 ; PRIOR APPLICATION NUMBER: EP 97403007.4
 ; PRIOR FILING DATE: 1997-12-11
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 2104
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 US-09-142-791A-5

Query Match 91.9%; Score 1897; DB 3; Length 2104;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1909; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 73 ATGGCGGCGGAGTTGCGGCTGCTGCTTTGCGCGGCTGCGGCATCGGTTGATG 132
 Db 1 ATGGCGGCGGAGTTGAGCTGCTGCTTTGCGCGGCTGCGGCATCGGTTGATG 60
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 Db 1321 TACCTGACAGCAAGCGCAACGCGCTCTCAACGAGGCGCTGAGCTGACGCGGACCCCA 1380
 QY 1453 GAAAGAGAGCATGGGCAAGACCACTCACTCATCGAGAGCAGCATCATCTGCTG 1512
 Db 1381 GAAAGAGAGCATGGGCAAGACCACTCACTCATCGAGAGCAGCATCATCTGCTG 1440

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DB 1441 CACTGCTGGAAAAAACCCTAACCAAGATTATGTATGATGACAGATGTTTGAAGACAAC 1500
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DB 1501 TGCATGAGAGATTTCATGACAGAACTACCAAGAAGTCCCTCACTGTCCAGCCAC 1560
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DB 1681 GGCAGTGAGAGCCCTCCCTCAACAACGATGCTCCAGCCTTAATTGAAAGCAGACAC 1740
QY 1813 GGACTGAGACCAAACTGCAAAACATCCAGATCAACAGCCATCATCAGCATCCCACT 1872
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DB 1801 CCCCCAGCGCTAACCCCGAGAGGGGAAAGTGGCCACCCCTGCCAGCCAGCCCAAC 1860
QY 1933 ACGAATCTCTTCCATTAACCAACGATGTTGTCAAGTCTCTGTCTTTGTAATAATCCGC 1992
DB 1861 ACGAATCTCTTCCATTAACCAACGATGTTGTCAAGTCTCTGTCTTTGTAATAATCCGC 1920
QY 1993 GGCATGGC 2001
DB 1921 ACAGAGGGC 1929

RESULT 5

US-09-142-791A-3
; Sequence 3, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-3

Query Match 89.1%; Score 1838; DB 3; Length 2072;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

QY 73 ATGCGCGCGAGATTGGCGCTGCTTTTCCCGGGGCTGCGGCATCGGATGATG 132

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QY 133 CCGGTGGCCAACTGCCCCCAATGCCCTTGCCCGGCCGCAAGAACAAGCCGAGATGAG 192
DB 61 CCGGTGGCCAACTGCCCCCAATGCCCTTGCCCGGCCGCAAGAACAAGCCGAGATGAG 120
QY 193 CTGATTGCTCTCAACGTGAGTGGGCGAGGTTCCAGACCTGAGAGACCACTGAGCGC 252
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QY 253 TAACCGGACACCTGCTGGGCGAGACCGAGAGAGATTCTTCAACGAGACCAACAG 312
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QY 313 GAGTACTTCTTCGACCGGGAACCCCGAGGTTCGCTGCTGCTCAACTTCTACCGCAG 372
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QY 373 GGGAGCTGCACTACCCCGCTACGAGTGCATCTGCTTACGACGACGACTGGCTTC 432
DB 301 GGGAGCTGCACTACCCCGCTACGAGTGCATCTGCTTACGACGACGACTGGCTTC 360
QY 433 TACGGATCTCTCCGAGATCATCGGGAATGCTGTCTACGAGAGTACAGACCGCAG 492
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QY 493 AGGAGAACCCCGAGCGGCTCATGACGACGACGACGACGACGACGACGACGACGAC 552
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DB 601 GTGTGAGACGCGTCCGCGGAGACGCTCCCGGCGAGCAAGAGCTGCCGTGGCGGAG 660
QY 733 CGCTACTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
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DB 721 TACCTCTGCGGCTTCTTCCGCGCTCCCAAGCGCTTACCTGCTGCTGCTGCTGCTGCT 780
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 Db 1321 TACCTGCACAGCAGCAGCGGCTCTCAACGAGCGCTGAGCTGACGGGACCCCA 1380
 QY 1453 GAAGAGGACACATGGGCAAGACCACTCACTCATCGAGAGCCAGCATCATCACTGCTG 1512
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 QY 1636 GGCTCTACTACCACTGCTGCTCCGCTGTAGTAAGAAAGACCAACCTGCCCAATTCT 1695
 Db 1621 GGCTCTACTACCACTGCTGCTCCGCTGTAGTAAGAAAGACCAACCTGCCCAATTCT 1680
 QY 1696 AACCTGCAGCTAATCTGCTGCGGACATGCAAGAGCTCAGACGATCCATCCAGGGC 1755
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 QY 1756 AGTAGAGAGCCCTCCCTCAACACGCTGCTCCAGCTTAATTGAAAGACAGACGGA 1815
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 QY 1876 CCAGGCTTAACCCAGAGGGGAAAGTCCGCCAACCCTGCCAGCCCAAGCCCAACAG 1935
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 QY 1936 AACATCTCTCATTAACGAGCAATGTGTCAAGGTCTCTGTTGTAATA 1985
 Db 1921 AACATCTCTCATTAACGAGCAATGTGTCAAGGTCTCTGTTGTAATA 1970

RESULT 6
 US-09-949-016-957
 ; Sequence 957, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231, 498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 957
 ; LENGTH: 5333
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-957

Query Match 48.5%; Score 1000.8; DB 4; Length 5333;
 Best Local Similarity 72.8%; Pred. No. 6.8e-211;
 Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 66 AGTACCATGCGCGCGAGTTGCGGCTGCTGCTTTTGGCCCGGCTGCCATCGG 125
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 Db 1019 GTGATGCGCTGCGCTGCGGCGCTATGCGGCTCCCGCAGGCGAGAGAAAGAC 1078
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 QY 363 CTACCGCAGCGGGAAGCTGACATACCGCGCTACAGTGCATCTTCTGCTTACAGACGA 422
 Db 1259 CTACCGCAGCTGGGAAGCTCCACATCTCTGCGACAGTGCATCTTCTGCTTACAGAGA 1318
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Db	1799	GATGACAGACAA TGAGGA CGTCAGCGGAGCC TTTGTCTCA CACTCCGAGTCTTCCGGGTCTT	1858
Qy	957	CAGGATCTTCAAGTTT TTTCCCGCACTCCCAAGGCGCTGCGGATCTTGGGCTTACACTGAA	1016
Db	1859	CAGGATCTTAAAGTTT TTTCCCGCACTCTCAAGGCGCTGCGGATCTTGGGGTACACTGAA	1918
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Db	1919	GAGTTGTGCTCAGAA TTTGGGCTTCTTGTCTTTCTCGCTCACATGGCTATCATCATCTT	1978
Qy	1077	TGCCACTGTGATGTTT TATGCGAGAGGGGCTCTCGGCGACGAA GTTCAAGACATCC	1136
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Qy	1377	AGGCACTTGAATGCATACCTGCA CAGCAAGCGCAAGCGGCTCTCAACGAGCGCTGGA	1436
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Qy	1437	GCTGACGGGCA CCCCAGAGAGAGACCATGGGCAAGACCACTCACTCATGAGAGCCA	1496
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Db	2396	GCACCAACCACTGCTTCACTGCTGTA AAAAAACAAGATCAAGATTTGTGAGCGAACA	2455
Qy	1557	GATGTTTGAGCAGAACTGCATGGA GAGTTCAATGCAAACTAACCATCCACAAGAGTCC	1616
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Qy	1617	CTCAGTGTCCAGCA CCCCAGGCTCTACCTACCACTGCTGCTCCGTGTAGTAAGAAAGAC	1676
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Qy	1797	TTTGAAGCAGACGACGCACTGAGACCAAACTGCAAAAACATCCCA GATCA CCAAGCCAT	1856
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1  /
2  / APPLICANT: Curran, Mark Edward
3  /
4  / APPLICANT: Hu, Ping
5  /
6  / APPLICANT: Ruteer, Marc
7  /
8  / APPLICANT: Wang, Jian-Wang
9  /
10 / TITLE OF INVENTION: NO. 6399761e1 Human Potassium Channels
11 /
12 / FILE REFERENCE: SEQ-15P
13 /
14 / CURRENT APPLICATION NUMBER: US/09/336,643A
15 /
16 / CURRENT FILING DATE: 1999-06-18
17 /
18 / PRIOR APPLICATION NUMBER: 60/076,687
19 /
20 / PRIOR FILING DATE: 1998-08-07
21 /
22 / PRIOR APPLICATION NUMBER: 60/116,448
23 /
24 / PRIOR FILING DATE: 1999-01-19
25 /
26 / PRIOR APPLICATION NUMBER: PCT/US99/03826
27 /
28 / PRIOR FILING DATE: 1999-02-22
29 /
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31 /
32 / SOFTWARE: FastSeq for Windows Version 4.0
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48 / OTHER INFORMATION: K+Hnov12
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Query Match	40.9%;	Score 843.2;	DB 3;	Length 3424;
Best Local Similarity	68.2%;	Pred. No. 3.2e-176;		
Matches 1287;	Conservative 1;	Mismatches 559;	Indels 39;	Gaps 7;
QY	65	GAGTCA	CCATGGCGCGGAGTTGGCGGCTGTGCTTGTGGCCGGGCTGCGCCATCG	124
DB	249	GTGGCAG	TGGCGGCGGAGGCTGTGGCCACGCTGGCTGTGCTTGTGCTGGGAGCAGCAGTGG	308
QY	125	GGTGATG	CCCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCCGACAAGAA	184
DB	309	GCTGGCTG	CCCCCGGCCGACCAACCCCTGCCCCCGGCCACCGGGGGTGAAGGCACTTCGAG	368
QY	185	AGGATAG	CGTGAATTGTCTCAACGTAGTGGGCGGAGTTCCAGACTTGGAGACCAACGC	244
DB	369	GAGATRG	GGTTCTGTGTGTAAGTGACGGGACGGCGCTTTGAGACTTGGAAAGATAACG	428
QY	245	TGAGCGC	TACCCGAGACCCCTGTGGGAGACGGAGAAAGAGTTCTTCTTCAACGAGG	304
DB	429	TGACCGC	TACCCAGACCACTTGTGTGGGAGCTCGAGAAAGAAATCTTCTACAGATGCTG	488
QY	305	ACACCAAG	AGAGTACTTCTTGACCGGGGACCCCGAGGTGTTCCGTGGTCTCAACTTCT	364
DB	489	ACTCAGG	CGAGTACTTCTTGCAATCGGACCTTGACATGTTCCGCATGTGCTGAATTTCT	548
QY	365	ACCGCAG	CGGGAGACTGCACTACCGCGGCTACGAGTGCATCTGTGCTTACGACGAGC	424
DB	549	ACCGAAC	CGGGCGGCTGCAATTGCCACGCGAGAGTGCATCCAGGCTTTCAGCAAGAGC	608
QY	425	TGGCTTT	CTTACGGCATCTCCCGAGATCATGGGAGCTGTGCTTACGAGAGTACAAGG	484
DB	609	TGGCTTT	CTTACGGCCTGTGTTCCGAGCTAGTGGTACTGTGCTTGAAGAGTATCGGG	668
QY	485	ACCGCAA	AGGAGAAACGCCGAGCTGCTATGACGACAACGACTGGAGAAACAACGAG	544
DB	669	ACCGAA	AAGAGAAATGCCGAGCGCTGCGAGAGATGAGGAGGACGAGCGCGGGG	728
QY	545	AGTCATG	CCCTGCGC-----TCAGCTTCCGCGACGACCATGTGGCGGGCCTTCGAGA	595
DB	729	ACGCCCA	GCCTGCGACAGGCAAGCTCCCTGCGGACGCGCTTGGCGGGCCTTCGAGA	788
QY	596	ACCCCA	CACACGACGCTGGCCCTGTGTTCTTACTACGTGAGCTGGCTTCTTATGCTG	655
DB	789	ATCCACA	CACGAGCACCGCAGCCCTCGTTTCTACTATGTAAACCGGCTTCTTATCGCGG	848
QY	656	TCTCGG	CATCAACCAAGTGTGAGACGGTGCAGTGGCGGACAGGTCCCGGCGAG-----	710
DB	849	TGTGGG	CATCGCCCAATGTGTGAGAACCATCCCATGCGCGGCTCTGCACAGCAGTCT	908

QY 711 -CAAGAGCTGCGGTCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGACACGCGGT 769
 Db 909 CAAGGAGACGCTGTCGGGAGCGCTTCCACAGGCTTTTCTGTCATGACACAGCTT 968
 QY 770 GCGTCATGATCTTACCGGTGAGTACTCTGCGGCTCTTGCGGCTCCGACCGCTACC 829
 Db 969 GTGTACTCATATTCACAGGATATCTCTGCGGCTGTTTGCGGCTCCGACCGCTTGGC 1028
 QY 830 GCTTCATCCGACGCTCATGACATGACGTGTCGTCGTCATGACCTTACTACATCG 889
 Db 1029 GCTTCCTGCGGAGTGTATGAGCTCATGACGTGTGTGCTCATCTGCGCTTACTACATG 1088
 QY 890 GTCTGTCATGACCAACAAGAGAGCTGTCCGCGCTTCTGTCACGCTCCGGGTCTTCC 949
 Db 1089 GGCTTTTGGTGGCCCAAGAGAGAGATGTCTGTGGCGCTTGTGTCACCTGCTGTGTTCC 1148
 QY 950 GCGTCTTCAAGATCTTCAAGTTTCCCGCACTCCGAGGCTGCGGATCCTGGGCTACA 1009
 Db 1149 GGGTGTTCGCACTTCAAGTTCTCCAGGCACTCACAGGCTTGAAGATCTGGGCTACA 1208
 QY 1010 CACTGAGAGCTGTGCTCCGAACTGGGCTTCTTCTCTCTCTCCCTCACCATGGCCATCA 1069
 Db 1209 CACTCAAGAGCTGTGCTTGTAGCTGGGCTTCTCTCTTCTTCCCTTACCATGGCCATCA 1268
 QY 1070 TCATCTTTGCTGCTGTGATGTTTATGTCGAGAGAGGCTCTCCGACGACAACTTACAA 1129
 Db 1269 TCATCTTTGCTGCTGTGATGTTTATGTCGAGAGAGGCTCACAAACGACAACTTACAA 1328
 QY 1130 GCATCCCTGCTGCTTGTGTCACCATGTCACCATGTCACCATGTCGATGTCGAGACA 1189
 Db 1329 GCATCCCTGCTGCTTGTGTCACCATGTCACCATGTCACCATGTCGATGTCGAGACA 1388
 QY 1190 TGTGCTTAAAGAGATTGAGAGGAAATCTTGGCTCCATCTGCTCTTGAAGTGGCTCC 1249
 Db 1389 TGTGCTTAAAGAGATTGAGAGGAAATCTTGGCTCCATCTGCTCTTGAAGTGGCTCC 1448
 QY 1250 TGTGCTTAAAGAGATTGAGAGGAAATCTTGGCTCCATCTGCTCTTGAAGTGGCTCC 1309
 Db 1449 TGTGCTTAAAGAGATTGAGAGGAAATCTTGGCTCCATCTGCTCTTGAAGTGGCTCC 1508
 QY 1310 ATCAGAGCTGATTAACGAGGAGCAAAAAGAGGCGCTTCCAGATCCGTGTGG 1369
 Db 1509 ACCAGCGGCTGACAGGCGCGAGAGACAGCAGAAAGTGGCTTGGCAAGATCCGATGG 1568
 QY 1370 CCAAAACAGGAGCTTGAATGATCTGTCACAGAGGCAAGGCTCTCTCAACGAGG 1429
 Db 1569 CAAAGAGTGTACCAACCAATGCTCTCTGAGTACAGAGAGATGGGCGCTTGA----- 1623
 QY 1430 CGCTGAGCTGACGGGACCCCAAGAGAGACATGGGCAAGACCACTCATCTATCG 1489
 Db 1624 ---GGACAGCGGACAGTGGCGAGAGACAGGCTTGTGTAGAGAACCGTCTGCTTGTG 1679
 QY 1490 AGAGCAGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
 Db 1680 AACAGCAATCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1739
 QY 1550 ATGAGCAGATGTTT-GAGCAGACCTGATGAGAGTTCATGCAAGTTCAGTACCATCACA 1608
 Db 1740 ATGAGCTCACTTCACTGAGAGCTGAGAGGAGCGTCTGCGCGGAGGCGGACGAGTA 1799
 QY 1609 AGAAGTCCCTCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1663
 Db 1800 GCACTCTTGTGTCTTCCAGCGAGAGGAGCGGAGCGGAGCGTGTCTTCTGCTGCTGCT 1859
 QY 1664 GTAGTAGAAGACACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1720
 Db 1860 GCAGGCGCAAGCGCGCGCATCCGCTTGCACACTGCTGCTGCTGCTGCTGCTGCTGCTG 1919
 QY 1721 GCATGCAAGAGCTCAGCAGATCCATCCAGGAGGAGTGAAGAGGCTCTCTCACAACA 1780
 Db 1920 GCATGCAAGAGCTGAGACATGCTGAGAGGAGGCTGCGAGAGCCATGCTCCCTCAG--A 1973

QY 1781 GTGCTCCAGCTTAATTGAAAGAGACGACGCTGAGACCAACTGCAAAATCC 1840
 Db 1974 GCGCTCCAGCTCAATGCAAGCGCCATGACGCTTGAACCTGACAGAGCGCGG 2033
 QY 1841 AGATCACACAGCCATCATCAGATCCCACTCCCGCAGCGTTAAACCCAGAGGGGAAA 1900
 Db 2034 ACTTCGTGCTGCTGCTTATCAGATCCCTACCTCTGCGCAACACCCAGATGAGAGCC 2093
 QY 1901 GTGCGCCACCCCTGCGACCCAGGC 1926
 Db 2094 AACCTTCTCCCTGCGCGGCTGCGC 2119

RESULT 8
 US-09-949-016-2456
 ; Sequence 2456, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2456
 ; LENGTH: 3260
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-2456

Query Match 15.8%; Score 326.4; DB 4; Length 3260;
 Best Local Similarity 66.2%; Pred. No. 2.4e-62;
 Matches 487; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 1173 ACTGGATACGAGACATGCTGCTTAAGACATGTCAGGAGAAATCTGCGCTCATCTG 1232
 Db 2 ACTCAGTATGCTGACATGCTGCTCAAAAACCATAGCAGGAAATTTGCTTCTATCTG 61
 QY 1233 CTCCTTGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1292
 Db 62 TTCCTGAGTGGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
 QY 1293 CCGGATTTACCAACCAATCAGAGCTGATTAACGAGGCAAAAAGAGGCGCGCT 1352
 Db 122 TCGCATCTACCAACCAATCAGAGCTGATTAACGAGGCAAAAAGAGGCTGACT 181
 QY 1353 TGGCAGATCGCTGTGGCAAAACAGGCACTTGAATGCTATCTGACAGCAACGCGCAA 1412
 Db 182 GGCCAGGATCGGGCAGCCAAAGCGGAAAGCTTACATGACAGCAACGCGAA 241
 QY 1413 CGGGCTCTCAACGAGGCGCTGAGCTGACGGGCAACCCAGAGAGAGCAATGGGCAA 1472
 Db 242 TGGTTTACTAGTAATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
 QY 1473 GACCACTCATCATCAGAGACGACGATCATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1532
 Db 299 ATCCGGCTCAGCTTGAACACGAGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
 QY 1533 TAACCAAGATTTATGATGAGAGATTTGAGCAGAACTGATGAGAGTTCATGCA 1592
 Db 359 GAATCAAGATTTGATGAGAGAACTTTGAGAGAAAGCTGATGAGAGTTCATGCTGT 418
 QY 1593 GAATCAAGATTTGATGAGAGAACTTTGAGAGAAAGCTGATGAGAGTTCATGCTGT 1652
 Db 419 TAATGCTCTTCAAGTACAGTCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCA 478

QY	1653	CTGCTCCCGCTGTAAGTAAAGAACACACACCTGCCCAATTTTAACTGCCAGCTACTG	1712
Db	479	CTGTTACGACGACACAAAAAACTTTTCGATCCAAATGCCAATGTATCAGGAAGCA	538
QY	1713	CCTGCGCAGCATGCAAGAGCTCAGCAGCATTCACATTCAGGGCAGTGACAGCCTCCT	1772
Db	539	TCAAGGTAGTATACAGAACTCAGCAGCATTCAGATCAGATGTGTGGAGAAACACTT	598
QY	1773	CACAACCAAGTCGCTCCAGCCTTAATTGAAGCAGACGACGACTGAGACCAACTGCA	1832
Db	599	GTTTAAcAGCCGATTCAGTTTAAATGcCAAAATGAAAGAGTGTGTTAACTTAACTGTGA	658
QY	1833	AACATCCAGATCACACACGCCATATCAGATCCCACTCCCCAGCGCTAACCCGAGA	1892
Db	659	ACAACCTTATGTGACTACAGCAATATAAGATCCCAACACTCCAGTAACCAcACACAGA	718
QY	1893	GGGGGAAAGTCGGCCA	1908
Db	719	AGGAGACGATAGGCCA	734

RESULT 9

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US-09-949-016-2293
; Sequence 2293, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2293
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2293

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Query Match 11.6%; Score 240; DB 4; Length 3004;

Best Local Similarity 53.4%; Pred. No. 2.5e-43;
Matches 712; Conservative 0; Mismatches 555; Indels 47; Gaps 8

QY 19 CAAGCTGTGTGCTAGCGTTCGCGCGGCTGCGGCCCAAGAGCTGAGTTCACCATGGCG 78
DB 72 CGAGCTGCCGCCCGACATGACCGTGTGTCCCGGGAGACCACTGCTTGAG--CCGAGAGTG 129
QY 79 GCCGAGTTGCCGGCCTGGCTGCTTTTTCGCCGGGCTGGCGCCATCGGGTGGATGCCGGTG 138
DB 130 GCCGATGTGTGAGGGGGCCCCCGCTCAAGGGCGCTGTGGCGCGCGGCTCGACCGCTAC 189
QY 139 GCCAACTGCCCCCATGCCCCCTGGCCCCCGGCCGACAAAGACAGCGGACGATGAGCTGATT 198
DB 190 GAGCCGCTGCCCGCTCACTGCGCGCGCGGGGAGACGAGACTGTGCGGGGAGCGCGTG 249
QY 199 GTCTCTCAACGTGAGTGGGCGGAGTTCAGACCTGAGGACCAAGCTGAGCGCTACCCG 258
DB 250 GTCATCAACATCTCCGGCTGCGCTTCGAGACGACGTGAAGACCTTGTCCAGTTCGCC 309
QY 259 GACACCTCTGCTGGCGACGACGAGAAAGAGTTC--TTCTTCAACGAGACACCAAGAG 315
DB 310 GAGACGCTGCTGGCGACCCCAAGCGCGCATGAGTACTTCGACCGCTCCGCAACGAG 369
QY 316 TACTTCTTCGACCGGAGCCCGAGGTGTTCGCTGCTGCTCAACTTCTACCGACGGGG 375

Db	370	TACTTCTTCGACCGCAACCGGCCAGCTTCGAGCCATCCTCTACTATCATGATCCGGG	429
QY	376	AAGC---TGCACTACCGCGGCTACGAGTGCATCTCTGCTACGACGACGAGCTGGCCTTC	432
Db	430	GGCCGCATCCGCGCGGCGGTCAACGTGCCCATGACATTTTCTCCGAGAGATCCGCTTC	489
QY	433	TACGGCATCTCCCGGAGATCATCGGGAGCTGCTCTACGAGAGTACAAGACCGCAAG	492
Db	490	TACCACTGGGCGAGGAGGCCATGAGAAATTCCCGAGGACGAGGGCTTCTCGCGGAG	549
QY	493	AGGAGAACCGCCGAGCGGCTCATGAGCAACAAGCACTCGGAGAAACACGAGAGTCCATG	552
Db	550	GAGGAGCGGCTTGGCCCCGCGCGCATCTTCCAGGGCCAGGTG---TGGCTGCTTTCGAG	606
QY	553	CCCTGCTCAGCTTCCGCCAGAACCATGTGGCGGCTTCGAGAACCCCAACACGACGACG	612
Db	607	TACCCGAGAGCTCCGGGCGCGGCGGCATCGCCATGCTGTGCTGGTGCATCTTC	666
QY	613	CTGGCCCTGGTCTTCTACTACGTGACTGGCTT-----CTTCATCGCTGTCTCGGTATC	666
Db	667	ATCTCCATTTGTCATCTTCTGCTTGAGACGCTGCCGAGTTCCGCGACGAGAAAGGACTAC	726
QY	667	ACCAACGTGTGAGAGACGCTGCCGTGCCGACCGTCCCGGCGACGAAAGAGCTGCCGTGC	726
Db	727	CCCGCTCGACGTCCGAGGACTCATTTGGAAGCACCGCGGCAACGACGATGGGGGTCCCGC	786
QY	727	GGGGAG-----CGCTACTCGGTGGCTTCTTCTGCTCGGACACGGCGTGGCTATGATC	780
Db	787	GCAGAGACCTTCAGCTTCTCCGATCCCTTCTTGTTGAGAGACGCTGTGCATCATCTGG	846
QY	781	TTCAACGTGAGTACCTCTCTGCGGCTCTTCGCGGCTCCAGCCGCTACCGCTTCATCCGC	840
Db	847	TTCTCTTCGAACGTGCTGTGGGTTCTTCGCTTGTCTTAACAAAGCCACCTTCTCGCGA	906
QY	841	AGCGTATGAGCATCATCGACGTGTGGCCATCATGCCCCATCTACATCCGCTGTGCATG	900
Db	907	AACATATGAACCTGATCGACATGTGTGGCATCATCTTATTTATCATCTGTGGTAAC	966
QY	901	ACCAA-----CAACGAGGACGTGTCCGGCGCTTCGTCAACGCTCCGGGTC	945
Db	967	GAGCTGGCCGAACGACAGGCAATGACAGACGAGCCATGTCTTGCCCATCTGAGGGTTC	1026
QY	946	TTCCGC-----GTCTTCAGGATCTTCAAGTTTCCCGCACTCCAGGGCTTCGG	996
Db	1027	ATCCGCTGTGTAAGGATCTTCCGCACTTTCAGGCTGTCCGCGCACTCCAGGGGCTGCAG	1086
QY	997	ATCTCGGGCTACACATGGAAGAGCTGTGCTCCGAACCTGGGCTTCTTCTTCTCCCTC	1056
Db	1087	ATCCTGGGGCAAAACGCTGAAGGGTCCATGCGGAGAGCTGGGATTGCTCATCTTCTTCCTC	1146
QY	1057	ACCATGGCCATCATCTTTGGCCACTGTGATGTTTATGCGGAGAAAGGGCTCTCGGCC	1116
Db	1147	TTTATTGGGGTCACTCTTTCCTCCAGCGCGGTCTACTTTGCGGAGGACGAGACCCCACT	1206
QY	1117	AGCAAGTTCACAGCATCTCCCTGCTGTTTGTGTACACCATTTGTCAACCATGACACACTG	1176
Db	1207	TCAGTTTCAGAGCATCTCCGGAATGCTTCTGTGTGGGCACTGTGTAAACATGACAACTG	1266
QY	1177	GGATACGGAAGACATGTGCTTAAGACGATTTGCAGGGAAAGATCTTGGGCTCATCTGCTCC	1236
Db	1267	GGTACGGCGAATGACACCCAGTACCATAGGGGCAAGATTTGTGGGATCTCTGTGCC	1326
QY	1237	TTGAGTGGCGTCTGTGATTTGCTTGGCCCTGCAGTCCCTGTGATTTGTTCCAATTTAGCCGG	1296
Db	1327	ATGCGCGGTGTCTTGACCATCGCATTTGCCAGTTCCGATGTGTTCCAACTTCAATTAC	1386
QY	1297	ATTTACCACGAGAA	1310
Db	1387	TTCTTACCACCGGGA	1400

RESULT 10

US-09-949-016-12066

```
; Sequence 12066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12066
; LENGTH: 7055
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12066

Query Match      11.6%; Score 240; DB 4; Length 7055;
Best Local Similarity 53.4%; Pred. No. 3.2e-43;
Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

QY 19 CAAGCTGTGTGCTAGCTCCGCGGCTGCGGCCCAAGAGCTGAGTCAACATGGCG 78
DB 2072 CGAGTGCCTCCGCGGACATGACCTGTGTGCGCGGGACCACTGCTGGAG--CCGAGGTG 2129
QY 79 GCGGAGTTGCGCGCTGCTGCTTTTCCCGCGCTGCGGCCATGCGGTGATGCCGTG 138
DB 2130 GCCGATGTGAGAGGGGCGCCGCTCAAGCGGCTGTGCGCGCGCTGCGACCGCTAC 2189
QY 139 GCCAATGCCCCCATGCCCCCTGGCGCCCGCCGACAAAGACGCGCAGATGAGCTGATT 198
DB 2190 GAGCGGTGCGCGCTTCACTGCGCGCGCGCGCGGAGCAGAGACTGTGCGGGAGCGGTG 2249
QY 199 GTCTCAACGTGAGTGGGCGGAGTTCCAGACTGAGAGCAACGCTGAGCGCTACCGG 258
DB 2250 GTGATCAACATCTCCGGCTGCGCTTCAAGCAGCAGTGAAGACCTTTGCGAGTTCCG 2309
QY 259 GACACCTGCTGGGCGAGCAGCAGAGAGAGTTC--TTCTTCAAGAGAGACCAAGAG 315
DB 2310 GAGACGCTGCTGGGCGAGCAGCAGAGAGAGTTC--TTCTTCAAGAGAGACCAAGAG 2369
QY 316 TACTTCTTGAACCGGAGACCCCGAGGAGTTCGCTGCGTCACTTCTTACCGCAGCGG 375
DB 2370 TACTTCTTGAACCGGAGACCCCGAGGAGTTCGCTGCGTCACTTCTTACCGCAGCGG 2429
QY 376 AAGC---TGACATAACCGGCTACGAGTGCATCTTCTGCTACGAGCAGCGCTGCTTC 432
DB 2430 GCGCGCATCCGCGCGCGCGCTCAACGTCGATGACATTTTCTCGAGAGATCCGCTTC 2489
QY 433 TACGCGATCTCTCCGAGATCATCGGGAGTGTGCTGCTACGAGAGTACAAAGACCGCAAG 492
DB 2490 TACGAGTGGGAGAGGAGGATGAGAGTTCGCGAGAGCAGAGGCTTCTGCGGGAG 2549
QY 493 AGGAGAAAGCGGAGCGGCTCATGAGCAAGAGACTGCGAGAGAAACAAGAGAGTGCATG 552
DB 2550 GAGGAGCGGCGCTTGGCGCGCGCGCTTCAAGCGCGCAGGTG---TGCTGCTCTTCGAG 2606
QY 553 CCCTGCTGAGCTTCCGCGAGACCATGTGGCGGCGCTTTCGAGAAACCCCAACAGCAGAG 612
DB 2607 TACCGGAGAGCTCCGCGCGCGCGCGCGCGCGCATCGCATCTGTGCTGTGCTGCTC 2666
QY 613 CTGCGCTGTGCTTCTACTAGTGAAGTGT---CTTCACTGCTGTCTCGGTATC 666
DB 2667 ATCTCAATGTGATCTTCTGCTGAGAGAGCTGCGGAGTTCGCGAGCAGAGAGGACTAC 2726
QY 667 ACCAAGTGTGTGAGAGCGGTGCGCGGAGCAGGTCCCGGCGAGCAAGAGCTGCGGTGC 726
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DB 2727 CCCGCTTCGACGTCGAGAGACTCATTTGAAGCAGCGCGCAACAGCAGTCCGGTCCGC 2786
QY 727 GGGAG-----CGTACTTCGGTGCGCTTCTTCTGCTCGGAGACAGCGCGTCAATGATC 780
DB 2787 GCAGAGCCTTCAGCTTCCCGATCCCTTCTGCTGAGAGAGCGTGTGATCATCTGG 2846
QY 781 TTCACGCTGAGTACCTCCGCGCTTTCGCGCGCTCCAGCGGCTACCGCTTCAATCCG 840
DB 2847 TTCTCTTGAAGTGTGCTGCGGTCTTCTGCTGCTTGAAGAGCAGCTTTCGCGA 2906
QY 841 AGCGTATGAGCATCATGAGTGTGGCCATCATGCGCTTCAATCATGCTGTGCTATG 900
DB 2907 AACATCATGAAGTGTGAGTGTGCGCATCATCTTATTTATCATCTGTGGTAAC 2966
QY 901 ACCAA-----CAACGAGAGCGTGTCCGCGCGCTTCTGCTACGCTCCGGGTC 945
DB 2967 GAGTGGCGGAACGAGCAGGCGCAATGAGACAGAGCGCATGTCTGTGCGCATCTGAGGTC 3026
QY 946 TTCGC-----GTCTCAGGATCTTCAAGTTTCCCGGCACTCCAGGGCGCTGCGG 996
DB 3027 ATCCGCTGTGAAGGTCTTCCGATCTTCAAGCTGTGCGGCACTCCAGGGCGCTGAG 3086
QY 997 ATCCGCGCTACACATGAAAGAGCTGTGCTCCGAGTGGCGCTTCTTCTTCTTCTC 1056
DB 3087 ATCCGCGGCAACGCTGAAGCGTCCATGCGGAGCTGGAGTTGCTCATCTTCTTCTC 3146
QY 1057 ACCATGCGCATCATCTTTCGCACTGTGATGTTTATGCGGAGAGCGCTCTCGGCC 1116
DB 3147 TTTATGCGGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3206
QY 1117 AGCAAGTTCACAGCATCTCTGCTGCTTGTGTATACCATGTTCACATGACCACTG 1176
DB 3207 TCAGTTTCAAGACATCCCGATGCTTGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3266
QY 1177 GATAGGAGAGATGTGCTTACAGATTCAGAGAGATCTTCCGCTCATCTGCTCC 1236
DB 3267 GGTACGCGCATATGACACCATGACATGAGGCGGAGATGTGAGTGTGAGTGTGAG 3326
QY 1237 TTGAGTGGCGTCTGCTGATTCCTTCCAGTCCCTGTGATGTTTCAACTTGAACGG 1296
DB 3327 ATGCGCGGTGCTTGAACCATGCAATGCGAGTTCGCGATGTTTCAACTTGAATAC 3386
QY 1297 ATTACCAACAGAA 1310
DB 3387 TTCTACCAACGCGGA 3400

RESULT 11
US-09-949-016-14035
; Sequence 14035, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14035
; LENGTH: 7056
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14035

Query Match      11.6%; Score 240; DB 4; Length 7056;
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Qy 433 TACGAGATCTCCCGAGAGATCATCGGGGACTGCTGTCTACGAGAGATCAAGAACCGCAAG 492
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Db 546 GAGGAGCGGCGCTTGGCCCGCGCGGCACTTCCAGCGCAGGTG---TGGCTCTCTTGAG 602
Qy 553 CCCTCGCTCAGCTTCCCGCAGAACCATGTGGGGGCTTGAAGACCCCGACACGACAG 612
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Qy 613 CTGACCTGCTTCTTACTACTAGTGAAGTGGCTT-----CTTCATGCTGTCTGCTCATC 666
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Qy 727 GGGAG-----CGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGGCTGCGTATGATC 780
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US-09-949-016-1604
; Sequence 1604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 1604
; LENGTH: 1802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1604

Query Match 10.5%; Score 216; DB 4; Length 1802;
Best Local Similarity 53.7%; Pred. No. 4.2e-38;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy 294 CTTCACGAGAGACCAAGAGTACTTCTTCGACCGGACCCCGAGTGTCCGCTGCT 353
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Db 267 CATGAGGTGATATTTGCGGAGGTGCAATGAGAGGAGATGCTGCTGCTGCT 326
Qy 414 CGACGAGAGCTGCTTCTTACCGCATCTCCGAGATCATGCGGAGTGTGCTGCT 470
Db 327 CAAGACGAGATGAGCTTCTGAGAGTGAAGCTCAAGTCTTCTGAGCAGTGTGCAAG 386
Qy 471 -----CGAGGATACAGGACCGCAAGAGGAGAGAGCGGCTCATGACGA 521
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Qy 702 CCGGCGAGAGAGAGTGTGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 761
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Qy 882 CTACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920
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Db 978 GCTGCTCATGTACCTGCGAGTGGGTATCTTCTTCTGCGCTGGGCTACCATGGA 1037
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Db 1218 CAACAACTTGTCTAGGTAATCAACAAGCAGC 1249

RESULT 14

US-08-464-340A-3
Sequence 3, Application US/08464340A
Patent No. 5710019

GENERAL INFORMATION:

APPLICANT: LI, ET AL.

TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESS: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,340A

FILING DATE: June 5, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-415

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2483 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

US-08-464-340A-3

Query Match 10.5%; Score 216; DB 1; Length 2483;

Best Local Similarity 53.7%; Pred. No. 4.7e-38;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

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(without alignments)
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1000.8	48.5	2351	17	US-10-361-811-253
5	1000.8	48.5	2351	17	US-10-369-186-253
6	1000.8	48.5	5333	15	US-10-212-677-252
7	1000.8	48.5	5333	15	US-10-212-677-254
8	1000.8	48.5	5333	17	US-10-361-811-252
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10	1000.8	48.5	5333	17	US-10-369-186-252
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12	843.2	40.9	3424	14	US-10-121-746-9	Sequence 9, Appli
13	823	39.9	2578	17	US-10-296-115-373	Sequence 373, App
14	679	32.9	5404	15	US-10-212-677-255	Sequence 255, App
15	679	32.9	5404	17	US-10-361-811-255	Sequence 255, App
16	679	32.9	5404	17	US-10-369-186-255	Sequence 255, App
17	634.2	30.7	1121	16	US-10-029-386-24777	Sequence 24777, A
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26	240	11.6	3004	18	US-10-322-281-95	Sequence 95, Appl
27	240	11.6	3303	19	US-10-772-636-9	Sequence 9, Appli
28	240	11.6	23055	18	US-10-322-281-94	Sequence 94, Appl
29	230	11.1	1408	16	US-10-029-386-20260	Sequence 20260, A
30	221.2	10.7	2565	17	US-10-435-935-10	Sequence 10, Appl
31	221.2	10.7	3756	18	US-10-377-139-18	Sequence 18, Appl
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41	213	10.3	6823	9	US-09-989-920-16	Sequence 16, Appl
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44	207.6	10.1	1587	18	US-10-322-281-92	Sequence 92, Appl
45	207.6	10.1	21587	18	US-10-322-281-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-10-062-879-3
; Sequence 3, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hual-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
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US-10-062-879-3

Query Match 100.0%; Score 2064; DB 13; Length 2064;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1081 ACTGTGATGTTTATGCGGAGAGGCTCTCGGCGAGAGTTTCAAGATCCCTGCTGCTGCTG 1140
Db 1081 ACTGTGATGTTTATGCGGAGAGGCTCTCGGCGAGAGTTTCAAGATCCCTGCTGCTGCTGCT 1140
QY 1141 TCGTTTGTGTAACCATGTGTCAACATGACCAACATGCGGATCGGAGATCGGAGATGCTGCTAAG 1200
Db 1141 TCGTTTGTGTAACCATGTGTCAACATGACCAACATGCGGATCGGAGATCGGAGATGCTGCTAAG 1200

QY 1201 ACGATTGCAAGGGAAGATCTTCGGCTCCATCTGCTCTTGAAGTGGCGTCTGCTCATTTGCC 1260
Db 1201 ACGATTGCAAGGGAAGATCTTCGGCTCCATCTGCTCTTGAAGTGGCGTCTGCTCATTTGCC 1260
QY 1261 CTGCGAGTCCCTGATGATTTGTTCCAACTTTAGCCGATTTTACCAACGAATTCAGAGAGCT 1320
Db 1261 CTGCGAGTCCCTGATGATTTGTTCCAACTTTAGCCGATTTTACCAACGAATTCAGAGAGCT 1320
QY 1321 GATTAACGAGGAGCAAAAAGAGGCGGCTTGGCCAGATCCGTGTGGCCAAAACAGGC 1380
Db 1321 GATTAACGAGGAGCAAAAAGAGGCGGCTTGGCCAGATCCGTGTGGCCAAAACAGGC 1380
QY 1381 AGTTGATGATATCTGCAACGAGCGCAACGGGCTCTCAACGAGGCGCTGAGCTG 1440
Db 1381 AGTTGATGATATCTGCAACGAGCGCAACGGGCTCTCAACGAGGCGCTGAGCTG 1440
QY 1441 ACGGCAACCCAGAGAGAGACATGCGGCAACCACTACTACTATCGAGAGCCAGCAT 1500
Db 1441 ACGGCAACCCAGAGAGAGACATGCGGCAACCACTACTACTATCGAGAGCCAGCAT 1500
QY 1501 CATCACTGCTGCACTGCTGCGGAAAAACCACTAACCGAGTTTATGAGAGAGATG 1560
Db 1501 CATCACTGCTGCACTGCTGCGGAAAAACCACTAACCGAGTTTATGAGAGAGATG 1560
QY 1561 TTGAGCAGAACTGATGAGAGTTCAATGAGAACTAACCATCCACAAGAGTCCCTCA 1620
Db 1561 TTGAGCAGAACTGATGAGAGTTCAATGAGAACTAACCATCCACAAGAGTCCCTCA 1620
QY 1621 CTGTCCAGCCACCAAGGCTCTACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 CTGTCCAGCCACCAAGGCTCTACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 CACCTGCCAATTTAACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 CACCTGCCAATTTAACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 ATCCACATTCAGGCGAGTGAAGACGCTCTCCCTCAACCAAGTCCGCTCAAGCTTAATTG 1800
Db 1741 ATCCACATTCAGGCGAGTGAAGACGCTCTCCCTCAACCAAGTCCGCTCAAGCTTAATTG 1800
QY 1801 AAAGCAGACGAGCTGAGACCAAACTGCAAAATCCAGATCCAGATCCAGAGCCATCATC 1860
Db 1801 AAAGCAGACGAGCTGAGACCAAACTGCAAAATCCAGATCCAGATCCAGAGCCATCATC 1860
QY 1861 AGCATCCCACTCCCGCAGGCTAACTCCAGAGGAGGAAAGTCCGCTCAAGCTTAATTG 1920
Db 1861 AGCATCCCACTCCCGCAGGCTAACTCCAGAGGAGGAAAGTCCGCTCAAGCTTAATTG 1920
QY 1921 CCAAGGCCCAACAGAACTTCTTCCATTAACAGAAATGTTGTAAGGTCTGCTGCTG 1980
Db 1921 CCAAGGCCCAACAGAACTTCTTCCATTAACAGAAATGTTGTAAGGTCTGCTGCTGCTG 1980
QY 1981 TAAATAATCCCGGCGCATGCGGCGGAGCATGCGAGCATGCGGCGCAATTGCGCCCTATA 2040
Db 1981 TAAATAATCCCGGCGCATGCGGCGGAGCATGCGAGCATGCGGCGCAATTGCGCCCTATA 2040
QY 2041 GTGAGTCTGTTAAAGCCGAATTC 2064
Db 2041 GTGAGTCTGTTAAAGCCGAATTC 2064

RESULT 2
US-10-062-879-1
; Sequence 1, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Thereof


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; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-10-062-879-1

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Query Match	96.8%	Score 1997;	DB 13;	Length 2121;
Best Local Similarity	97.3%	Pred. No. 0;		
Matches 2064;	Conservative	0;	Mismatches 0;	Indels 57;
				Gaps 11

QY	I	GATTGTGTAAC	CTA	ACTCCAA	AGCTGTGTGCT	TAGCGTCCGCGCGCTG	CCGGCCCAAGA	60
Db	1	GATTGTGTAAC	CTA	ACTCCAA	AGCTGTGTGCT	TAGCGTCCGCGCGCTG	CCGGCCCAAGA	60
QY	61	GCTGAGTCAC	CAATG	CGCGCCGAG	TTCGCGCTG	CGCTTTTGGCCCGGCTG	CGGCGC	120
Db	61	GCTGAGTCAC	CAATG	CGCGCGCGAG	TTCGCGCTG	CGCTTTTGGCCCGGCTG	CGGCGC	120
QY	121	ATCGGTTGATG	CCGCTG	GGCCA	CTGCCCCATG	CCCCCTGGCCCCCGGCGCA	CAAGAA	180
Db	121	ATCGGTTGATG	CCGCTG	GGCCA	CTGCCCCATG	CCCCCTGGCCCCCGGCGCA	CAAGAA	180
QY	181	CGGAGAGTAG	CTGATT	GTCTT	CAAGT	AGTGGCGGAGGTT	CCAGACTG	240
Db	181	CGGAGAGTAG	CTGATT	GTCTT	CAAGT	AGTGGCGGAGGTT	CCAGACTG	240
QY	241	ACGCTGAGCG	CTACCCG	GACAC	CCCTGCTGG	CGACGAGAGAGATT	CTTCTT	300
Db	241	ACGCTGAGCG	CTACCCG	GACAC	CCCTGCTGG	CGACGAGAGAGATT	CTTCTT	300
QY	301	GAGGACACCA	AGAGTACT	CTTTC	GACCGGAG	CCCCGAGGTTC	CGCTCGT	360
Db	301	GAGGACACCA	AGAGTACT	CTTTC	GACCGGAG	CCCCGAGGTTC	CGCTCGT	360
QY	361	TTCTACCGC	CACGGGG	AAGCTG	CACTAC	CCGCGCTAC	GAGTGCAT	420
Db	361	TTCTACCGC	CACGGGG	AAGCTG	CACTAC	CCGCGCTAC	GAGTGCAT	420
QY	421	GAGCTGGCT	CTTACG	GCACT	CTCCG	GAGATCAT	CGGGGACT	480
Db	421	GAGCTGGCT	CTTACG	GCACT	CTCCG	GAGATCAT	CGGGGACT	480
QY	481	AAGGACCGC	CAAGAGG	AGAA	CGCCGAG	CGGCTCAT	TGACGAC	540
Db	481	AAGGACCGC	CAAGAGG	AGAA	CGCCGAG	CGGCTCAT	TGACGAC	540
QY	541	CAGGAGTC	CATGCC	CTCGCT	CAGCTT	CCGCGAC	CAATGTG	600
Db	541	CAGGAGTC	CATGCC	CTCGCT	CAGCTT	CCGCGAC	CAATGTG	600
QY	601	CACACCA	GACACG	CTGGCC	CTGTCTT	CTACTA	CGTAGT	660
Db	601	CACACCA	GACACG	CTGGCC	CTGTCTT	CTACTA	CGTAGT	660
QY	661	GTATATCA	CAACG	TGTGAG	ACGCGT	CGGCA	CGGTCCG	720
Db	661	GTATATCA	CAACG	TGTGAG	ACGCGT	CGGCA	CGGTCCG	720
QY	721	CCGTGCGGG	AGCGCT	ACTTC	GGTGCTT	CTTCTG	CTCGAC	780
Db	721	CCGTGCGGG	AGCGCT	ACTTC	GGTGCTT	CTTCTG	CTCGAC	780
QY	781	TTTACCG	TGAGAGT	ACTCT	CGCGGCTT	TGCGGCT	CCAGCGCT	840
Db	781	TTTACCG	TGAGAGT	ACTCT	CGCGGCTT	TGCGGCT	CCAGCGCT	840

QY	841	AGCGTCATGAGCATCATCGACGCTGGTGGCCATCATGCCCTACTACTACATCGGCTCTGGTCATG	900
Db	841	AGCGTCATGAGCATCATCGACGCTGGTGGCCATCATGCCCTACTACTACATCGGCTCTGGTCATG	900
QY	901	ACCAACAACGAGGAGCGTGTCCGGCGCCTTCGTCAAGCTCCGGGCTTCGGCGTCTTCAGG	960
Db	901	ACCAACAACGAGGAGCGTGTCCGGCGCCTTCGTCAAGCTCCGGGCTTCGGCGTCTTCAGG	960
QY	961	ATCTTCAAGTTTTTCCCGCACCTCCAGGCGCTGCGGATCCTGGGCTACACACTGAAGAGC	1020
Db	961	ATCTTCAAGTTTTTCCCGCACCTCCAGGCGCTGCGGATCCTGGGCTACACACTGAAGAGC	1020
QY	1021	TGTGCCCTCCGAACTGGGCTTCTTCTCTTCTCCCTCACCATGGCCATCATCTTTGGCC	1080
Db	1021	TGTGCCCTCCGAACTGGGCTTCTTCTCTTCTCCCTCACCATGGCCATCATCTTTGGCC	1080
QY	1081	ACTGTGATGTTTTATGCGGAGAGGGCTCTCGGCGACGAAGTTCAACAAGCATCCCTGCC	1140
Db	1081	ACTGTGATGTTTTATGCGGAGAGGGCTCTCGGCGACGAAGTTCAACAAGCATCCCTGCC	1140
QY	1141	TGCTTTTGTATACACCATTTGTCAACCATGACACACTGGGATATCGAGACATGTTGCCCTAAG	1200
Db	1141	TGCTTTTGTATACACCATTTGTCAACCATGACACACTGGGATATCGAGACATGTTGCCCTAAG	1200
QY	1201	ACGATTTGCAGGGAGAGATCTTGGGCTCCATCTGCTCTTGAATGGCGTCTGTCAATTGCC	1260
Db	1201	ACGATTTGCAGGGAGAGATCTTGGGCTCCATCTGCTCTTGAATGGCGTCTGTCAATTGCC	1260
QY	1261	CTGGCCAGTCCCTGTGATTTGTTTCCAACTTTAGCCGGATTTTACCACCAATCAGAGAGCT	1320
Db	1261	CTGGCCAGTCCCTGTGATTTGTTTCCAACTTTAGCCGGATTTTACCACCAATCAGAGAGCT	1320
QY	1321	GATTAACGCGAGGGGACAAAGAAGGCCCGCTTGCCAGGATCCGTTGGCCAAACAGAGC	1380
Db	1321	GATTAACGCGAGGGGACAAAGAAGGCCCGCTTGCCAGGATCCGTTGGCCAAACAGAGC	1380
QY	1381	AGTTGGAATGCATACCTGACACAGCAAGCGCAACGGGCTCTCAACGAGCGCTGAGAGCTG	1440
Db	1381	AGTTGGAATGCATACCTGACACAGCAAGCGCAACGGGCTCTCAACGAGCGCTGAGAGCTG	1440
QY	1441	ACGGGGCAACCCGAGAAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCCAGCAT	1500
Db	1441	ACGGGGCAACCCGAGAAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCCAGCAT	1500
QY	1501	CATCAACCTGCTGCACTGCCCTGGAACCACT-----	1533
Db	1501	CATCAACCTGCTGCACTGCCCTGGAACCACTGCCCTGCTATCTTGTGATGATATCCC	1560
QY	1534	-----AACCAAGATTTATTGATGAGCAGATGTTT	1563
Db	1561	CTGTATTCTGTACGAACCTCCACCATCAAGAACCAAGATTTATTGATGAGCAGATGTTT	1620
QY	1564	GAGCAGAATCTGCATGAGAGAGTTCAATGACAGAACTAACCATCCACAAGAAAGTCCCTCACTG	1623
Db	1621	GAGCAGAATCTGCATGAGAGAGTTCAATGACAGAACTAACCATCCACAAGAAAGTCCCTCACTG	1680
QY	1624	TTCAGGCCAACCAGGCTCACTACCTACCACTGCTGCTGCCGTGCTAGTAAGAAGACCAACAC	1683
Db	1681	TTCAGGCCAACCAGGCTCACTACCTACCACTGCTGCTGCCGTGCTAGTAAGAAGACCAACAC	1740
QY	1684	CTGCCCAATTTCTAACTGACCACTACTGCTGCTGCGCAGCATGCAAGAGCTCAGCAGATC	1743
Db	1741	CTGCCCAATTTCTAACTGACCACTACTGCTGCTGCGCAGCATGCAAGAGCTCAGCAGATC	1800
QY	1744	CACATCCAGGGGCAGTGAGCAGGCTCTCCCTCACAACCAAGTGGCTCCAGGCTTAAATTTGAAA	1803
Db	1801	CACATCCAGGGGCAGTGAGCAGGCTCTCCCTCACAACCAAGTGGCTCCAGGCTTAAATTTGAAA	1860
QY	1804	GCAGAGCAGCGAGCTGAGACCAAACTGCAAAACATCCAGATCACAAGCCATCATCAGC	1863
Db	1861	GCAGAGCAGCGAGCTGAGACCAAACTGCAAAACATCCAGATCACAAGCCATCATCAGC	1920
QY	1864	ATCCCCACTTCCCCAGCGCTAACCCGACAGGGGGAAAGTGGGCCACCCCTTGCCAGGCCA	1923

Db 1921 ATCCCACTCCCCCGCGCTAACCCCGAGGGGGAAGTGGCCACCCCTGCCAGCCCA 1980
QY 1924 GCGCCCAACAGAACATCTCTTCATTAACAGCAATGTTCTCAAGGTCTCTGTGTA 1983
Db 1981 GCGCCCAACAGAACATCTCTTCATTAACAGCAATGTTCTCAAGGTCTCTGTGTA 2040
QY 1984 AAATCCCGCGCCATGCGCGCGGAGAGATGCGACGTGCGGCCCAATTGCGCCCTATAGT 2043
Db 2041 AAATCCCGCGCCATGCGCGCGGAGAGATGCGACGTGCGGCCCAATTGCGCCCTATAGT 2100
QY 2044 AGTCGATTAAGCCGAATTC 2064
Db 2101 AGTCGATTAAGCCGAATTC 2121

RESULT 3

US-10-212-677-253
; Sequence 253, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-253

Query Match 48.5%; Score 1000.8; DB 15; Length 2351;
Best Local Similarity 72.8%; Pred. No. 1.2e-267;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 66 AGTCACCATGCGCGCGAGTTGCGGCTGCTGCTTTCGCCGCGCTGCGCCATCG 125
Db 423 AGTAATCATGCGCGCGGCGGTGCGAGCGTGCCTTTGCAAGGCGAGCGCTATCG 482
QY 126 GTGATGCGCGGTGCGCACTGCGCCCATGCGCCCTGCGCCCGCGCGCGCG 182
Db 483 GTGATGCTGCTGCGCGCGCTATGCGCGCTGCGCGCGCGCGCGCGCGCGCG 542
QY 183 GCAGATGAGTGAATGCTCTCAACGTGAGTGGCGGAGGTTCCAGACCTGAGACCA 242
Db 543 CCAAGATGCTCTCATTTGTGTAATGTAAGTGGCAACCGCTTCCAGACGTGAGACCA 602
QY 243 GCTGAGCGCTACCGCGAGACCTGCTGCGGAGAGCAAGAGAGAGTCTTCAACGA 302
Db 603 CTTGGAACGTTAACCGAGACACTCTACTGCGGAGTTCTGAGAGGAACTTTTCTAACACCC 662
QY 303 GGAACCAAGAGTACTTCTTGAACCGGAGACCGCGAGGTGTTCCGCTGCTCACTT 362
Db 663 AGAAACTCAGCAGTATTTCTTGAACCGGAGACCGAGACATCTTCCGCAATCTGAATTT 722
QY 363 CTACCGCAGCGGGAAGTGAATACCGCGCTACAGAGTGAATCTCTGCTTACAGACGA 422
Db 723 CTACCGCAGCTGGGAAGTCACTATCTTCCGCGAGAGTGAATCTCTGCTTACAGTGAAG 782
QY 423 GCTGCGCTTCTACCGGATCTCTCCGAGATCATGCGGAGCTGCTGCTACAGAGATCAA 482
Db 783 ACTGCGCTTCTTGGCTCATCCGGAATCATGCGGAGCTGCTGTTATGAGAGTACAA 842
QY 483 GGAACGAGAGAGAGAGAGCGCGGCTCATGAGAGACAGACTCGAGAGAACAA 542

Db 843 GATCGAGCGGAGAGAACCGCGAGCGCTGCGAGAGACGCGGATACCGAACCCGCTG 902
QY 543 GGAG--TTCATGCGCTCGCTCAGCTTCCGCGAGACCATGTGCGCGCTTTCGAGAACCC 599
Db 903 GGAAGCGCGCTTCCGCGAGACCATGTGCTGAGAGAGAGGCTTTCGAGAACCC 962
QY 600 CCACACGAGACGCTGCGCGCTTCTTCACTGAGTGAAGTCTTCTTCAATGCTGCTC 659
Db 963 CCACACGAGACGATGCGCGCTGCTTCTTCACTGAGTGAAGGCTTTCGAGAACCC 1022
QY 660 GATCATCAACCAAGTGTGAGACGCGTCCGCGAGACGCGTCCGCG--CAGCAAGA 716
Db 1023 TGTATCGCAATGTGTGAGAAACAGTCCGCGAGATCAAGCCGATGATCAATTAAAGA 1082
QY 717 GCTGCGCGCGGAGCGCTACTCGGTGCGCTTCTTCTGCTGAGACAGGCTGCTCAT 776
Db 1083 ACTGCCGTGTGAGAGCGGTATGCTGTGCGCTTCTTCTGCTTGAACAGCGCTGCTCAT 1142
QY 777 GATCTTCAACGAGTGAATCTCTGCGCGCTCTTCCGCGCTCCAGCGCTTCAACGCTTCA 836
Db 1143 GATCTTCAACGAGTGAATCTCTGCGCGCTCTTCCGCGCTCCAGCGCTTCAACGCTTCA 1202
QY 837 CCGAGCGCTCATGAGCATATCGACGCTGTGCGCATATGCCCTTACTACATCGCTGCT 896
Db 1203 GCGTAGTGTATGATATATCGAGTGTGCGCATCTGCGCTTATTAATGCGCTGCT 1262
QY 897 CATGACCAACAGAGAGTGTGCGCGCTTCTGCTCAAGCTCCGCGCTTCCGCGCTT 956
Db 1263 GATGACCAACAGAGAGTGTGCGCGCTTCTGCTCAAGCTCCGCGCTTCCGCGCTT 1322
QY 957 CAGGATCTTCAAGTGTGCGCGCTTCTGCTCAAGCTCCGCGCTTCCGCGCTTCA 1016
Db 1323 CAGGATCTTCAAGTGTGCGCGCTTCTGCTCAAGCTCCGCGCTTCCGCGCTTCA 1382
QY 1017 GAGCTGTGCTCCGAGTGTGCTTCTCTCTCTCCCTCAACATGCGCATCATCTT 1076
Db 1383 GAGTGTGCTCCGAGTGTGCTTCTCTCTCTCTCCCTCAACATGCGCATCATCTT 1442
QY 1077 TGCCACTGTGATGTTTATGCGCGAGAGAGGCTCTCCGCGAGAGTTCACAGCATCTCC 1136
Db 1443 CGCTACAGTATGTTTATGCGCGAGAGAGGCTCTCTCCGCGAGAGTTCACAGCATCTCC 1502
QY 1137 TGCTCGTTTGTGTAACCATGTGACCATGACACATGCGGATACGAGACATGTGCTC 1196
Db 1503 TGCAAGCTTCTGTATACCATGTGACCATGACACATGCGGATACGAGACATGTGCTC 1562
QY 1197 TAAGACATGCGAGAGATCTTCCGCTCATCTGCTCTTGAAGTGGCGTCTGCTCAT 1256
Db 1563 AAAAACCATGACAGGAGAGATTTGCTTCTATCTGCTGAGTGGCGTCTGCTCAT 1622
QY 1257 TGCCCTGCGAGTCCCTGTGATGTTTCAACTTTAGCGGATTTACACAGATTCAGAG 1316
Db 1623 TGCTTACCTGTTCCGTTGATTTGATTCACATTCAGTGCATTCACACAGATTCAGAG 1682
QY 1317 AGCTGATTAACGAGGAGCAAAAAGAGGCGCGCTTGCAGAGATCCGTGCGCAAAAC 1376
Db 1683 AGCAGACAAAGAGGAGCAAAAAGAGGAGTGAAGTGCAGAGATCCGCGAGGCCAAAG 1742
QY 1377 AGCAGTTCGAATGATACCTGACACAGCAAGCGCAACGCGCTCTCAACGAGCGCTGGA 1436
Db 1743 CGGAAGCGCAAAAGTCTTACATGACAGGCAAAAGGATGTTTACTCAATTAACAGTGA 1802
QY 1437 GCTGACGCGGACCCGAGAGAGAGACATGCGGCAAGACCTCACTCATGAGAGCA 1496
Db 1803 GTCTCAGAGAG--TGAAGAGGCTTTTGTAGCAATTCGCGCTCAAGCTTGAACCA 1859
QY 1497 GCATCATCACTGCTGACCTGCGTGAAGAAACCACTAACCAAGGTTTATGATGAGCA 1556
Db 1860 GCAACCAACCTGCTTCACTGCGTGAAGAAACCAAGATCAAGAGTTGTGAGAGCA 1919
QY 1557 GATGTTGAGCAGAGCTGATGAGAGGTTCAATGACAGACTAACCATTCACAGAGTCC 1616
Db 1920 AGCTTTGAAGAAAGCTGATGAGAGTTGCAACTGTTAATGCTCTTCAAGTCAAGTCC 1979


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OY      1557 GATGTTTGAGCGAAGACTGCATGGAGAGTTCATGACGAAGTAACCCTCCACAAGAAGTCC   1616
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Db      1920 AGCTTTGAGAAAGCTGCATGGAAAGTTGCAACTGTGTTAATGCTCTTCAAGTCACAGTCC   1979
OY      1617 CTCATCTGCCAGCCACCGAGCCTCACTAACACCTGCTGCTCCCCTGCTAGTAAAGAAAGAC   1676
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1980 TTCACTGTCTTCACAAACGAAGAGTCACCGACCTGCTGTTCACGACGACAAAAAANAAC   2039
OY      1677 CACACACCTGCCCCAATTCTAACCTGCCAGCTACTGCGCTGCGCAGCATGCAAGACTCAG   1736
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2040 TTTTCGCATCCCAAATGCCAATGATATCAGGAAGCCATCAAGSTAGTATACAGAAGACTCAG   2099
OY      1737 CACGATCCACATCCAGGGCAGTAGACAGCCCTCCTCACAAACCAAGTCGCTCCAAGCCTTAA   1796
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2100 CACGATTCAGATCAGATGTGTGGAGAGAACACCTCTGTCTAACAGCCGATCCAAGTTTAAA   2159
OY      1797 TTTGAAAGCAGACGACGAGCTGAGACCAAACTGCAAAAACATCCAGATCACACAGCCAT   1856
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2160 TGCCAAATGGAAGAGTGTGTTAAACTTAAACTGTGAACAACTTATGTGACTTACAGCAAT   2219
OY      1857 CATCAGCATCCCACTCCCCCAGCGCTAAACCCAGAGGGGGAAAAGTCGGCCA   1908
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2220 AATAAGCATCCCAACACTCTCCAGTAAACCAACACGAGGAAGAGAGATAGGCCA   2271

RESULT 5
US-10-369-186-253
; Sequence 253, Application US/10369186
; Publication No. US20030232056a1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-253
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	Query Match	48.5%	Score 1000.8	DB 17	Length 2351
	Best Local Similarity	72.8%	Pred. No. 1.2e-267		
	Matches 1348	Conservative 0	Mismatches 492	Indels 12	Gaps 4
QY	66	AGTCACCATGGCGCCGAGTGTGGGCGCTGGCTGCTTTTGGCCCGGCTGCGGCCATGG	125		
DB	423	AGTAATCATGGCGCGCGGGGTGGCAGCGTGGCTGCTTTTGCAGAGGCGCAGCGGCTATGG	482		
QY	126	GTGATGCGCGGTGGCCAACTGCCCATGCCCCCTGGCCCC---GGCCGACAAACAAGCG	182		
DB	483	GTGATGCGCTGTGGCTTCGGGGCTTATGTGCGGCTCCCCCGAGGCAGAGAGGAAAGAGC	542		
QY	183	GCAGATGAGCTGATTGTCTCAACGTGAGTGGGGCGAGAGTTCCAGACTGTGAGGACAC	242		
DB	543	CCAAGATGCTCTCATTTGTGCTGAATGTGATGTGCACCCCGCTTCCAGACTGTGCAGACAC	602		
QY	243	GCTGAGCGCTACCCGAGACACCTGCTGGCGCAGCAGAGAGAGATTCTTCTTCAACGA	302		
DB	603	CCTGGAACGTTACCCAGACACTTACTGGGCACTTGTGAGAGGACATTTTCTTACACCC	662		
QY	303	GGACACCAAGAGTACTTTCGACCGGGACCCCCGAGGTGTTCCGCTGCGTCTCAACTT	362		
DB	663	AGAACTCAGCAGTATTTTGTGACCGTGAACCCAGACATCTTCCGCCACATCTGAATTT	722		
QY	363	CTACCGCAGCGGGAGCTGCACTAACCGCGCTACGAGTGACATCTGCTACGACGAGA	422		
DB	723	CTACCGCAGTGGAGATCCACATTAATCTCCGACAGGTGCATCTCTGTACATGAAGA	782		

QY	423	GCTGGCTTCTTAACGGCATCTCTCCCGAGATCATCTGGGGACTGCTGCTACGAGAGATCAAA	482
Db	783	ACTGGCTTCTTTGGCTCATCCCGAAATCATCGCGCACTGCTTTATGAGAGTACAA	842
QY	483	GGACCGCAAGGGAGAACGCCGAGCGGCTCATGAGACGCAACGACTCGGAGAACAA	542
Db	843	GGATCGCAGGCGAGAGAAACCGCAGCGCTTGACGAGACGACGGATTACCGCACCCGCTGG	902
QY	543	GGAG---TCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGCGGGCTTTCAGAAACC	599
Db	903	GGAGAGCGCTTTGCCCAACCATGACTGCAAGGACAGAGGCTGTGAGGGCTTTTCAGAAACC	962
QY	600	CCACACCAGCAGCCTGGGCTTGATCTTCTACTACGTGACTGGCTTCTTCATCGCTGCTC	659
Db	963	CCACACCAGCAGCAGTGGGCTTGATCTTCTACTACTGTCAAGGGGTTTTCATTTGCCGCTC	1022
QY	660	GGTCAATCAACCACTGGTGGAGACGGTCCGTGGCGACGGTCCCGG---CAGCAAGGA	716
Db	1023	TGTCAATCGCGAATGTGGTGAAGACAGTCCGTGGCGATCAAGCCAGGTGACATTAAAGA	1082
QY	717	GCTGCGGTGCGGGAGCGCTACTCGTGGCCTTCTCTGCTGGAACAGCGGCTGCTCAT	776
Db	1083	ACTGCCCTGTGAGAGCGGTATGCTGTGGCCTTCTCTGCTTGGACACGGCTGCTCAT	1142
QY	777	GATCTTCAACCGTGGAGTACCTCTGCGGCTCTTTCGCGGCTCCAGCGCTCAACCGCTTCAT	836
Db	1143	GATCTTCAAGTTGAGTATTGCTTCCGCTGGCTGACGGCCCTAGTCTTACCGTTTGT	1202
QY	837	CCGACGCTCATAGACATCATGACGCTGGTGGCCATCATGCCCTACTACATCGGCTGGT	896
Db	1203	GCGTAGTGTCAATGAGTATCATGACGCTGGTGGCATCTGCTTATTAATGAGGCTGGT	1262
QY	897	CATGACCAACAAGAGACGCTGTCCGCGCTTGTCAAGCTCCGAGCTTTCGCGCTT	956
Db	1263	GATGACAGACATAGAGACGTGACGGAGCCTTGTGACACTCCGAGCTTTCGCGCTT	1322
QY	957	CAGGATCTTCAAAGTTTTCGCGCACTCCAGGGCTTGGGATCTTGGGCTTACACACTGAA	1016
Db	1323	CAGGATCTTAAAGTTTTCGCGCACTCTCAAGGCTTGGCATCTTGGGGTACACACTGAA	1382
QY	1017	GAGCTTGGCTCCGAATGGGGCTTCTCTCTCCCTACCATGGCCATCATCTT	1076
Db	1383	GAGTTGGCTCCGAATGGGGCTTCTCTCTCTCCCTACCATGGCTCATCTT	1442
QY	1077	TGCCACTGTGATGTTTATGCGAGAGAGGGCTCTCGGCGCAGCAATTCACAAAGATCCC	1136
Db	1443	CGCTACAGTTATGTTCTTACGACAGAGAGGGGTCTTCGGCTTACAGATTCACAGCATCCC	1502
QY	1137	TGCCTGCTTTGGTATACCATGTGTACCATGACCACTGGGATACGAGACATGTGCC	1196
Db	1503	TGCAGCTTCTGGTATACCATGTGTACCATGACCACTAGGGTATGGTACATGTGCC	1562
QY	1197	TAAGACGATTGCAAGGGAAGATCTTCGGCTCATCTGCTCTTGAAGTGGCGCTCTGTCAT	1256
Db	1563	AAAAACCATAGCAGGGAAGATTTTGGTCTATCTGTTGCTGAATGGGGCTTGTGCAT	1622
QY	1257	TGCCCTGCCAGTCCCTGATGATGTTTCAACTTATAGCCGATTTACACAGAAATCAGAG	1316
Db	1623	TGCTCTAATCTGTTCCGGGATGTATCCAATTCAGTCGATCTTACACAGAAATCAACG	1682
QY	1317	AGCTGATAAACGAGGGGCAAAAAGAGGCCCGCTTGCCAGATCCGTGTGGCCAAAC	1376
Db	1683	AGCAGACAAACGAGGGGCAAAAAGAAAGCTAGACTGGCCAGATCCGGGCGACCCAAAG	1742
QY	1377	AGGCAGTTGCAATGATACCTGCAAGCAAGCGCAACGGGCTCTTCAACGAGGGCGCTGGA	1436
Db	1743	CGGAAGCGCAATGCTTATCATGCAAGCAACGGAATGTTTACTAGTAATCAGCTGCA	1802
QY	1437	GCTGACGGGCAACCCAGAAAGAGACATAGGCAAGACCACTCACTCATCGAGACCA	1496
Db	1803	GTCCTGAGAGGA--TGAGACAGGCTTTTGTAGCAAAATCCGGCTCAGCTTGAAGACCA	1859
QY	1497	GCATCATCACTGCTGCACTGCTGAAAAAACCACTAACGAGTTTATGTATGAGCA	1556

Db	1860	GCACCAACCACTGCTTCACTGCTGGAAAAAACCAAGAAATCAAGATTGTGGACGAACA	1919
Qy	1557	GATGTTTGAGCAGAACTGTCATGGAGATTCAATGCAAGAACTACCCATCCACAAGAGTCC	1616
Db	1920	AGTCTTTGAGAGAAAGCTGCATGGAAAGTTGCAACTGTTAATGTCCTTTCAGATCACAGTCC	1979
Qy	1617	CTCACTGTCCAGCCACCAGGCGCTCACTAACCCCTGCTGCCCTGGTAGTAAGAGAC	1676
Db	1980	TTCACGTCTTCAACAAGAGAGTCCACCAGCACTGCTGTTCAAGACGACACAAAAAAC	2039
Qy	1677	CACACACCTGCCCAATTCTAACCTGCCAGCTACTGCGCTGGCAGCATGCAAGCTCAG	1736
Db	2040	TTTTTCGATCCCAATGCCAAATGATATCAAGAAAGCATCAAGSTAGTATCAAGAACTCAG	2099
Qy	1737	CACGATCCACATCCAGGGCAGTGAGCAGCCCTCCCTCACAAACAGTGGCTCCAGCCTTAA	1796
Db	2100	CACGATTCAGATCAGATGTGTGGAGAAACACTGTCTTAAACAGCCGATCCAGTTTAAA	2159
Qy	1797	TTTGAAGCAGACGACCGGACTGAGACCAAACTGCAAAACATCCAGATCAACCAAGCCAT	1856
Db	2160	TGCCAAATGGAAGAGTGTGTTAACTTAACTGTGTAACAACCTTATGTGACTTACAGCAAT	2219
Qy	1857	CATCAGATCCCACTCCCGCAGCGCTAACCCACAGGGGGGAAAGTCGGCCA	1908
Db	2220	AATAAGATCCCAACCTTCACAGTAACCAACCAAGAGGAGACGATAGGCCA	2271

RESULT 6

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; Sequence 252, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-252

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Query Match	48.5%;	Score 1000.8;	DB 15;	Length 5333;
Best Local Similarity	72.8%;	Pred. No. 1.4e-267;		
Matches 1348;	Conservative	0;	Mismatches 492;	Indels 12;
				Gaps 4;

OY	66	AGTCACCATGCGGCCGGAGTTGCGGCCTTGCTTTTGGCCGGGCTGCGGCATCCG	125
Db	959	AGTAATATATGGCGCGGGGGGTGGCAGCGTGCGTGCCTTTTGGCAAGGGCAGCGGCTATCGG	1018
OY	126	GTTGATGCCGGTGGCCAACTGCCCCATGCCCCCTGGCCCC---GGCCGACAAGAACAACGG	182
Db	1019	GTGATGCCCTGTGGCCTCGGGGCTATGCGGCTCCCCCGAGGCAAGAGAGAAAAAGAC	1078
OY	183	GCAGATGAGCTGATTGTCTCTCAAAGTAGTGGGCGGAGGTTCCAGACTGGAGAACAC	242
Db	1079	CCAAGATGCTCTCATTTGTGCTGAATGTAGTGGCACCCGCTTCCAGACGTGGCAGACAC	1138
OY	243	GCTGAGCGCTAACC CGAGACACCTGTGCTGGGCGACGACGAGAGAAGATTCTTCTTCAACGA	302
Db	1139	CCTGAACGTTTACC CAGACACTCTACTGGGCA GTTCTGAGAGGGA CT TTTTCTTACCA CCCC	1198
OY	303	GGACACCAAGAGTACTTTTCCAGCCGGGACCCCGAGTGTCCCGCTGCGTCAACTT	362

Db	1199	AGAAACTCAGCAGTATTCTTTGACCCTGTAACCCAGACATCTTCCGCCACATCTGAATTT	1258
QY	363	CTACCGCAGCGGGAGCTGCACTACCCCGGCTACGAGTGCACTCTGCTTACGACGCA	422
Db	1259	CTACCGCAGCTGGGAAGCTTCACCTACTCTTGCCACGAGTGCACTCTGCTTACGATGAAGA	1318
QY	423	GCTGGCTTCTACGGCATCTCTCCCGAAGATCATCGGGGACTGCTGCTACGAGAGTACAA	482
Db	1319	ACTGGCTTCTTTGGCCCTCATCCCGAATCATCGCGACTGCTGTATGAGAGTACAA	1378
QY	483	GGACCGCAAGAGGAGAAAGCCGAGCGGCTCATGGACGACAAAGCATCTCGAGAACCA	542
Db	1379	GGATCGAGGCGAGAGAAAGCCGAGCGCTTGACAGACGACGCGAATACGACACCGCTGG	1438
QY	543	GGAG--TCCATGCTCTGCTCAGCTTCCGCAGACCAATGTGGCGGCTTTCGAGAACCC	599
Db	1439	GGAGAGCGCTTGGCCACCATGACTGCAAGGAGGAGGCTTGAGAGGCTTTCGAGAACCC	1498
QY	600	CCACACGAGCAGCGCTGGCCCTGGCTTCTACTAGCTGACGCTTCTTTCATGCTGTCTC	659
Db	1499	CCACACGAGCAGATGGCCCTGGGTTCTACTATGTCAAGGGGTTTTCATGCGGCTCTC	1558
QY	660	GGTCATCAACCAAGTGGGAGACGAGTGGCGGCGGACGAGTCCCGGG--CAGCAAGGA	716
Db	1559	TGTCATCGCAATGTGTGGAAACAGTGCCTGGCGGATCAAGCCAGGTCACTTAAGA	1618
QY	717	GCTGCGGTGCGGGAGCGCTACTCTGAGCTTCTTCTGCTGAGACAGCGCGTCTCAT	776
Db	1619	ACTGCCCTGTGAGAGCGGTAGTGTGGCTTCTTCTGCTTGACACGCGCTGCTCAT	1678
QY	777	GATCTTCAACCGTGGAGTACCTCTGCGGCTCTTGCGGGCTTCCAGCGCTTACCGCTTCA	836
Db	1679	GATCTTCAAGTGGAGTATTTGCTTCCGCTGCGAGCGGCTTACGCTTACCGCTTGT	1738
QY	837	CCGAGCGTCATGAGCATCATGACGCTGGTGGCATCATGCCCTACTACATCGGTCTGT	896
Db	1739	GCGTAGTGTATGAGTATCATGACGCTGGTGGCATCTGCTTATACATTTGGGCTGGT	1798
QY	897	CATGACCAACACGAGACGTGTCCGCGCTTGTACAGCTCCGAGCTTCCGCGCTT	956
Db	1799	GATGACACACATGAGACGTGACGAGAGCTTGTGTACACTCCGAGCTTCCGCGCTT	1858
QY	957	CAGATCTTCAAGTTTTCGCGCACTCCAGAGGCTTGGCATCTGAGGCTTACACTGAA	1016
Db	1859	CAGATCTTCAAGTTTTCGCGCACTCTCAAGGCTTGGCATCTGAGGCTTACACTGAA	1918
QY	1017	GAGCTGTCCTCCGAACGAGGCTTCTTCTTCTCCCTACCATGGCCATCATCTT	1076
Db	1919	GAGTGTGCTCAGAAATGGGCTTCTTCTTCTGCTACCATGGCTATCATCTT	1978
QY	1077	TGCCACTGTGATGTTTATGCGAGAAAGGCTCCTCGCGCAGCAATTACAAAGCATCC	1136
Db	1979	CGCTACAGTTATGTTCTACGACAGAAAGGCTTTCGCTTACCAAGTTACACGATCC	2038
QY	1137	TGCTGCTTTGGTACACCATGTCTACCATGACCACTGGGATACGAGACATGTGCC	1196
Db	2039	TGCAGCTTCTGGTATACCATGTCTACCATGACCACTTGGGATGTGTGATGTGCC	2098
QY	1197	TAAGACGATTGACGGAAGATCTTCGGCTCCATGTCTCCTTGAGTGGCGTCTGTCTAT	1256
Db	2099	AAAAACCATAGACGGAAGATTTTGTGTTCTATCTGTTGCTGAGTGGGCTTGTCTAT	2158
QY	1257	TGCCCTGCGAGTCCCTGTGATGTTTCCAATTTAGCCGGAATTTACACCAAGATCAAG	1316
Db	2159	TGCTTACCTGTTCGGGTGATTGTATCCAATTCAGTCGATCTACACCAAGATCAAG	2218
QY	1317	AGCTGATTAACGAGGACCAAAAAGAGGCCCTTGGCAGAGATCCGTGTGGCCAAAAC	1376
Db	2219	AGCAGCAAAAGAGGACCAAAAAGAAAGCTAAGTGGCAGAGATCCGGCAGCCAAAAG	2278
QY	1377	AGGAGTTTGAATGACATCTGACAGACGCAAGCGGCTCTCAACGAGGCGCTGGA	1436
Db	2279	CGGAAGCGAAATGCTTACATGACAGACAAAGCAATGTTTACTACGATACAGCTGCA	2338

QY	1437	GCTGACGGGGCACCCCCAGAGAAGGAGACATGGGCAAGCAACTCTCATTCGAGAGCCA	1496
Db	2339	GTCCTTAGAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAALACCA	2395
QY	1497	GCATCATCACCTGCTGCACTGCTCGGAAAAAACCACTAACACGAGTTATTATGATGACA	1556
Db	2396	GCACCAACCACTGCTTCACTGCTCGGAAAAAACCAAGAAATCAGAGTTGTGAGCAACA	2455
QY	1557	GATGTTTGAGCAGAAGCTGCATGAGAGATTCAATGCAGAACTAACCCATCCACAAGAGTCC	1616
Db	2456	AGCTTTTGAGAAAGCTGCATGGAAGTTGCACACTGTTAATCGCTTCAAGTCACAGTCC	2515
QY	1617	CTCAGTGTCCAGCCACCCAGGCTCTACTACCACTGCTGCTCCGTCGTAGTAAAGAAC	1676
Db	2516	TTCACTGTCTTTCACAACAAGAGATCACCAAGCACTGCTGTTCACGACGACACAAAAAAC	2575
QY	1677	CACACACCTGCCAATTGTAACTGCAGCTACTGCGCTGGCAGCATGCAAGAGCTCAG	1736
Db	2576	TTTTGCGATCCCAATGCGCAATGTATCAGGAAGCATCAAGTAGTATACAAAGACTCAG	2635
QY	1737	CACGATTCACATTCAGGGCAGTGCAGAGCCCTCCCTCACAAACAGTGCCTCCAGCCTTAA	1796
Db	2636	CACGATTCAGATTCAGATGTGTGAGAGAAACACTTCTGTCTTAAACAGCGATCCAGTTTAA	2695
QY	1797	TTTGAAGCAGACGACGCACTGAGACCAAACTGCAAAAACATCCAGATCAACACAGCCAT	1856
Db	2696	TGCCAAATGGAAGAGTGTGTTAACTAACTGTGAACAACCTTATGTGACTACAGCAT	2755
QY	1857	CATCAGCATCCCACTCCCCAGCGCTAAACCCACAGAGGGGGAAGTCCGCCA	1908
Db	2756	AATTAAGATCCCAACACTCTCCAGTAAACCAACAGAGAGAGACGATAGGCCA	2807

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RESULT 7
US-10-212-677-254
; Sequence 254, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FaSTSeq For windows Version 4.0
; SEQ ID NO 254
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-254

```

Query Match	48.5%	Score 1000.8	DB 15	Length 5333
Best Local Similarity	72.8%	Pred. No. 1.4e-267		
Matches 1348	Conservative	0	Mismatches 492	Indels 12
			Gaps	4
Qy	66	AGTCACCATGCGCGCCGAGTTGCGCGCTTGCTTTTGC	CGGCGTGC	CGCCATCGG 125
Db	959	AGTAATCATGCGCGCGGGGTGCGACGCTGCTGCTTTTGCAAGGCGACGGCTATTCG		1018
Qy	126	GTGATCGCGGTGGCCAACTGCCCATGCCCTTGCGCCC	-----GGCCGACA	GAACAACGG 182
Db	1019	GTGGATGCTGTGGCCCTCGGGGCTTATGCCGGCTCTCCCCGAGGCAAGGAGAAAAGAC		1078
Qy	183	GCAGATGACGTGATTGTCTCAACGTAGTGGGGCGGAGGTTCCAGACCTGAGACAC		242
Db	1079	CCAGATGCTCTCATTTGTCTGATGTGAGTGGCACCGGCTTCCAGACGTGGCAGAC		1138

QY	243	GCTGAGCGCTAACCCGGACA	CCCTGCTGGGAGACGAGAGAGAGTCTTCTTCAACGA	302	
Db	1139	CCTGGAACGTTAACCCGACA	CTTACTGGGAGTTTGAGAGGACTTTTCTACCAACC	1198	
QY	303	GGACACCAAGAGTACTTCTT	CGACCGGGACC	CGAGGTGTTCCGCTGCGNCTCACTT	362
Db	1199	AGAACTCAGCAGTATTTCTT	TGACC	GTGACCAGACATCTTCCGACACATCTGTAATTT	1258
QY	363	CTACCGCAGCGGGAAGCTG	CACTAACCCGCTACGAGTGCATCTTGCCTACGACGAGA	422	
Db	1259	CTACCGCAGCTGGGAAGCT	CACTATCTTCGCCACGAGTGCATCTTGTCTTACGATGAAGA	1318	
QY	423	GCTGGCTTCTAACGGCAT	TCTTCCCGAGATCATCGGGGACTGCTCTACGAGAGTACAA	482	
Db	1319	ACTGGCTTCTTTGGGCTCT	ATCCCGAAATCATCGGCGACTGCTGTATTATGAGAGTACAA	1378	
QY	483	GGACCGCAAGAGGGAGAAC	CGCGGCTCATGAGACGACACGACTCGGAGAACACCA	542	
Db	1379	GGATCGCAGCGAGAGAAC	CGCGAGCGCTGACGAGACGCGGATACCGACACCGCTGG	1438	
QY	543	GGAG--TCCATG	CCCTCGCTCAGCTTCCGCAGACCATGTGCGGGCTTTCGAAACCC	599	
Db	1439	GGAGAGCGCTTTGCCCA	CCATGACTGCAAGGAGGTTCTGAGGGCTTTTCGAAACCC	1498	
QY	600	CCACACACGACAGCTGG	CGCTGTCTTCTACTACGTGACTGCGTCTTTCATCGCTGTCTC	659	
Db	1499	CCACACGACGACGATGG	CGCTGTCTTCTACTACGTGACTGCGGTTTTCATTCGCGTCTC	1558	
QY	660	GGTATCATCAACGCTGG	NGAGACGCTGCGGACAGTCCCGG--CAGCAAGGA	716	
Db	1559	TGTCAATCGCGAATGTGG	TGAAACAGTGCCTGCGGATCAAGCCAGTTCATTAAAGA	1618	
QY	717	GCTGCCGTGCGGGAGCG	CTACTCGTGGCTTCTTCTGCTGACACGCGGTGCGTCA	776	
Db	1619	ACTGCCGTGTGAGAGCG	GTATGCTGTGCTTCTTCTTGAACACGGCTGCGTCA	1678	
QY	777	GATCTTCAACCGTGA	GTAACTCTTGGCGCTTTCGCGGCTTCCAGCGCTAACCGCTTCA	836	
Db	1679	GATCTTCAAGTGA	GTAACTTGTGCTTTCGCTGCGGCTTCCAGCGCTTACCGTCTTGT	1738	
QY	837	CCGACGGTCATGAGCAT	CATGACGCTGGTGCATCATGCCCTACTACATCGGTCTGGT	896	
Db	1739	GCGTAGTGTCAATGAG	TATCATCGACGTGGTGCATCTGCTTATTAATGGGCTGGT	1798	
QY	897	CATGACCAACACGAG	ACGTGTCCGGCGCTTGTCACGCTCCGGGTCTTCCGCTCTT	956	
Db	1799	GATGACACACATGAG	ACGTGACGGAGCTTGTTCACACTCCAGTCTTCCGGGTCTT	1858	
QY	957	CAGGATCTTCAAGTT	TTCGCGCACTCCAGAGGCTTGGCATCTCTGGGCTACACATGAA	1016	
Db	1859	CAGGATCTTAAAGTT	TTCGCGCACTTCAAGGCTTGGCATCTCTGGGCTACACATGAA	1918	
QY	1017	GAGCTGGCCCTCCGA	CTGGGCTTCTTCTTCTTCCCTACCAATGGCCATCATCTT	1076	
Db	1919	GAGTTGGCCCTCAGA	ATTGGGCTTCTTGTCTTCTTCTGCTACCAATGGCTATCATCTT	1978	
QY	1077	TGCCACTGTGATGT	TTTATGCGGAGAGGGCTCCTCGGCGACCAATTCACAAAGCATCCC	1136	
Db	1979	CGCTACAGTTATGT	TTCTACGAGAGAGGGCTTTCGGCTTAGCAATTCACCAAGCATCCC	2038	
QY	1137	TGCTCGTTTGTGTAC	ACCATTGTCAACATGACACACTGGGATACGAGACATGTGCC	1196	
Db	2039	TGCAGCTTCTGTGT	ATACCATGTCAACATGACCAACTAGGGGTATGTGTACATGTGTCC	2098	
QY	1197	TAAAGCATTTGACG	GGAAGATCTTCGCGCTCCACTGTCTCTTGAAGTGGCGTCTGTCTAT	1256	
Db	2099	AAAAACATAGCAG	GGAAGATTTTGTGTTCTATCTGTTCCGTGAGTGGGGTCTTGTCTAT	2158	
QY	1257	TGCCCTGCAGTCC	CTGTGATTGTTTCAACTTTAGCCGGAATTTACCAACGAATCAGAG	1316	
Db	2159	TGCTCTACTGTTC	CGGTGATTGTATCAACTTCAGTCCGATCTACCAACGAATCAG	2218	
QY	1317	AGCTGATMAACG	AGGGAACAAAGAGGCCGCTTGCAGAGATCCGTGTGGCCAAAC	1376	

Db 2219 AGCAGACAAACGAAAGGGCACAAGAAAGCTAAGACTGGCCAGAGATCCGGGACAGCCAAAAG 2278

Qy 1377 AGCGAGTTGCAATGCATACCTGCA CAGCAAGCGCAACGGGCTCTCAACGAGCGCTGGA 1436

Db 2279 CGGAAGCGCAAAATGCTTACATGCAGAGCAAA CGGAATGGTTTACTCAATATCAGCTGCA 2338

Qy 1437 GCTGACGGGGCAACCCAGAAAGAGACACATGGGCAAGACCACTTCACTCATTCGAGACCCA 1496

Db 2339 GTCTTCAGAGAA--TGAGCAGGCTTTTGTTAAGCAATCCGGCTCCAGCTTTTGAACCCA 2395

Qy 1497 GCATCATCACCTGCTGCACTGCCCTGGAAGAAACCACTAACCAAGATTATTTGATAGCA 1556

Db 2396 GCACACCACACTGCTTCACTGCTGGAAGAAACCAAGATTCAGAGTTGTGAGCAACA 2455

Qy 1557 GATGTTTGAGCAGAACTGCAAGAGAGTTCAATGCAGAACTAACCATTCACAAGAGTCC 1616

Db 2456 AGTCTTTGAAGAAAGCTGCATGGAAGTTGCACTGTTAATCGTCTTCAAGTCACAGTCC 2515

Qy 1617 CTCACTGTCCAGCCACCCAGGCTCACTACCACTGTGCTCTCCCGTCGATGTAAGAGAC 1676

Db 2516 TTCACTGTCTTCAACAAGAGAGTCAACGACCACTGTGTTCAACGACGACACAAAAAAC 2575

Qy 1677 CACACACCTGCCCAATTCTAACCTGCCAGCTACTGCGCTGCGAGCATGCAAGAGCTCAG 1736

Db 2576 TTTTCGATCCCAATGCAATGTATCAGAAAGCATCAAGGTATATACAAAGACTCAG 2635

Qy 1737 CAGCATCCACATCCAGGGCAGTAGAGCAGCGCTCCCTCACAAACGAGTCCGCTCAGCCTTAA 1796

Db 2636 CACGATTCAGATCAGATGTGTGAGAGAAACACTCTGTCTAACAGCCGATCCAGTTTAAA 2695

Qy 1797 TTGGAAGCAGACGACGAGCTGAGACCAAACTGCAAAACATCCAGATCAACCAAGCCAT 1856

Db 2696 TGCCAAATAGAAAGAGTGTGTTAACTAATACTGTGAACAACCTTATGTACTACGCAAT 2755

Qy 1857 CATCAGCATCCCACTCCCCACGCGCTAACCCAGAGGGGGAAGTCCGCCA 1908

Db 2756 AATAAGCATCCCAACACTCCAGTAAACCAACCCAGAGAGAGCATAGGCCA 2807

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RESULT 8
US-10-361-811-252
; Sequence 252, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-252

Query Match          48.5%; Score 1000.8; DB 17; Length 5333;
Best Local Similarity 72.8%; Pred. No. 1.4e-267;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY      66 AATCCCATGGCGGCGCGAGTTCGGCTTGCTTTTGCCCCGGGTGCGCCATCGG 125
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       959 AGTAATCAATGCGCGCGGGGTGACAGCTGTGCTTTTGCAAGGCGGCTATCGG 1018

QY      126 GTGATGCCGGTGGCCAATGCCCATGCCCTTGCCCC---GGCCGAACAAGAAGCG 182
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1019 GTGATGCTGTGGCTTCGGGGGCTATGCCGCTCCCGGAGGAGAAAGAAC 1078

QY      183 GCAGGATGACTGATTGTCTCAACGTAAGTGCGGCGAGGTTCCAGACTGAGACCAC 242

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Db	1079	CCAAAGATGCTCTCATTTGTGTGTAATGTGATGTGCACCCGGCTTCCAGAGCTGGCAGAGAC	1138
Qy	243	GCTGGAGCGCTAACCCCGGACACCCCTGCTGGGCGAGCAGGAGAGAGATTCTTCTTCAACGA	302
Db	1139	CTTGGAACGTTAACCCAGACACTTACTGGGCAAGTTCTGAGAGGACTTTTCTACCAACC	1198
Qy	303	GGACACCAAGAGATATTCTTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTCTCAACTT	362
Db	1199	AGAAACTCAGCAGATATTTCTTTGACCCGTGACCAGACATCTTCCGCCACATCTGTAATTT	1258
Qy	363	CTAACCGCAGCGGGAGAGCTGCATTAACCCGGCTACGAGTGCAATCTGCGCTACGACAGCA	422
Db	1259	CTAACCGCAGCGGGAGAGCTGCATTAACCCGGCTACGAGTGCAATCTGCGCTACGAGTAAGA	1318
Qy	423	GCTGGCCTTCTTACGGCACTCCCTCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAA	482
Db	1319	ACTGGCCTTCTTGGCCTCATCCGGAATCATCGGCACTGCTGTATGAGAGATACAA	1378
Qy	483	GGACCGCAAGAGGAGAAACGCGGAGCGGCTCATGACGACAAAGACTCGGAGAACAAACA	542
Db	1379	GGATCGCAGCGCAGAGAAACGCGGAGCGGCTCGAGAGACGACCGGATATCCGACACCGCTGG	1438
Qy	543	GGAG--TTCATGCCCCCTCGCTCAGCTTCCGCCAGACCATGTGCGGGCTTCGAGAACCC	599
Db	1439	GGAGAGCGCCTTGCCCAACCATGACTGCAAGGAGAGGGGTCTGAGAGGGCTTCGAGAACCC	1498
Qy	600	CCAACCAAGCAGCTGGCCCTGGTCTTCTACTACGTAAGTGGCTTCTTATCGCTGTCTC	659
Db	1499	CCACACCAAGCAGATGGCCCTGGTGTCTTACTATGTCAACGGGGTTTTCATGCGGCTC	1558
Qy	660	GGTCATCACCAACGCTGTGTGAGACGGGTGCGGCAACGGTCCCGG--CAGCAAGGA	716
Db	1559	TGTCTATCGGAATGTGTGTGAAACAGTGGCTGCGGATCAAGCCAGGTCAATTTAAAGA	1618
Qy	717	GCTGCCGTGGGGGAGAGCGCTACTCGGTGGCTTCTTCTGCTGAGACAGGGCTGGCTCAT	776
Db	1619	ACTGCCCTGTGGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACACGGCCCTGGCTCAT	1678
Qy	777	GATCTTACCGGTGAGTACCTCCTGCGGCTTTCGCGGCTCCAGCGGCTACCGCTTCAT	836
Db	1679	GATCTTACAGTTGATGATTTGCTTCGCTGCTGACGCGGCTTACCTAGTGGTTACCGTTTGT	1738
Qy	837	CCGACGCTCATGAGCATCATCGACGTGTGGCCATCATGGCCTACTACATCGGCTGTGT	896
Db	1739	GCGTAGTGTATGAGTATCATTCAGCGTGTGGCCATCTGCTTATTAACATTGGGCTGT	1798
Qy	897	CATGACCAACAACGAGAGCGTGTCCGGCGCTTGTCAACGCTCCGGGCTTCCGCGTCTT	956
Db	1799	GATGACAGACATGAGGAGCGTCAAGCGGACCTTGTCACTCCGAGCTTCCGGGCTT	1858
Qy	957	CAGGATCTTCAAGTTTCCCGCACCTCCAGGGGCTGCGGATCCTGGGCTACACTGAA	1016
Db	1859	CAGGATCTTAAAGTTTCCCGCACCTCAAGGCTGCGGATCCTGGGCTACACTGAA	1918
Qy	1017	GAGCTGTGCTCCGAACCTGGGCTTCTTCTTCTTCCCTACCATGGCCATCATCTT	1076
Db	1919	GAGTGTGCTCAGAAATTGGGCTTCTTCTTCTTCTGCTACCATGGCTATCATCTT	1978
Qy	1077	TGCCACTGTGATGTTTATATGCGGAGAAAGGGCTCTCGGCCAGCAAGTTCAACAGCATCC	1136
Db	1979	CGCTACAGTTATGTTCTACGACAGAGAGAGGGGTCTTGGGCTTAGCAAGTTCAACAGCATCC	2038
Qy	1137	TGCGCTGTTTTGTACACCATTTGTACATGACACACACTGGGATACGAGACATGTGCGC	1196
Db	2039	TGCAAGCTTCTGTATACCATCGTCAACATGACAACTATGGGTATGTGACATGTGCGC	2098
Qy	1197	TAAAGCAGTTGACGGAAGATCTTCCGCTCATCTGCTCTTGTAGTGGCGTCTGTGTCAT	1256
Db	2099	AAAAACATAGCAGGGAAGATTTTGTGTTCTATCTGTTGCTGAGTGGGGTCTTGTGTCAT	2158
Qy	1257	TGCGCTGCGAGTCCCTGTGATGTTTTCACACTTAAGCCGATTTACCAAGAAATCAGAG	1316

QY	1197	TAAGACGATTGCAGGGGAAGATCTTCGGCTCCATCTGCTCCTTTGAGTGGCGCTCTGGTCAT	1256
Db	2099	AAAAACCATAGCAGGAAGATTTTGGTTCTATCTGTTCGCTGAGTGGGCTTGGTCAT	2158
QY	1257	TGCCCTGCCAGTCCCTGTGATTTTCCAACTTTAGCCGGATTTTACCACCAGATCAGAG	1316
Db	2159	TGCTCTACCTGTTCGGGTGATTGTATCCAACTTAGTCGATCTACCACCAGATCAACG	2218
QY	1317	AGCTGATTAACGCAAGGCGACAAAGAAGGCCCGCTTGGCCAGATTCGTGTGGCCAAAC	1376
Db	2219	AGCAGACAAACGAAGGCGACAAAGAAGAACTAGACTGGCCAGGATCCGGGCGCCAAAG	2278
QY	1377	AGGCAGTTGGAATGCATPACTCTGCACAGCAAGCGCAACGGGCTCTCAACGACGGCGCTGGA	1436
Db	2279	CGGAACGCAAAATGCTTACATGCAGAGCAAAACGAATGTTTACTCAGTAATCAGCTGCA	2338
QY	1437	GCTGACGGGCAACCCCAAGAGAGACACATGGGCAAGAACCACTCACTCATCTGAGAGCCA	1496
Db	2339	GTCCTCAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAAACCA	2395
QY	1497	GCATCATCACCTGTGCACTGCTCGAATAAAAAACAATAACAGAGATTATATGATGAGCA	1556
Db	2396	GCACCAACCACTGTCTTCACTGCTCGAATAAAAAACAAGATCAAGATTTGTGACGAAACA	2455
QY	1557	GATGTTTGAGCAGAACTGCATGAGAGATTCAATGCAGAACTAACCAATCCACAGAAGTCC	1616
Db	2456	AGCTTTTGAAGAAAGCTGCATGGAAGTTGCACACTGTTAATGTCCTTCAAGTCACAGTCC	2515
QY	1617	CTCAGTGTCCAGCCACCAGGCGCTCACTAACCCGCTGCTCCCTGCTAGTAAAGAAC	1676
Db	2516	TTCACTGTCTTCAAAACAGAGATCACCAAGCACTGCTGTTTACGACGACACAAAAAAC	2575
QY	1677	CACACACCTGCCCAATTCTAACCTGCAGCTACTGCTGCGCAGCATGCAAGACTCAG	1736
Db	2576	TTTTGGATCCCAATGCCCAATGTATCAGGAAGCCATCAAGGTAGTATACAGAACTCAG	2635
QY	1737	CACGATCCACATCCAGGGCAGTGAAGCAGCCCTCCCTCACAACAAGTGTCTCCAGCCTTAA	1796
Db	2636	CACGATTCAGATCAGATGTGTGAGAGAAACACCTCTGTCTTAAAGCCGATCCAGTTTAA	2695
QY	1797	TTTGAAGCAGACGCACTGAGACCAAACTGCAAAACATCCAGATCAACCAAGCCAT	1856
Db	2696	TGCCAAATGAGAAGTGTGTTAACTTAACTGTGAACAACCTTATGTGACTTACAGCAAT	2755
QY	1857	CATCAGATCCCACTCCCCAGCGCTAAACCCAGAGGGGGAAGTTCGGCCA	1908
Db	2756	AATAAGCATCCCAACCTTCCAGTAAACACACACAGAGGAGAGACGATAGGCCCA	2807

```

RESULT 11
US-10-369-186-254
; Sequence 254, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-369-186-254

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Query Match	48.5%	Score 1000.8;	DB 17;	Length 5333;
Best Local Similarity	72.8%;	Pred. No. 1.4e-267;		
Matches 1348;	Conservative	0;	Mismatches 492;	Indels 12;
				Gaps 4;

QY	66	AGTCACCATGGGGCCCGAGTGTGGCGCTGGCTGCTTTTGCCGGGGCTGGCCATCGG	125
Db	959	AGTAATCATGCGCGGGGGGTGGAGCGTGGCTGCTTTTGCAAGGCGAGCGGCTATCGG	1018
QY	126	GTGATGCCGGTGGCCAACTGCCCATGCCCCCTGGCCCC--GGCCGACAAGAACGCG	182
Db	1019	GTGATGCCCTGTGGCCCTCGGGGCTTATGCGCGCTCCCCCGAGCGAGGAGAGAAAGGAC	1078
QY	183	GCAGATGAGCTGATTTGTCTCAACGTGATGGGCGGAGTTCCAGACTGGAGACCAC	242
Db	1079	CCAAGATGCTCTCATTTGTGCTGAATGTGATGGCACCCGCTTCCAGACGTGGCAGGACAC	1138
QY	243	GCTGAGCGCTACCCGGAACCCCTGCTGGCGAGCACGGAGAAAGATTCTTCTTCAAGCA	302
Db	1139	CCTGAACGTTACCCAGACACTTACTGGGAGTTCTGAGAGGACTTTTCTACACACC	1198
QY	303	GGACACCAAGAGTACTTCTTCGACCCGGGACCCCGAGTGTTCGCTGCGTGTCAACTT	362
Db	1199	AGAAACTCAGCAGTATTTCTTTGACCGTGACCAGACATCTTCCGCCACATCTGAAATTT	1258
QY	363	CTACCGCACTGGGGAAGCTGCATPACCCCGCTACGAGTGCATCTCTGCTTACGACGACA	422
Db	1259	CTACCGCACTGGGAAGCTCCACTATTCCTCGCACAGAGTGCATCTGTGCTTACGATGAGA	1318
QY	423	GCTGGCTTCTACGGCATCTTCCCGGAGATCATGGGGAGCTGCTGCTACGAGAGTACAA	482
Db	1319	ACTGGCTTCTTTGGCTCATCCCGAAATCATCGGAGACTGTGTTATGAGGAGTACAA	1378
QY	483	GGACCGCAAGAGGAGAACGCCCGAGCGGCTCATGACGACAAAGACTTCGAGAACAAACCA	542

QY	483	GGACCGGAAGGGAGAAAGCCGAGCGGCTCATGACGACAACGACTGGAGAACAAACCA	542
Db	1379	GGATCGCAGCGGAGAAACGCCGAGCGCTGCGACGACGACGGGATACCGAACCCGTGG	1438
QY	543	GGAG--TCCATGCCCTCGCTCAAGCTTCCGCGAGACCATGTGGCGGGCCTTCGAAACCC	599
Db	1439	GGAGAGCGCCTTGCACCACATGACTGCAGAGGCGAGAGGCTTGGAGGCGCTTCGAGAACCC	1498
QY	600	CCACACCAAGCAGCGCTGGCCCTGGTCTTCTACTACGTACCTGGCTTCTTATCGCTGTCTC	659
Db	1499	CCACACCAAGCAGCATGGCCCTGGTGTCTTCTACTATGTACACGGGTTTTTTCATTGGCGTCTC	1558
QY	660	GGTCATCAACCAAGTGTGGAGACGGTGGCGTGGCGGACAGTCCCGG--CAGCAAGA	716
Db	1559	TGTCAATCGCAATGTGTGTGGAACAAGTCGCGGATCAAGCCAGGTACATTAAGA	1618
QY	717	GCTGCCGTGCGGGAGCGCTACTCGGTGGCCCTTCTTCTGCTGGAACACGGCGTGCAT	776
Db	1619	ACTGCCCTGTGGAGAGCGGTATGCTGTGGCCCTTCTTCTTGTGGACACGGCCTGCGTCAT	1678
QY	777	GATCTTCAACCGTGAAGTACCTCCTGCGGCTCTTTCGCGGCTCCCAAGCCGTACCGCTTCAT	836
Db	1679	GATCTTCAAGTGAATTTGCTTCGCGCTGGCTGAGCGCCAGTCTGTTAACCGTTTTGT	1738
QY	837	CCGACGCGTCATGAGCATCATTCGACGCTGTGGCCATCATGACCCTACTACATCGGTCTGT	896
Db	1739	GCGTAGTGCATGAGTATCATTCGACGCTGTGGCCATCCTGCTTATTCATATGGGCTGT	1798
QY	897	CATGACCAACAACGAGACGTGTCCGGCGCCTTGTGTCACGCTCCGGTCTTCCGGCTTT	956
Db	1799	GATGACAGACAAATGAGAGAGCTCAGCGGAGCCTTTGTACACACTCCGAGTCTTCCGGGCTTT	1858
QY	957	CAGGATCTTCAAGTTTTCCCGCCACTTCCCAAGGCGCTGCGGATCTTGGGCTACACA CTGAA	1016
Db	1859	CAGGATCTTAAAGTTTTCCCGCCACTCTCAAGGCGCTGGGCACTCTGGGGTACACA CTGAA	1918
QY	1017	GAGCTGTGCGCTCCGAACCTGGGCTTCTTCTCTTCTCCCTACCATGGCCATCATCTTT	1076
Db	1919	GAGTGTGCGCTCAGAAATTGGGCTTCTTCTTCTCGCTACCATGGCTATCATCTTT	1978
QY	1077	TGCCACTGTGATGTTTTTATGCGGAGAGGGCTCTCGGCGACGAAGTTCAACAAGCATCCC	1136
Db	1979	CGCTACAGTTATGTTCTACGCGAGAGAGGGGCTTTCGGCTAGCAAGTTCAACAAGCATCCC	2038
QY	1137	TGCGCTGTTTTGTACACCAATGTGTACCATGACCAACTGGGATACGGAGACATGGTGGC	1196

Db	2039	TGACAGCTTCGGTATATACCATCGTCACACATGACAAACACTAGGGGTATGTGACATGTGGCC	2098
Qy	1197	TAAGACATTGACAGGGAAGATCTTCGGCTCCATCTGCTCTTGAATGGCGCTCGTGCAT	1256
Db	2099	AAAAACATAGCAGGGGAAGATTTTGTCTTATCTGTTCCGTGAGTGGGTCTTGTGCAT	2158
Qy	1257	TGCCCTGCCAGTCCCTGTGATTTGTTCCAACTTAAGCCGGAATTACACCAATCAGAG	1316
Db	2159	TGCTCTAACCTGTTCGGTGTATGTATCCAACTTCAATGTCGATCTACCAACCAATCAACG	2218
Qy	1317	AGCTGATTAACGACAGGCGACAAAAGAGGCCCGCTTGCCAGATCCGTGTGGCCAAAAC	1376
Db	2219	AGCAGCAAAACGAAAGGGGACAAAAGAAAGCTAGACTGGCCAGATCCGGGACGCAAAAG	2278
Qy	1377	AGGCAGTTGCAATGATCATCTGACAGACGCAACGGCGCTCTCAACGAGCGCTGGA	1436
Db	2279	CGGAAGCGCAATGCTTATCATGACAGACGAAATGTTTACTAGTAATCAGCTGCA	2338
Qy	1437	GCTGACGGGCAACCCAGAAAGAGACATGGGGACCACTGCACTCATGAGAGCCA	1496
Db	2339	GTCTCTAGAGGA--TGACAGGCTTTGTTAGCAAAATCGGCTCAGCTTTGAAACCA	2395
Qy	1497	GCATCATCACTGCTGCACTGCTCTGGAATAAAACCACTAACACGATTTATGATGACA	1556
Db	2396	GCACCAACCACTGCTTCACTGCTCGGAATAAAACCAAGATCAGAGTTTGGAGCGAACA	2455
Qy	1557	GATGTTGAGCAGAACTGCATGGAGAGTTCAATGACAACTAACCCATCCAAAGAGTCC	1616
Db	2456	AGTCTTGAAGAAAGCTGCATGGAAGTTGCAACTGTTAATCGTCTTCAAGTCAAGTCC	2515
Qy	1617	CTCACTGTCAGCCACCCAGCCTCACTAACCACTGCTGCTCCCGTGTAGTAAGAAGAC	1676
Db	2516	TTCACTGTCTTCAACAAGAGAGTCAACGACCTGCTGTTCAACAGACACAAAAGAAC	2575
Qy	1677	CACACACCTGCCAATTTCTAACCTGCGAGCTACTGCGCTGCGCAGCATGCAAGAGCTCAG	1736
Db	2576	TTTTGCGCATCCCAATGCGAATGTATCAGGAAGCATCAAGTAGTATACAGAATCAG	2635
Qy	1737	CACGATCCACATCCAGGGCAGTGAGAGAGCCCTCCCTCAACAACAGTGCCTCAGCTTAA	1796
Db	2636	CACGATTCAGATCAGATGTGTGAGAGAGAACACCTCTGTCTTAACAGCCGATCCAGTTAAA	2695
Db	2696	TGCCAAATGGAAGAGTGTGTTAACTTAACCTGTGAACAACCTTATGTGACTTACAGCAAT	2755
Qy	1857	CATCAGCATCCCCACTCCCCCAGCGCTAAACCCGAGAGGGGAAAGTCGGCCA	1908
Db	2756	AATAAGCATCCCAACACTCTCCAGTAACCAACACCGAAGAGAGCATGATAGGCCA	2807
RESULT 12			
US-10-121-746-9			
; Sequence 9, Application US/10121746			
; Publication No. US20030036648A1			
; GENERAL INFORMATION:			
; APPLICANT: Miller, Andrew P.			
; APPLICANT: Curran, Mark Edward			
; APPLICANT: Hu, Ping			
; APPLICANT: Ruteer, Marc			
; APPLICANT: Wang, Jian-Wang			
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels			
; FILE REFERENCE: SEQ-15P			
; CURRENT APPLICATION NUMBER: US/10/121,746			
; CURRENT FILING DATE: 2002-04-11			
; PRIOR APPLICATION NUMBER: US/09/336,643A			
; PRIOR FILING DATE: 1999-06-18			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687			
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448			
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826			

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-10-121-746-9

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Query Match	40.9%	Score 843.2;	DB 14;	Length 3424;
Best Local Similarity	68.2%;	Pred. No. 8.7e-224;		
Matches 1287;	Conservative 1;	Mismatches 559;	Indels 39;	Gaps 77;

[illegible]

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QY 890 GTCTGTCATGACCAACAACGAGAGCGTTCGGCGCTTGTCTACGCTCCGGGTCTTCC 949
Db 1089 GCGTTTGGTGGCCCAAGAACGACGATGTTCTTGGCGCTTGTCTACCTGTGTGTCTC 1148
QY 950 GCGTCTTACGAGATCTTCAAGTTTCCCGCAGCTCCAGGGCTCGGATCTGGGCTACA 1009
Db 1149 GGGTGTGGCATCTTCAAGTTCTCCAGGACCTACAGGGCTTGAGATTTGGGCTACA 1208
QY 1010 CACTGAAGAGCTGTGCTCCGAATGCGGCTTCTCTCTCTCCCTCAACCATGGCCATCA 1069
Db 1209 CACTCAAGAGCTGTGCTCCGAATGCGGCTTCTCTCTCTCCCTCAACCATGGCCATCA 1268
QY 1070 TCATCTTGGCAGCTGTGATGTTTATGCGGAGAGGGCTCTCGGCCAGCAAGTTACAA 1129
Db 1269 TCATCTTGGCAGCTGTGATGTTTATGCGGAGAGGGCTCTCGGCCAGCAAGTTACAA 1328
QY 1130 GCATCCCTGCGCTGTTTGTACACCATTTGTACCATGACACACTGGGATACGGAGACA 1189
Db 1329 GCATCCCTGCGGCTTCTGTGTATACCATTTGTACCATGACACAGCTTGGCTACGGAGACA 1388
QY 1190 TGGTGCTTAAGACGATTTGACGGGAAGATCTTGGCTCCATCTGCTCTGAGTGGCGTCC 1249
Db 1389 TGGTGCTCCAGCACCATTGCTGGCAAGATTTTGGGTCTCATCTGCTCACTCAGTGGCGTCT 1448
QY 1250 TGGTCATTTGCGCTGCGAGTCCCTGTGATGTTTCCACTTTAGCCGATTTACACCCAGA 1309
Db 1449 TGGTCATTTGCGCTGCGAGTCCCTGTGATGTTTCCACTTTAGCCGATTTACACCCAGA 1508
QY 1310 ATCAGAGAGCTGATTAACGACGAGGACAAAGAGGCGCCCTTGGCCAGATCCGTGTG 1369
Db 1509 ACCAGCGGCTGACAGAGCGCCGAGACAGACAGAGAGTGGCTTGGCAAGATCCGATTGG 1568
QY 1370 CCAAAACAGGAGTTGATGATGATACCTGACAGCAAGCGGCTCTTCAACGAGG 1429
Db 1569 CAAAGAGTGTACCAACCAATGCTCTTCCGACAGTACAAAGAGATGGGGGCTTGA----- 1623
QY 1430 CGCTGAGCTGACGGGACACCCAGAGAGAGGACATGGGCAAGACCACTCACTCATCG 1489
Db 1624 ----GGACAGCGGACAGTGGCGAGGAAACAGGCTCTTGTGTACGAAACCGTTGCGCTTGG 1679
QY 1490 AGAGCCAGCATCATCACTGCTGCACTGCTGTGAAAAAACCTAAACACAGATTATG 1549
Db 1680 AACAGCAACATCAACCACTTGTCTGCACTGCTGTAGAGAAACAGTGCATGAGTTCAAG 1739
QY 1550 ATGAGCAGATGTTT--GAGCAGAACTGCAATGAGAGTTCAATGACAGATACCATCCACA 1608
Db 1740 ATGAGCTCACTTCACTGAGAGCCCTGGAGCCGTCTCGCCGGGTGGCCGACACAGCCGTA 1799
QY 1609 AGAAGTCCCTCACTGTCCAGGCAACCCAGGCTCTCACTACCACTGCG-----TGTCCCTC 1663
Db 1800 GCACTCTGTGTCTTCCAGGCGAGTGGAGACCCCGAAGCTGTGTCTTCTTGTGCTTCC 1859
QY 1664 GTAGTAAGAAAGACACACACCTGCCAATTCTAACCTGCACTACTC--GCCTGGCGA 1720
Db 1860 GCAAGGCGCAAGCGCGCGCCCACTCCGCTTGGCACTCCACTGCTCAGTCAAGCCGTGGCA 1919
QY 1721 GCATGCAAGAGCTCAGACGATCCACATCCAGGCGAGTGAAGAGCCCTCCCTCAACCA 1780
Db 1920 GCATGCAAGAGCTCAGACGATCCACATCCAGGCGAGTGAAGAGCCCTCCCTCAG-----A 1973
QY 1781 GTGCTCCAGCTTAAATTGAAAGCAGACGAGAGCTGAGACCAAACTGCAAAACATCC 1840
Db 1974 GCGGCTCCAGCTCAATGCAAGCCCATGACAGCTTGAAGTGAAGTGGAGAGCGCGG 2033
QY 1841 AGATCACCACAGCCATCATCAGATCCCACTCCCGCAGGCTAACCCCAAGAGGGGAAA 1900
Db 2034 ACTTCGTGGCTGCAATATCAGCATCCCTAACCCCTCTGCAACACCCCAAGATGAGAGCC 2093
QY 1901 GTGCGCCACCCCTGCGAGCCAGGC 1926
Db 2094 AACCTTCTCTCCCTGCGCGGCTGGC 2119
```

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RESULT 13
US-10-296-115-373
; Sequence 373, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hysq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT FILING DATE: 2002-11-18
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-373
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Query Match 39.9%; Score 823; DB 17; Length 2578;
Best Local Similarity 67.7%; Pred. No. 3.3e-218;
Matches 1270; Conservative 0; Mismatches 575; Indels 32; Gaps 7;
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QY 73 ATGCGCGCGAGTTCGCGGCTGCTGCTTGTCCCGGCTGCGGCATCGGGTGAATG 132
Db 1 ATGCGCGGAGGCTTGGCCAGCTGCTGCTTGTCTCGGCGAGCAGCAGTGGGCTG 60
QY 133 CCGGTGCGCACTGCGCCCATGCGCCCTGCGCCCGCCGCAAGAACAGCGGAGATGAG 192
Db 61 CCCCTGGCCAGCAACCCCTGCGCCCGGCGACCGGGGTGAAGGCACTCGAGAGATGAG 120
QY 193 CTGATTGCTCTCAAGTGAAGTGGCGGAGTTCAGACCTGAGAGACCACTGAGCGC 252
Db 121 GTTCTGTGTGAACGTGACGAGCGCGCTTTGAGACTTGAAGATATCCCTGAGCCG 180
QY 253 TACCCGAGACCTGCTGCGGAGAGAGAGAGAGTCTTCTTCAACGAGACACCAAG 312
Db 181 TACCCAGACACTTGTGCGGAGAGTGGAGAGAGATTTCTTACGATGCTGACTGAGC 240
QY 313 GAGTACTTCTTGAACCGGAGACCCGAGTGTTCGCGTGGCTCAACTTCAACCGAG 372
Db 241 GAGTACTTCTTGAATCGCGACCCCTGACATGTTCCGCCATGTGCTCAACCGAAG 300
QY 373 GGAAGCTGCACTACCGCGCTACAGTGCATCTGCTTACGAGCAGAGCTGGCTTC 432
Db 301 GGGCGGCTGCACTTGGCCAGGAGAGAGTGCATCAGGCTTTCAGAGAGAGCTGGCTTC 360
QY 433 TACGCGATCTCCCGGAGATCATCGGGGAGCTGCTGTAAGAGATTAACAAGACCGAAG 492
Db 361 TACGCGCTGCTTCCGAGAGTACGTGAGTGTGCTGCTTGAAGAGATATCGGAGACCGAAG 420
QY 493 AGGAGAGACCGCGAGCGCTCATGAGCAGAACGACTCGAGAACCAACAGAGTCCATG 552
Db 421 AAGAGAGATGCGCGAGCGCTGAGAGAGATGAGAGAGCAGAGCGCGGAGCGGCCA 480
QY 553 CCTTGGC-----TCAGCTTCCGCGAGACCATGTGCGCGGCTTTCGAGAACCCCGAC 603
Db 481 GCGCTGCGAGAGGAGCTTCCCTGCGGAGCGGCTTGGCGGGGCTTTCGAGAGATCCACAC 540
QY 604 ACCAGCAGCTGCGCTGCTTCTTCACTAGTACTGAGCTTCTTCACTGCTGCTGCT 663
Db 541 AGGAGCAGCGAGCGCTTCTTCTTCACTATGTAACCGGCTTCTTCACTGCGGTGCTG 600
QY 664 ATCAGCAACGTGTGAGAGCGGTGCGGTGCGGAGCGGTCCGCGAG-----CAAGAG 717
Db 601 ATGCGCAATGTGTGAGAGACCATCCATGCGCGGCTTTCAGACGAGGTCTTCAAGGAG 660
QY 718 CTGCGGTGCGGAGCGCTTCTGCTGCTGCTTCTTCTGCTGAGACGCGGCTGCTG 777
Db 661 CAGCCCTGTGGGAGACGCTTCCACAGAGCGCTTCTTCTGCTGAGACAGCGCTGTGACTC 720
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QY 778 ATCTGACCGTGAGTACCTCTCGGGCTCTCGGGCTCCAGCCGCTACCGCTTATC 837
 Db 721 ATATTGACAGGTGTAATACTCTCTGCGGCTGTTGGCGCCCGCCAGCCGCTTGCGCTTCTG 780
 QY 838 CGCAGCGTATGAGCATCATCGACGTGTGGCCATCATGCCCTACTACATCGGTGTGTC 897
 Db 781 CGAGTGTATGAGCTCATCGACGTGTGGCCATCTGCCCTACTACATATGGGCTTTTG 840
 QY 898 ATGACCAACAACGAGAGAGCTGTCCGCGCTTCTGTCAGCGCTCCGGGTCTTCCGGCTTC 957
 Db 841 GTGCCAAGAAGACGATGTCTTGCGCCCTTGTCTACCCCTGCGGTGTTCGGGTGTT 900
 QY 958 AGGATCTTCAAGTTTCCCGCCACTCCAGGGCTGCGGATCCGGGCTTACACATGAAG 1017
 Db 901 CGCATCTTCAAGTTTCTCCAGGCATCAAGGGCTTGAGGATTTGGGCTACACATCAAG 960
 QY 1018 AGCTGTGCTCCGAAGCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1077
 Db 961 AGCTGTGCTCTGAGCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
 QY 1078 GCCACTGTGATGTTTATGCGGAGAGGGCTCTCGGCAAGCACTTCAACAAGATCCCT 1137
 Db 1021 GCCACTGTGATGTTTATGCGGAGAGGGCAACAACAAGACCACTTCAACAAGATCCCT 1080
 QY 1138 GCCTGTGTTGTATACACCATGTGTACCATGACACACTGTGGATACGAGACATGTGCT 1197
 Db 1081 GCGGCTTCTGTATACCATGTGTACCATGACACACTGTGGATACGAGACATGTGCT 1140
 QY 1198 AAGACGATTGACGGGAAGATCTTGGGCTCATCTGTCTCTGTAGTGGCGTCTGTGAT 1257
 Db 1141 AGCACCATTTGCTGGCAAGATTTTCCGGTCCATCTGTCTCACTAGTGGCGTCTGTGAT 1200
 QY 1258 GCCCTGCGAGTCCCTGTGATGTTTCCACTTTAGCCGATTTACCAACGAGATCAGAGA 1317
 Db 1201 GCCCTGCTGTGCGAGTATGTGTCTCACTTACCGCATCTACCAACGAGATCAGAGA 1260
 QY 1318 GCTGATAAACGAGGGGCAAAAAGAGCCGCTTGGCCAGATCCGTGTGCCAAACA 1377
 Db 1261 GCTGACAAAGCGCGAGACAGACAGAGGTGCGCTTGGCAAGATCCGATTTGGCAAGAGT 1320
 QY 1378 GGCAGTTGGAATGATACCTGTGACAGCAAGCGGCTCTTCAACGAGCGCTGGAG 1437
 Db 1321 GGTAACAACCAATGCTTCTGCAATGACAGAGATGGGGGCTTGA-----GGAC 1371
 QY 1438 CTGACGGGACACCCAGAGAGAGACATGCGGCAAGACCACTCACTCATCGAGGCGAG 1497
 Db 1372 AGCGGAGTGGGAGAGAACAGGCTGTTGTGTGAGAACCGTTTGCCTTGAACAGCAA 1431
 QY 1498 CATCATCACTGTGCTGACTGCTGTGAAAAAACCACTAACACGATTTATGTATGAGCAG 1557
 Db 1432 CATCACCACTTGTGCTGCTGTGTAGAGAGAACGTCATGAGTTTACAGATGAGCTC 1491
 QY 1558 ATGTTT-GAGCAGAACTGATGAGAGTTCAATGAGAACTACCATCCACAGAAAGTCC 1616
 Db 1492 ACCTTCAGTGAAGCCCTGGGAAGCGTCTGCGGGGTGGCCGACAGCGGTAGCACTCT 1551
 QY 1617 CTCACTGTCCAGGCAACCGGCTCTCACTACCACTGC-----TGCCTCCGTGTAGTAAG 1671
 Db 1552 GTGTCTTCCAGGCGAGTGGGAACCGGAAGCTGTGTCTTCTTGTGCGCCCTGCGAGGGCC 1611
 QY 1672 AAGACCAACACCTGCGCAATTCTAACCTGCGAGTACTGCGTGGCAGCATGCAAGAG 1731
 Db 1612 AAGCGCGCGCATCCGCTTGCACACTCACTGCTCAGTCAAGCGGTGGAAGCATGCA 1671
 QY 1732 CTACAGCAGATCCACATCAAGGGGAGTGAAGACCCCTCTCAACAACCAATGCTGCAGC 1791
 Db 1672 GGAGCTGGACATGCTGGAGGGCTTGGCAGAGACCATGCCCCCTTCAAGCGGCTCAGC 1731
 QY 1792 CTTAATTGAAAGCAG-ACGACGAGCTGAGACCAAACTGCAAAA-CATCCAGATACCA 1849
 Db 1732 CTTCAATGCCAAGCCCCCATGACAGCTTGAAGTGAATGCGAGACGGGGGACTTCTGTG 1791
 QY 1850 CAGCATCATCAGCATCCCACTCCCGCAGCGCTAACCCAGAGGGGGAAGTGGCGAC 1909

Db 1792 CTGCCATATACAGCATCCCTTACCCCTCTGCGCAACACCCAGATGAGAGCAACTTCT 1851
 QY 1910 CCGCTGGCAGCCAGGC 1926
 Db 1852 CCCCTGGCGCGGTGGC 1868

RESULT 14
 US-10-212-677-255
 ; Sequence 255, Application US/10212677
 ; Publication No. US20030129192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenault, Ruth A.
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Panger, Gary R.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.484C7
 ; CURRENT APPLICATION NUMBER: US/10/212,677
 ; CURRENT FILING DATE: 2002-08-02
 ; NUMBER OF SEQ ID NOS: 288
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 255
 ; LENGTH: 5404
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-212-677-255

Query Match 32.9%; Score 679; DB 15; Length 5404;
 Best Local Similarity 77.0%; Pred. No. 4.6e-178;
 Matches 868; Conservative 0; Mismatches 250; Indels 9; Gaps 3;

QY 66 AGTCAACATGCGGCGCGGAGTGTGGGCTGTGCTTGTGCGGCGCTGGCCATCGG 125
 Db 1362 AGTATCATGCGGCGGCGGAGTGTGGGCTGTGCTTGTGCGGCGCTGGCCATCGG 1421
 QY 126 GTGATGCGGCGGCGGAGTGTGGGCTGTGCTTGTGCGGCGCTGGCCATCGG 182
 Db 1422 GTGATGCGGCGGCGGAGTGTGGGCTGTGCTTGTGCGGCGCTGGCCATCGG 1481
 QY 183 GCAGATGAGCTGATTTGTCTTCAAGTGTGGGCGGAGTGTCCAGACCTGAGAGCCAC 242
 Db 1482 CCAAGATGCTCTCATTTGTGTGAGTGTGAGTGTGACCGCGCTTCCAGACGTGGCAGACAC 1541
 QY 243 GCTGAGCGCTACCCGAGACCTGTGCTGGGAGACGAGAGAGAGTCTTCTTCAACGA 302
 Db 1542 CCTGGAAGCTTACCCAGACACTTACTGGGAGTGTGAGAGGAGCTTTTCTACACCC 1601
 QY 303 GGACACCAAGAGTACTTCTTGAACCGGAGCCCGGAGGTGTTCCGCTGCTCAACTT 362
 Db 1602 AGAACTCAGCAGTATTTCTTGAACCGTGAACCGACATCTTCCGACATCTGAATTT 1661
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; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; NUMBER OF SEQUENCE: 2003-02-05
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Job time : 2141.06 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 08:07:28 ; Search time 6052.92 Seconds
(without alignments)
12979.627 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hic:*
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7: gb_est6:*
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9: gb_gss2:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1828.4	88.6	1911	9	AY419308 Pan trogl
3	1643.8	79.6	1911	9	AY419309 Mus muscu
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11	676.8	32.8	1939	9	AY408064 Pan trogl
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15	529.6	25.7	628	8	BZ20318
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17	465.2	22.5	647	9	CE500599
18	447	21.7	695	1	AL120075
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20	428.8	20.8	567	4	BI033106
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ALIGNMENTS

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ACCESSION AY419307
VERSION AY419307.1 GI:39775264
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
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DEFINITION      genomic survey sequence.
ACCESSION      AY419308
VERSION      AY419308.1 GI:39775265
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
REFERENCE      1 (bases 1 to 1911)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
      Adams,M.D. and Cargill,M.
      Inferring nonneutral evolution from human-chimp-mouse orthologous
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JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1911)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrieres,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
JOURNAL Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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DB 781 ATCATGACGTGTGGCCATCATGCCCCCTNNACATCGGTCTGTGCATGACCAACAGAG 840
QY 913 GACGTGCGGCGCTTCTGCTACAGCTCCGGGCTTCCGCTTTCAGAGATCTTCAAGTTT 972
DB 841 GACGTGCGGCGCTTCTGCTACAGCTCCGGGCTTCCGCTTTCAGAGATCTTCAAGTTT 900
QY 973 TCCCGCACTCCCAAGGCGCTGCGGATCTGCGGCTACACACTGAAGAGCTGCTCCGAA 1032
DB 901 TCCCGCACTCCCAAGGCGCTGCGGATCTGCGGCTACACACTGAAGAGCTGCTCCGAA 960
QY 1033 CTGGGCTTCTTCTTCTTCTCCCTCAACATGGCCATCATCTTTGCCACTGTATGTTT 1092
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QY 1093 TATGCCGAGAGGCGCTCTCGGCGCAAGTTCAAGACATCCCTGCTGTTTGATAC 1152
DB 1021 TATGCCGAGAGGCGCTCTCGGCGCAAGTTCAAGACATCCCTGCTGTTTGATAC 1080
QY 1153 ACCATTGTCAACATGACCACTGGGATACGAGACATGTGCTTAAGACGATTGACAGG 1212
DB 1081 ACCATTGTCAACATGACCACTGGGATACGAGACATGTGCTTAAGACGATTGACAGG 1140
QY 1213 AAGATCTTGGGCTCCATGCTGCTCTGAGTGGCGCTGCTGCTGATGCTGCTGCTGCT 1272
DB 1141 NNNNNCTTGGGCTCCATGCTGCTCTGAGTGGCGGNNNNNNNNNNNNNNNNNNNNNNNN 1200
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QY 1333 GCACAAAGAGAGGCGGCTTCCAGGATCCGTGTGGCCAAAACAGGAGTTGCAATGCA 1392
DB 1261 GCACAAAGAGAGGCGGCTTCCAGGATCCGTGTGGCCAAAACAGGAGTTGCAATGCA 1320
QY 1393 TACCTGACAGCAAGCGGCTCTCAACGAGCGCTGAGAGCTGACGGGCAACCCA 1452
DB 1321 TACCTGACAGCAAGCGGCTCTCAACGAGCGCTGAGAGCTGACGGGCAACCCA 1380
QY 1453 GAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCCAGCATATCACTGCTG 1512
DB 1381 GAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCCAGCATATCACTGCTG 1440
QY 1513 CACTGCTGAAAAAACCACTAACCAAGATTATGATGAGAGAGATTTGAGCAGAAC 1572
DB 1441 CACTGCTGAAAAAACCACTAACCAAGATTATGATGAGAGAGATTTGAGCAGAAC 1500
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DB 1561 CCAGGCTCACTAACCACTGCTGCTCCCGTGTAGTAAGAAGACCAACACCTGCCAAT 1620
QY 1693 TCTAACCTGCAAGTACTGCTGCTGCGAGCATGCAAGAGCTGACGACGATCCACATCCAG 1752
DB 1621 TCTAACCTGCAAGTACTGCTGCTGCGAGCATGCAAGAGCTGACGACGATCCACATCCAG 1680
QY 1753 GGCAGTGAAGAGCCCTCCCTCAACCAAGTGTGCTCCAGCCCTTAATTGAAAGACAGAC 1812
DB 1681 GGCAGTGAAGAGCCCTCCCTCAACCAAGTGTGCTCCAGCCCTTAATTGAAAGACAGAC 1740
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QY 1873 CCCCAGCGCTAACCCAGAGGGGAAAAGTCGGCCACCCCTGCCAGCCAGCCCAAC 1932
DB 1801 CCCCAGCGCTAACCCAGAGGGGAAAAGTCGGCCACCCCTGCCAGCCAGCCCAAC 1860
QY 1933 AGCAACATTCCTTCCATTAACCAAGCAATGTTGTCAGAGTCTCTGTGTTAA 1983
DB 1861 ACGAACATTCCTTCCATTAACCAAGCAATGTTGTCAGAGTCTCTGTGTTAA 1911

RESULT 3
AY419309
LOCUS 1911 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus KCND3 gene, VIRUTAL TRANSCRIPT, partial sequence,
AY419309
ACCESSION AY419309
VERSION AY419309.1 GI:39775266
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1911)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..1911
location/Qualifiers
gene /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1911
/gene="KCND3"
/locus_tag="HCM6847"

ORIGIN
Query Match 79.6%; Score 1643.8; DB 9; Length 1911;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 1744; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 73 ATGCGCGCGGAGTGGCGGCTGCTTTGGCCCGGGCTGCGGCATCGGGTGATG 132
DB 1 ATGCGCGGAGAGTGGCGGCTGCTTTGGCCCGGGCTGCGGCATCGGGTGATG 60
QY 133 CCGGTGGCAACTGAGCCCATGCGCCCTGGCCCGGCGGACAGAAACAAGCGGAGATG 192
DB 61 CCAAGTGGCAACTGAGCCCATGCGCCCTAGCTCCAGCGGACAAACAAGCGGAGAGCG 120
QY 193 CTGATTTGCTCAACGAGTGGGCGGAGTTCCAGACCTGAGAGACCGCTGGAGCGC 252
DB 121 CTGATTCGCTCAACGAGTGGGCGGAGTTCCAGACCTGAGAGACCGCTGGAGCGC 180
QY 253 TACCCGAGACCCCTGCTGGGAGCAGCAGAGAGAGTTCTTCAACGAGAGACCAAG 312
DB 181 TATCCGAGACCCCTGCTGGGAGCAGCAGAGAGAGTTCTTCAACGAGAGACCAAG 240
QY 313 GAGTACTTCTTGAACCGGAGACCCGAGGTGTTCCGCTGCGTCACTTCAACGAGAG 372
DB 241 GAGTACTTCTTGAACCGGAGACCCGAGGTGTTCCGCTGCGTCACTTCAACGAGAG 300

QY 373 GGAAGCTGCACTAACCCGGCTACAGGTGATCTTGCTTACGACGAGAGCTGGCCTTC 432
DB 301 GGAAGCTGCACTAACCCGGCTATGATGATGATCTTGCTTACGACGATGAACTGGCCTTC 360
QY 433 TACGGATCTTCCCGAGATCATCGGGAGTGTGCTGTAAGAGAGTACAAAGACCGCAAG 492
DB 361 TATGGATCTTCCCGAGATCATCGGAGACTGTCTTACGAGAGTACAAAGACCGCAAG 420
QY 493 AGGAGAACCGGAGCGGCTCATGAGACGACAAAGACTGGAGAACCAAGAGAGTCCATG 552
DB 421 CGGAGAGATGCGAGCGGCTCATGATGACATGACTCTGAAAACAACGAGAGTCCATG 480
QY 553 CCTGCTCAGCTTCCGCGAGACCAATGTGGCGGCTTCCGAGAACCCCAACAGCAGACG 612
DB 481 CCTCTCTCAGCTTCCGCGAGACCAATGTGGCGGCTTCCGAGAACCCCAACAGCAGAC 540
QY 613 CTGGCCCTGCTTCTTACTACTAGCTGAGCTGCTTCTTCAATGCTGCTGCTATCACCAC 672
DB 541 CTGGCACTGCTTCTTACTAGTGTGACTGCTTCTTCAATGCTGCTGCTGCTATCACCAC 600
QY 673 GTGTGAGACCGGTGCGGCGGACAGGTCCGCGGACAGCAAGAGAGCTGCGGCGGAG 732
DB 601 GTGTGAGACCGGTGCGGCGGACAGGTCCGCGGACAGCAAGAGAGCTGCGGCGGAG 660
QY 733 CGCTACTGCTGCTTCTTCTTCTGCTGCTGACACGCGGTGCTATGATCTTCAACGAGAG 792
DB 661 CGCTATTCGCTGCTTCTTCTTCTGCTGCTGACACTGCTGCTGCTGCTGCTGCTGCTG 720
QY 793 TACCTCTGCGGCTTCTGCGGCTCCAGCGCTACCGCTTATCCGAGAGGTATGAGC 852
DB 721 TACCTCTGCGGCTTCTGCGGCTCCAGCGCTACCGCTTATCCGAGAGGTATGAGC 780
QY 853 ATCATGCAAGTGTGCGCATCATGCTTACTATCATGCTGCTGCTGCTGCTGCTGCTGCT 912
DB 781 ATTATGCAAGTGTGCGCATCATGCTTACTATCATGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 913 GACGTGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
DB 841 GACGTGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 973 TCCCGCACTCCAGAGGCTGCGGATCTGCGGCTACACACTGAAGAGCTGCTCCGAA 1032
DB 901 TCCCGCACTCCAGAGGCTGCGGATCTGCGGCTACACACTGAAGAGCTGCTCCGAA 960
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DB 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
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QY 1153 ACCATTGTCACCATGACCACTGAGATACGAGACATGCTGCTTAAGACATGTCAGGG 1212
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QY 1393 TACCTGACAGAGAGGCAAGGCTTCTTCAAGAGAGGCGCTGAGCTGAGCGGACCCCA 1452
DB 1321 TACCTGACAGAGAGGCAAGGCTTCTTCAAGAGAGGCGCTGAGCGGACCCCA 1380

OY		1453	GAAAGGAGCACAATGGGGAGAAGACCCTCACTCATGTAGAGCGCAGCATTCATCACTGCTG	15112
Db		1381	GAAAGGAGCAGATGGGCAAGACCACTCTACTCATGTAGAGCCAGCATTCATCACTGCTGA	1440
OY		1513	CACCTGCCTGAAAAAACCACTAACCAGAGTTTATTGATGAGCAGATGTTTTGAGCAGAAC	15722
Db		1441	CACCTGCTTAAGAAAAGACCACTAACCATGAGTTTATTGATGAGCAGATGTTTGAGCAGAAC	15000
OY		1573	TGCATGAGAGAGTTCAATGAGAACTAACCCATCCACAAGAGTCCCCTCACTGTCCAGCCAC	16322
Db		1501	TGCATGAGAGAGCTCGATGAGAACTAACCCCTCCACAGAAAGTCTTCTGTGCCAGCCAC	15600
OY		1633	CCAGGCTCACTAACCACTGCTGTCTCCCGTGTAGTAAGAAAGCACACACCTGCCCAAT	16922
Db		1561	TCGGGCTTACCACCACTGCTGTCTCCCGTGTAGCAAGAAAGACCAACACACTGCCCAAC	16200
OY		1693	TCTAACCTGCCAGCTACTTCTGCTCTGGCGCAGATGCAAGAGCTTCAGCAGATCCATCCAG	17522
Db		1621	TCTAACCTGCCCTGCCACCCCGCTGGCGCAGATGCAAGAGCTTCAGCAGCTCCACATCCAG	16800
OY		1753	GGCAGTAGAGAGCCCTCCCTCACAACCAAGTCGCTCAGCCCTTAATTTGAAGCAGACGAC	18122
Db		1681	GGCAGGAGAGAGCCCTCCCTCACCACCAAGTCGCTCAGCCCTTAATTTGAAGCAGACGAT	17400
OY		1813	GGACTGAGACCAAACCTGCAAAAACATCCAGATTACCA CGGCATCATCAGCATCCCCACC	18722
Db		1741	GGACTGAGACCAAACCTGCAAAAACATCCAGATTACCA CGGCATCATCAGCATCCCCACC	18000
OY		1873	CCCCCAGCGCTAACCCCGAGAGGGGAAAGTCGGCCACCCCTCTGCCAGCCAGCCCCCAAC	19322
Db		1801	CCCCCAGCTCTGACCCCGAGAGGAAAGTCGGCCACCCCTCTGCCAGCCAGCCCCCAAC	18600
OY		1933	ACGAACATTCCTCCATAACCCAGCAATGTTGTCAAGGTCTCTGTCTGTAA	1983
Db		1861	ACGAACATTCCTCCATAACCCAGCAATGTTGTCAAGGTCTCTGTCTGTAA	1911
RESULT 4				
AKO33962				
LOCUS		3730 bp	mRNA	linear
DEFINITION		Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330129C02 product:potassium voltage-gated channel, Shal-related family, member 3, full insert sequence.		
ACCESSION		AKO33962		
VERSION		AKO33962.1	GI:26329580	
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE		1	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253	
JOURNAL MEDLINE PUBMED		10349636		
REFERENCE AUTHORS		2	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
TITLE		JOURNAL MEDLINE PUBMED		
JOURNAL MEDLINE PUBMED		20499374		
REFERENCE		11042159		
AUTHORS		3	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komno,H., Akiyama,J., Nishi,K., Kitsunai,T., Taehiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Otoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format	
TITLE				

JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	5 Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	6 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
		Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroaka,T., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akchira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
			cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. Location/Qualifiers
			FEATURES source
			1..3730 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:9330129C02" /db_xref="taxon:I0090" /clone="9330129C02" /sex="male" /tissue_type="diencephalon" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 224..1819 /note="unnamed protein product; potassium voltage-gated channel, Shal-related family, member 3 (MGP MG1:1928743, GB NM_019931, evidence: BLASTN, 100%, match=1462) putative"
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ORIGIN

II PRESSVPFQSKTIVSLPLG"

Query Match	62.3%;	Score 1285.6;	DB 3;	Length 3730;
Best Local Similarity	90.2%;	Pred. No. 2e-287;		
Matches 1375; Conservative	0;	Mismatches 149;	Indels 0;	Gaps 0;

OY	10	AACTAATCCAAAGCTGGTGTGCTTAAGCCTCCGCGGGCTGGCGGCCCAAGACTGAGTCC	69
Db	161	AAACCACTCCAAAGCTGGTGTGTATCAAGTGTCAAGAGCACTACACAGCCCAAAAGCTGAGTCC	220
OY	70	ACCAATGGCGCGCGGAGTTGGCGGCTGGCTGCTTTTGGCCCGGGCTGGGCCATCGGCTGG	129
Db	221	ACCAATGGCGCGGAGAGTTGGCAAGCTGGGCTGGCTTTTGGCCCGGGCTGGGCCATTGGATGG	280
OY	130	ATGCGCGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCCCAAGAACAGCGCGCAGAT	189
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OY	190	GAGCTGATTTGCTCTCAACGTGAGTGGCGGAGGTTTCCAGACTTGAAGACCACTGTGAG	249
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OY	250	CGCTACCCGGAGACACCTGCTGGGAGACACGAGAAAGAGTTCTTCTTCAACGAGACACC	309
Db	401	CGCTATCCCGAACACTTGTCTGGTGAAGACAGAGAGAGGTTCTTCAATGAGACACG	460
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OY	430	TTCTACGCGACTCTCCCGGAGATCATCGGGGACTGCTGCTTACGAGAGTACAAAGACCGC	489
Db	581	TTCTATGGCATCTCTCCCGAGATCATCGGAGACTGCTGCTTACGAGAGTACAAAGACCGC	640
OY	490	AAAGAGGAGAACCCCGAGCGGCTATGAGACGAACAGACTGGAGAACAAACGAGATCC	549
Db	641	AAAGCGGAGAAATCGAGCGGCTATGATGACAAATGACTCTGAAAACAAACGAGATCC	700
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Db	701	ATGCCCTCTCTCAGCTTCCGTCAGACCAATGTGGCGGGCTTCCGAGAACCCCAACACGACG	760
OY	610	ACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCAATGCTGTCTCGTCAATCAC	669
Db	761	ACCTTGCACTGGTCTTCTACTAATGTGACTGGCTTCTTCAATGCTGTCTCGTCAATCAC	820
OY	670	AACGTGGTGAAGACGCTGCGGCGGACCGTCCCGGGCAGCAAGAGCTGCCGTGCGGG	729
Db	821	AATGTGGTGAAGACGCTGCGGCGGACCGTCCCGGGCAGCAAGAGCTGCCGTGCGGG	880
OY	730	GAGCGCTACTCGGTGGCCTTCTTGTGCTGGAGACACGCGTGCATGATCTTCAACCGTG	789
Db	881	GAGCGCTAATCGGTGGCTTCTTGTGCTGGAGACACTGCTGTGTAATGATCTTCAACAGTG	940
OY	790	GAGTACTCTTCGCGGCTCTTTCGCGGCTCCCAAGCCGTAACCGTCTCATCCGACGCTATG	849
Db	941	GAGTACTCTTCGCGACTCTTTCGCGGCAACCAAGATACCGCTTCAATCCGACGCTATG	1000
OY	850	AGCATCATCGACGTGTGGCCATCATGCCCCCTACTACATCGCTGTGTCATGACCAACAC	909
Db	1001	AGCATTATCGACGTGTGTGGCCATCATGCCCCCTATTACATTTGGCTGTGTCATGACCAACAT	1060
OY	910	GAGGAGCTGTCCGGCGCCTTCTGTACAGCTCCGGGTCTTCCGCGTCTTCAAGATCTTCAAG	969
Db	1061	GAGGAGCTGTCTGGGGGCAATTTGTACACTCCGGGTCTTCCGCTCTTCAAGATCTTCAAG	1120
OY	970	TTTTCCGCCCACTCCACAGGCGCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCTCC	1029

Db	1121	TTCTCCGACATTCCAGAGGTCATCGGATCTG6GGCTACACCCGAAGAGCTGTGCTCA	1180
QY	1030	GAACTGGGCTTTCTCTCTCTCCCTCACCATGGCCATCATCTTTGGCAGCTGGATG	1089
Db	1181	GAACTGGGCTTTCTCTCTCTCTCCCTTAACATG6CCATCATCTTTGGCAGCTGGATG	1240
QY	1090	TTTTATGCCGAGAGGGGCTCCTCGGCCAGCAAGTTCAACAAGCATCCCTGCTCGTTTGG	1149
Db	1241	TTTTATGCTGAGAGGGGCTCCTCTGCCAGCAAGTTCAACAAGCATCCCTGATCTTTCTGG	1300
QY	1150	TACACCATGTGHCACCATGACCACTGAGGATACGGAGACATGTTGCTTAAGACATTTGCA	1209
Db	1301	TACACCATGATGACCATGACCACTGAGGATATGAGACATGTTGCTTAAGACATTTGCA	1360
QY	1210	GGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCTGTGTCATTTGCCCTGCCAGTC	1269
Db	1361	GGAAGATATTTGGCTCCATCTGCTCCTCAGGGGTGTCCTGTGTCATTTGCCCTGCCAGTC	1420
QY	1270	CCTGTGATTTGTTCCAACTTTAAGCCGGAATTTACCAACGAAATCAGAGAGCTGATTAACGC	1329
Db	1421	CCTGTGATGATGCTCCAACTTTAAGCAGGATCTTACCAACGAAATCAGAGAGCATTAACGC	1480
QY	1330	AGGGCAAAAGAAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAACAGGCAGTTGCAAT	1389
Db	1481	AGGGCAAAAGAAAGGCCCGCCTTGCCAGGATCCGGGTGGCCAAACGGGAAGCTTCAAT	1540
QY	1390	GCATPACTTGCA CAGCAAGCGCAAGGGGCTCTCTCAACGAGGGCGCTGGAGCTGACGGGCAAC	1449
Db	1541	GCTPACTTGCA CAGCAAGCGCAATGGGCTCTCTAATGAGGGCCCTGGAGCTGACGGGCAAC	1600
QY	1450	CCAGAAAGAGGACATGGGGCAAGACCACTGACTCATGAGAGGCGAGCATCATCACTG	1509
Db	1601	CCAGAAAGAGGACATGGGGCAAGACCACTGACTCATGAGAGGCGAGCATCATCACTG	1660
QY	1510	CTGCACTGCTGAAAAAACCACT 1533	
Db	1661	CTTACTGCTTAAGAAAGACCACT 1684	

RESULT 5	2997 bp	mRNA	linear	HTC 03-APR-2004
AK032268				
LOCUS				
DEFINITION	Mus musculus adult male olfactory brain cDNA, RIKEN full-length			
	enriched library, clone:6430513P12	product:potassium channel Kv4.2		
	mRNA, full insert sequence.			
ACCESSION	AK032268			
VERSION	AK032268.1	GI:26328092		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Harada, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,			

TITLE
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
REFERENCES
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
AUTHORS
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
REFERENCE
6 (bases 1 to 2997)
AUTHORS
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
TITLE
Direct Submission
JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:ftp://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:ftp://genome.gsc.riken.jp/
URL:ftp://fantom.gsc.riken.jp/.
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Best Local Similarity 72.0%; Pred. No. 8.7e-218;
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Db	1982	CTATCATTCATTTTTCGTACCCGTTATGTTCTAAGCAGAGAAAGGGCTCTTTCAGCAAGCAAGT		2041
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QY	1304	ACCAGAATCAGAGAGCTGATTAACGACAGGCGACAAAGAAGGCCCGCTTGCAGATCC		1363
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QY	1784	GCTCCAGCTTAAATTTGAAAGACAGACGAGCTGAGACCAAACTGCAAAAACATCCCA		1843
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DEFINITION	1893 bp DNA linear GSS 15-DEC-2003
ACCESSION	Homo sapiens KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,
VERSION	AY406812 genomic survey sequence.
	AY406812
	AY406812.1 GI:39762783

KEYWORDS	SSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
AUTHORS	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
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LOCUS			linear
DEFINITION			GSS 15-DEC-2003
ACCESSION	AY406814		
VERSION	AY406814.1	GI:39762785	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1893)		
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1893)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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Matches 1275;	Conservative	0; Mismatches 557;	Indels 12; Gaps 4;
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Qy	190	GAGCTGATTTGCTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGAGACCAAGCTGAG	249
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ORIGIN

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Matches 1284; Conservative 0; Mismatches 555; Indels 39; Gaps 7;

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QY 1849 ACAGCATCATGACATCCCACTTCCCGCAGGCTAAACCCAGAGGGGAGAAAGTGGCCA 1908
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LOCUS AY408065
DEFINITION Mus musculus KCND1 gene, VIRUTAL TRANSCRIPT, partial sequence,
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RESULT 10

AY406813

LOCUS 1893 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes KCND2 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY406813

VERSION AY406813.1 GI:39762784

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
1 (bases 1 to 1893)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

2 (bases 1 to 1893)

Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

location/Qualifiers
1..1893

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DEFINITION	1939 bp DNA linear GSS 15-DEC-2003
ACCESSION	Pan troglodytes KCND1 gene, VIRTUAL TRANSCRIPT, partial sequence,
VERSION	AY408064
KEYWORDS	AY408064.1 GI:39764035
SOURCE	GSS.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Pan troglodytes
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
TITLE	1 (bases 1 to 1939)
JOURNAL	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
PUBMED	Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
REFERENCE	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
AUTHORS	Adams, M.D. and Cargill, M.
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous
JOURNAL	gene trios
PUBMED	Science 302 (5652), 1960-1963 (2003)
REFERENCE	14671302
AUTHORS	2 (bases 1 to 1939)
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
JOURNAL	Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
PUBMED	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
REFERENCE	Adams, M.D. and Cargill, M.
AUTHORS	Direct Submission
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
JOURNAL	Rockville, MD 20850, USA

COMMENT	FEATURES	source
This sequence was made by sequencing genomic exons and ordering them based on alignment.	location/Qualifiers	1..1939
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Query Match	32.8%; Score 676.8; DB 9; Length 1939;	
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Qy 1258 GCGCTGCGAGTCCCTGTGATGTTTCCAACTTTAGCCGATTTACCAACGAATCAGAGA 1317
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Qy 1318 GCTGATTAACGAGGAGCAAAAGAGGCGCGCTTGCAGAGATCCGTGTGGCCAAACA 1377
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RESULT 12

AK033805
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DEFINITION Mus musculus adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230112B12 product:potassium voltage-gated channel, Shal-related family, member 1, full insert sequence.
ACCESSION AK033805
VERSION AK033805.1 GI:26329482
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Carninci, P. and Hayashizaki, Y.
1 High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalizetion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
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Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
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Nature 420, 563-573 (2002)
6 (bases 1 to 3302)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

Source

Location/Qualifiers
1. .3302

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ORIGIN

Query Match 28.0%; Score 577.6; DB 3; Length 3302;

Best Local Similarity 68.1%; Pred. No. 4.8e-123;

Matches 917; Conservative 0; Mismatches 399; Indels 30; Gaps 7;

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LOCUS CNS059UA 993 bp DNA linear GSS 01-SEP-2000

DEFINITION

Tetradon nigroviridis genome survey sequence T3 end of clone

ACCESSION

AL327691

VERSION

AL327691.1

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetradon nigroviridis

ORGANISM

Tetradon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

1 Roest Crolius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Frazmes, C., Winkler, P., Brotlier, P., Quetier, F., Saurin, W., and Weissenbach, J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633

PUBMED 10835645

REFERENCE 2

AUTHORS Roest Crolius, H., Jallou, O., Dasilva, C., Ozouf-Costaz, C., Frazmes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE 20359837

PUBMED 10899143

REFERENCE 3 (bases 1 to 993)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source 1..993

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Best Local Similarity 79.7%; Pred. No. 6.3e-123;

Matches 723; Conservative 0; Mismatches 178; Indels 6; Gaps 4;

QY 279 GGAGAGAGAGTCTTCTTCAACGAGACACCAAGAGTACTTCTTCAACCGGAGACCCCGA 338

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QY 339 GGTGTCGCGTGCCTGCTCAACTTCTTCAACGAGGAGGAGTGCATACCGCGCTGAGA 398

Db 932 TGCCTTCAGAGCATCTCAACTTNTACCGGACGGGNAAGCTCCANTACCTCCGACGA 873

QY 399 GTGCATCTTGCCTTACGACGAGCTGCGCTTCTTACGGCATCTCCCGAGATCATCGG 458

Db 872 GTGCATCTCAGCTTATGATGACGAGNTGACATTTCTTGGCATCATCCAGAGCTCATCGG 813

QY 459 GAGTGTGCTGCTACGAGAGTACAGAGACCGCAAGAGGAGAGACCGCGAGGCTCATGGA 518

Db 812 CGACTGCTGCTACGAGAGTACAGAGAGAGAGAGAGAGATTTAGAGGGGCTGACGA 753

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Db 695 GTGGGGGGGCTTGCAG 636

QY 639 TGGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698

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LOCUS DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 070F19 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL267651 GI:7989467

VERSION AL267651

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis

REFERENCE 1

AUTHORS Roest Crolius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Frazmes, C., Winkler, P., Brotlier, P., Quetier, F., Saurin, W., and Weissenbach, J.

TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633

PUBMED 10835645

REFERENCE 2

AUTHORS Roest Crolius, H., Jallou, O., Dasilva, C., Ozouf-Costaz, C., Frazmes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE 20359837

PUBMED 10899143

REFERENCE 3 (bases 1 to 1054)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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DB 710 ACCAATGAGTACTTCTTGCAGCGGAGACCCGAGGTGTCGCTGCTCACTTCTAC 651
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B2203918
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CH230-390G12, genomic survey sequence.
ACCESSION B2203918
VERSION B2203918
KEYWORDS B2203918.1 GI:23861970
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 628)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvarzbein,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other_GSSs: CH230-390G12.TJ
CONTACT: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 390 row: G column: 12
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Location/Qualifiers
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Query Match 25.7%; Score 529.6; DB 8; Length 628;
Best Local Similarity 91.2%; Pred. No. 5.4e-112;
Matches 573; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
QY 457 GGGAGTGTGCTTACGAGAGTCAAGACCGCAAGAGAGGAGAAAGCGGAGCGGCTCATG 516
DB 2 GGGAGTGTGCTTATGAGAGTCAAA-TACCGCAAGCGGAGAAAGCGTGAAGCGGCTCATG 60
QY 517 GACGACAAGACTCGGAGAAACAACAGAGTCCATGCCCTGCTGAGCTTCCGCGAGACC 576

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Copyright (c) 1993 - 2005 CompuGen Ltd.

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4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3412	100.0	655	US-09-178-109-2	Sequence 2, Appli
2	3403	99.7	655	US-09-142-791A-4	Sequence 4, Appli
3	3300.5	96.7	636	US-09-178-109-4	Sequence 4, Appli
4	3291.5	96.5	636	US-09-142-791A-2	Sequence 2, Appli
5	3265.5	95.7	636	US-09-142-791A-6	Sequence 6, Appli
6	2498.5	73.2	630	US-09-949-016-6828	Sequence 6828, Ap
7	2102	61.6	646	US-09-336-643A-10	Sequence 10, Appli
8	846	24.8	260	US-09-949-016-8327	Sequence 8327, Ap
9	767	22.5	806	US-09-833-466-13	Sequence 13, Appli
10	742.5	21.8	854	US-09-833-466-12	Sequence 12, Appli
11	742.5	21.8	858	US-09-275-252A-6	Sequence 6, Appli
12	724	21.2	539	US-08-464-340A-13	Sequence 13, Appli
13	720.5	21.1	601	US-09-336-643A-4	Sequence 4, Appli
14	715.5	21.0	616	US-09-275-252A-4	Sequence 4, Appli
15	713.5	20.9	552	US-09-949-016-8164	Sequence 8164, Ap
16	712.5	20.9	523	US-09-949-016-6195	Sequence 6195, Ap
17	709	20.8	528	US-08-527-152-2	Sequence 2, Appli
18	704	20.6	446	US-10-162-012-8	Sequence 8, Appli
19	704	20.6	495	US-09-275-252A-5	Sequence 5, Appli
20	703	20.6	532	US-10-162-012-13	Sequence 13, Appli
21	696	20.4	757	US-09-949-016-7121	Sequence 7121, Ap
22	695	20.4	532	US-08-288-405A-10	Sequence 10, Appli
23	691	20.3	556	US-09-275-252A-8	Sequence 8, Appli
24	678	19.9	159	US-08-606-143-45	Sequence 45, Appli
25	675	19.8	529	US-09-949-016-6196	Sequence 6196, Ap
26	675	19.8	538	US-09-949-016-8017	Sequence 8017, Ap
27	636.5	18.7	490	US-09-336-643A-6	Sequence 6, Appli

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29	636.5	18.7	507	4	US-09-949-016-9860	Sequence 9860, Ap
30	635.5	18.6	162	2	US-08-606-143-44	Sequence 44, Appli
31	629	18.4	494	4	US-09-949-016-7475	Sequence 7475, Ap
32	627.5	18.4	491	4	US-09-181-339-7	Sequence 7, Appli
33	622	18.2	494	1	US-08-464-340A-4	Sequence 4, Appli
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35	614	18.0	499	3	US-09-336-643A-8	Sequence 8, Appli
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37	597	17.5	477	3	US-09-336-643A-18	Sequence 18, Appli
38	584	17.1	513	1	US-08-464-340A-2	Sequence 2, Appli
39	584	17.1	513	5	PCT-US94-08449A-2	Sequence 2, Appli
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41	564	16.5	519	4	US-09-719-919A-17	Sequence 17, Appli
42	557.5	16.3	545	4	US-09-833-466-3	Sequence 3, Appli
43	529	15.5	497	4	US-09-181-339-3	Sequence 3, Appli
44	414.5	12.1	423	4	US-09-181-339-9	Sequence 9, Appli
45	370.5	10.9	256	4	US-09-181-339-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-178-109-2
Sequence 2, Application US/09178109
Patent No. 6395477
GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
FILE REFERENCE: Polypeptides and Uses Therefor
CURRENT APPLICATION NUMBER: US/09/178,109
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 655
TYPE: PRT
ORGANISM: human
US-09-178-109-2

Query Match	Best Local Similarity	Score	DB 3	Length	655
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%;	3412;			
Query	1	MAAGVAAWLPFARAAAGWMPVANCMPPLAPADKNKRODELIVLVNVSGRFQWRTTLER	60		
Db	1	MAAGVAAWLPFARAAAGWMPVANCMPPLAPADKNKRODELIVLVNVSGRFQWRTTLER	60		
Query	61	YPTDILGSTEKEFFFNEDTKEYPEDRDPEVERFCVINFYRTGKLHYPREICISAYDELAF	120		
Db	61	YPTDILGSTEKEFFFNEDTKEYPEDRDPEVERFCVINFYRTGKLHYPREICISAYDELAF	120		
Query	121	YGLPELIGDCYEEYDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAFENPHTST	180		
Db	121	YGLPELIGDCYEEYDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAFENPHTST	180		
Query	181	LALVEYVVTGFFIAVSITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACWMIFTVE	240		
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Db 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELGTPEEHEMGKTTSLIESQHLL 480
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RESULT 2

US-09-142-791A-4
; Sequence 4, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmejs
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 655
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-4

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Best Local Similarity 99.7%; Pred. No. 1.6e-317;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 181 LALVFYVYTGFFIAVSITNVETVPCGTVPKSGKELPCGERYSVAFCLDTACVMIFTYE 240
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Db 241 YLRLFAAPSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVFRIFKE 300
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Db 481 HCLEKTTGLSYLVDDPLSVRTSTIKNHEFIDEQMFEOQNCMESSMONTPTSTRSPSLSSHP 540
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QY 541 GLTTCCSRSKKTHLPNSNLPATRLRSMOELSTIHIOGSEQPSLTSSSLNLKADG 600
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Db 541 GLTTCCSRSKKTHLPNSNLPATRLRSMOELSTIHIOGSEQPSLTSSSLNLKADG 600
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Db 601 LRPNCKTSQITTAIISIPTPALTPEGESRPPASPPTNTNIPSTSNVVKVSVL 655
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RESULT 3

US-09-178-109-4
; Sequence 4, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hui-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-09-178-109-4

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Best Local Similarity 97.1%; Pred. No. 1.1e-307;
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D 361 TIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHSKRNGLINEALELTGTPEEEMGKTSLSIESQHLL 480
D 421 AOKKARLARIRVAKTGSSNAYLHSKRNGLINEALELTGTPEEEMGKTSLSIESQHLL 480
QY 481 HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 540
D 481 HCLEKTT-----NHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 521
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSQPSLTSSSLNLKADDG 600
D 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSQPSLTSSSLNLKADDG 581
QY 601 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPSITSNVVKVSVL 655
D 582 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPSITSNVVKVSVL 636

RESULT 4
US-09-142-791A-2
; Sequence 2, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 2
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-2

Query Match 96.5%; Score 3291.5; DB 3; Length 636;
Best Local Similarity 96.8%; Pred. No. 7.9e-307;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
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D 241 YLRLFAAPSRYYRFRIRSVMSIIDVVAIMPYYIGLVNTNEDVSGAFVTLRVFRVRIKFK 300
QY 301 SRHSGRLRLGTYLTKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY 360
D 301 SRHSGRLRLGTYLTKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
D 361 TIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHSKRNGLINEALELTGTPEEEMGKTSLSIESQHLL 480
D 421 AOKKARLARIRVAKTGSSNAYLHSKRNGLINEALELTGTPEEEMGKTSLSIESQHLL 480
QY 481 HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 540
D 481 HCLEKTT-----NHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 521
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSQPSLTSSSLNLKADDG 600
D 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSQPSLTSSSLNLKADDG 581
QY 601 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPSITSNVVKVSVL 655
D 582 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPSITSNVVKVSVL 636

RESULT 5
US-09-142-791A-6
; Sequence 6, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 6
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-6

Query Match 95.7%; Score 3265.5; DB 3; Length 636;
Best Local Similarity 96.2%; Pred. No. 2.5e-304;
Matches 630; Conservative 1; Mismatches 5; Indels 19; Gaps 1;
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QY	121	YGLPEIIGDCCYEEYKDKORENAEMLDDNDSENNOCMSPLSFRQTMRAFAENHTST	180
Db	121	YGILPEIIGDCCYEEYKDKORENAEMLDDNDSENNOCMSPLSFRQTMRAFAENHTST	180
QY	181	LALVFYVYTGFFIAVSVTINVEIYVPCGTVPGSKELPCEGRYSVAFPCLDTCVMIFVE	240
Db	181	LALVFYVYTGFFIAVSVTINVEIYVPCGTVPGSKELPCEGRYSVAFPCLDTCVMIFVE	240
QY	241	YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVGSAFVTLKVERVRIKFF	300
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QY	301	SRHSQGLRILGYTLKSCASELGFLLFSLTMALIIIFATVMFYAEKSSASAKFTSIPASFWY	360
Db	301	SRHSQGLRILGYTLKSCASELGFLLFSLTMALIIIFATVMFYAEKSSASAKFTSIPASFWY	360
QY	361	TIIVMTTLGGYDMPKTIAGKIFGSIISLSGVLVIALPVPVIVSNFSRIYHONORADKR	420
Db	361	TIIVMTTLGGYDMPKTIAGKIFGSIISLSGVLVIALPVPVIVSNFSRIYHONORADKR	420
QY	421	AOKKARLARIRVAKTGSSNAVLHRSKNGLNEALLETGTPREEHNGKTTSLIESQHHL	480
Db	421	AOKKARLARIRVAKTGSSNAVLHRSKNGLNEALLETGTPREEHNGKTTSLIESQHHL	480
QY	481	HCLEKTTGLSYLDPLLSYRSTSTIKNHEFIDEQMEONCMESMWQNPSTRSPSLSSH	540
Db	481	HCLEKTT-----NHEFIDEQMEONCMESMWQNPSTRSPSLSSH	521
QY	541	GLTTTCGRSRKKTTHLPNSNLPATRLRSMQELSTIHQGSQOGLTTSASSLNLKADG	600
Db	522	GLTTTCGRSRKKTTHLPNSNLPATRLRSMQELSTIHQGSQOGLTTSASSLNLKADG	581
QY	601	LRPNCKTSQITTAIISIPTEPALTPGESRPPASPGENTNIPISITSNVVKSVL	655
Db	582	LRPNCKTSQITTAIISIPTEPALTPGESRPPASPGENTNIPISIASNVKVSAL	636

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RESULT 6
US-09-949-016-6828
; Sequence 6828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SEQ ID NO 6828
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6828

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	Query Match	73.2%;	Score 2498.5;	DB 4;	length 630;
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Dd	1	MAAGVAANLPPARAAALIGMMFPASGEMPA	PRPQERKRRQDALIVLN	VS	SGTRFGQTQDTLE 60
QY	60	RYPDTLLGSTEKEFFENEDTKKEYFFEDRDP	EVEVCVLNFERYTGKLHYPRYCIS	I	SAYDELA 119
			:::::	: :::::	: : :
Dd	61	RYPDTLIGSSSERDFFYHPETQQYFFRD	PDIFRHILNFTYRTGKLHYPRHCIS	A	YDELA 120
			:::::	: :::::	: : :

Qy	120	FYGLPEIIGDCCYEEXKDRKRENAERLMDNDNSENNQES--MPSLSFRQTMWRAFENPHT	178
Db	121	FFGLPEIIGDCCYEEXKDRRRENAERLDDADPTGAGESALPTMTARORWRAFENPHT	180
Qy	179	STALVEFYVTGFFIAVSVITNVETVPCGTVPGS--KELPCGERYSVAFFCLDTACVMIF	237
Db	181	STMALVEFYVTGFFIAVSIVIANVETVPCGSSPGHMKELPCGERYAVAFCLDTACVMIF	240
Qy	238	TVEYLRLFAAPSRRYRFIRSVMSIIDVVAIMPYTIGLVMTNEDVSGAFVTLRVRVFR	297
Db	241	TVEYLRLFAAPSRRYRFIRSVMSIIDVVALPYTIGLVMTNEDVSGAFVTLRVRVFR	300
Qy	298	EKFSRHSOGLRILGYTLKSCASELGFLLBSLTMATIIIFATVMFYEAKSSASAKETSIPAS	357
Db	301	EKFSRHSOGLRILGYTLKSCASELGFLLBSLTMATIIIFATVMFYEAKSSASAKETSIPAA	360
Qy	358	FWYITVMTTIGYDMVPKTIAGKIFGSIKSLSGVLVIALPVPVIVSNFSRIYHQNORAD	417
Db	361	FWYITVMTTIGYDMVPKTIAGKIFGSIKSLSGVLVIALPVPVIVSNFSRIYHQNORAD	420
Qy	418	KRPAOKKARLARIRVAKTGGSSNAYLHKSNGCLNEMLELTGTPREEHNGKTTLSLESQHH	477
Db	421	KRPAOKKARLARIRAKSGSANAYMQSKNGLLSNLQ--SSEDEQAFAFSKSGSSRETQHH	479
Qy	478	HLHCEKTTGHSYLVDDELVSRTSTIKNEHFIIDOMEFQONCMSSMONTYPTSTRPSLS	537
Db	480	HLHCELEKTT-----NHEFVDEQVFEESCEMEVATVNRPPSSHSPSL	520
Qy	538	SHRGLTTTCCSRRSKKTTHLPNSNULPATRLRSMOELSTIHIOGSEOPSLTTSRSLSLKA	597
Db	521	SOQGVLTSTCCSRRAHKTFERIPNANVSGSHOGSIQELSTIQICVERTPLTNSRSLSLNAMK	580
Qy	598	DGGLRPNCKTSOITTAIISIPTPPALTPEGESRP--PPASPGENTNIPISITSNVVKVSVL	655
Db	581	BECKVKNCEOPVYTTAISIPTPPVTTPEGDREPESEPYSGG-----NIVRVSAL	630

```

RESULT 7
; US-09-336-643A-10
; Sequence 10, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 646
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(646)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-10

```

Query Match 61.6%; Score 2102; DB 3; length 646;
 Best Local Similarity 63.3%; Pred. No. 1.3e-192;
 Matches 428; Conservative 78; Mismatches 116; Gaps 14;

```

Qy 1 MAAGVAAWLPAPAAAGMMPVANCMPPLAPADKNKQDELIVLVNSGRRFQWTTLER 60
Db 1 MAAGLATWLPAPAAAGMMPVANCMPPLAPADKNKQDELIVLVNSGRRFQWTTLER 60
Qy 61 YPDTLLGSTEKEFFENEDKKEYFEDRDEPFRVCLNPFRTGKLYHPRYECISAYDELA 120
Db 61 YPDTLLGSSSEKEFFEDKKEYFEDRDEPFRVCLNPFRTGKLYHPRYECISAYDELA 120
Qy 121 YGILPEIIGDCYEEYKDKRENAERLMDNDSENNOESMPSL----SPRQTMWRAENP 176
Db 121 YGILPEIIGDCYEEYKDKRENAERLMDNDSENNOESMPSL----SPRQTMWRAENP 176
Qy 177 HTSTLALVFFYTTGFFIYAVITNVETVPC--GTVPGSKELPCGERYSVAFCLDTACV 234
Db 177 HTSTLALVFFYTTGFFIYAVITNVETVPC--GTVPGSKELPCGERYSVAFCLDTACV 234
Qy 180 HTSTALVFFYTTGFFIYAVITNVETVPC--GTVPGSKELPCGERYSVAFCLDTACV 239
Db 180 HTSTALVFFYTTGFFIYAVITNVETVPC--GTVPGSKELPCGERYSVAFCLDTACV 239
Qy 235 MIFTEYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRERV 294
Db 235 MIFTEYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRERV 294
Qy 240 LIFTEYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRERV 299
Db 240 LIFTEYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRERV 299
Qy 295 FRIFKFSRHSGGRLILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASKFTSI 354
Db 295 FRIFKFSRHSGGRLILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASKFTSI 354
Qy 300 FRIFKFSRHSGGRLILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASKFTSI 359
Db 300 FRIFKFSRHSGGRLILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASKFTSI 359
Qy 355 PASFWYTIWTTTLYGDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQ 414
Db 355 PASFWYTIWTTTLYGDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQ 414
Qy 360 PAFWYTIWTTTLYGDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQ 419
Db 360 PAFWYTIWTTTLYGDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQ 419
Qy 415 RADKRAQKARLARIRVAKTGSSNAYLHSGKNGLNALDELGTPEEBHM--GKTTSLIE 473
Db 415 RADKRAQKARLARIRVAKTGSSNAYLHSGKNGLNALDELGTPEEBHM--GKTTSLIE 473
Qy 420 RADKRAQKARLARIRVAKTGSSNAYLHSGKNGLNALDELGTPEEBHM--GKTTSLIE 475
Db 420 RADKRAQKARLARIRVAKTGSSNAYLHSGKNGLNALDELGTPEEBHM--GKTTSLIE 475
Qy 474 SQHHHLHCLTKTTGLSTLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRS 533
Db 474 SQHHHLHCLTKTTGLSTLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRS 533
Qy 476 QQHHHLHCLTKTTGLSTLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRS 515
Db 476 QQHHHLHCLTKTTGLSTLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRS 515
Qy 534 PLSGHP---GLTTCSSRSK--KTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTT 588
Db 534 PLSGHP---GLTTCSSRSK--KTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTT 588
Qy 516 TSVSQPVGPGSLSSCCPRRAKRAIRLANSTASVSR--GSMQELDM--LAGLRSHAPQ 572
Db 516 TSVSQPVGPGSLSSCCPRRAKRAIRLANSTASVSR--GSMQELDM--LAGLRSHAPQ 572
Qy 589 SRSSLNKADGDLRPNCKTSQITTAIISIPPPALPEGESRPPASPG----- 637
Db 589 SRSSLNKADGDLRPNCKTSQITTAIISIPPPALPEGESRPPASPG----- 637
Qy 573 SRSSLNKADGDLRPNCKTSQITTAIISIPPPALPEGESRPPASPG----- 629
Db 573 SRSSLNKADGDLRPNCKTSQITTAIISIPPPALPEGESRPPASPG----- 629
Qy 638 PNTNIPSITSNVKVS 653
Db 638 PNTNIPSITSNVKVS 653
Qy 630 SSGTPTCLPPEVTKIS 645
Db 630 SSGTPTCLPPEVTKIS 645

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RESULT 8

```

US-09-949-016-8327
; Sequence 8327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8327
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Human

```

```

US-09-949-016-8327
Query Match 24.8%; Score 846; DB 4; Length 260;
Best Local Similarity 60.0%; Pred. No. 1.1e-72;
Matches 174; Conservative 35; Mismatches 49; Indels 32; Gaps 4;
Qy 368 LGYDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQADKRAQKARL 427
Db 1 LGYDMVNPKTIAKIFGICSLGVLVIALPVPVIVSNFSRIYHQNQADKRAQKARL 60
Qy 428 ARIRAKTGSSNAYLHSGKNGLNALDELGTPEEBHMKTSLIESQHHHLHCLTKT 487
Db 428 ARIRAKTGSSNAYLHSGKNGLNALDELGTPEEBHMKTSLIESQHHHLHCLTKT 487
Qy 61 ARIRAKTGSSNAYLHSGKNGLNALDELGTPEEBHMKTSLIESQHHHLHCLTKT 119
Db 61 ARIRAKTGSSNAYLHSGKNGLNALDELGTPEEBHMKTSLIESQHHHLHCLTKT 119
Qy 488 GLSYLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRSPSLSHPGTLTTC 547
Db 488 GLSYLVDPDLSVSTIKNHEPIDQMEQNCMESSMONTPTSTRSPSLSHPGTLTTC 547
Qy 120 -----NHEFVDEQVEESCMETVATVNRSSSPSLSSQGVSTCC 160
Db 120 -----NHEFVDEQVEESCMETVATVNRSSSPSLSSQGVSTCC 160
Qy 548 SRRSKKTTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTSTRSSLNKADGDLRPNCKT 607
Db 548 SRRSKKTTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTSTRSSLNKADGDLRPNCKT 607
Qy 161 SRHAKTFRIRANVSGSHQSGIQLSTIQIRCVERTPLSNRSSLNAKMECYKLNCEQ 220
Db 161 SRHAKTFRIRANVSGSHQSGIQLSTIQIRCVERTPLSNRSSLNAKMECYKLNCEQ 220
Qy 608 SQITTAIISIPPPALPEGESR--PPASPGPNTNIPSITSNVKVSVL 655
Db 608 SQITTAIISIPPPALPEGESR--PPASPGPNTNIPSITSNVKVSVL 655
Qy 221 PYVTAAIISIPPPALPEGESR--PPASPGPNTNIPSITSNVKVSVL 260
Db 221 PYVTAAIISIPPPALPEGESR--PPASPGPNTNIPSITSNVKVSVL 260

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RESULT 9

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US-09-833-466-13
; Sequence 13, Application US/09833466
; Patent No. 6727353
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.2
US-09-833-466-13

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Query Match 22.5%; Score 767; DB 4; Length 806;
Best Local Similarity 27.5%; Pred. No. 2.7e-64;
Matches 223; Conservative 115; Mismatches 243; Indels 230; Gaps 27;
Qy 27 MPLAPAD--KNKQDELIVLVNSGRRFQWRTTLERYPTLLG-----STEKEFF----- 74
Db 20 LPPEVDIISKTSKSRKINVGGLNHEVLMR--TIDRLPRRLGKLDCNTHESLLEVC 78
Qy 75 -FNEDEKYEPRDRDPEVFRVCLNPFRTGKLYHPRYECISAYDELAFGILPEIIGDCCY 133
Db 75 -FNEDEKYEPRDRDPEVFRVCLNPFRTGKLYHPRYECISAYDELAFGILPEIIGDCCY 133
Qy 79 DYNLENENYFDRHPGAFTSILNFYRTGKLHMEEMCALSGQELDYWGIDEIYLESQ 138
Db 79 DYNLENENYFDRHPGAFTSILNFYRTGKLHMEEMCALSGQELDYWGIDEIYLESQ 138
Qy 134 EBYKDK-----RENAERLMDNDSENNOESMPSLSFQTMWRAENPHTSTLALV 186
Db 134 EBYKDK-----RENAERLMDNDSENNOESMPSLSFQTMWRAENPHTSTLALV 186
Qy 139 ARYHQKEQWNEBELREAEATMDGEGEDNTCCGDK--KKGLMDLLEKPNSSVAAKILA 196
Db 139 ARYHQKEQWNEBELREAEATMDGEGEDNTCCGDK--KKGLMDLLEKPNSSVAAKILA 196
Qy 187 YVTGFFIYAVITNVETVP-----GTVPGSKELPCGERYSVAFCLDTACVMIFTV 239
Db 187 YVTGFFIYAVITNVETVP-----GTVPGSKELPCGERYSVAFCLDTACVMIFTV 239
Qy 197 IVSILFIVLSTIALSINTLPEIQETDERGQLNDNRQLA-----HVEAVCIAMFTM 246
Db 197 IVSILFIVLSTIALSINTLPEIQETDERGQLNDNRQLA-----HVEAVCIAMFTM 246
Qy 240 EYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVP 292
Db 240 EYLLRLFAAPSRFRYSVSIIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVP 292

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QY 27 MPLAPAD--KMKRQDELIVLVNSGRFQT-WRTTLERYPDITLG-----STEKEFF---- 74
D 16 LPPEMEIVRSACSRVRVNLVGLAHEVLMR-TLDRLPRTLRGLKRDNCNTHDSLLEVC 74
QY 75 -FNEDEKREYFDRDPEVRCVNLNRYRTGKLYPRYECISAYDELAIFYGLPEIGDCY 133
D 75 DYSLDNEYFDRHPGAFTSILNFRYRTGRLHMEEMCALSFQGLDYGWIDEIYLESCCQ 134
QY 134 EBYKDRKRENAERLMDNDSENNOE-----SMPLSFQTMWRAFENPHTSTLALVFYV 188
D 135 ARYHOKKEQNMELKREAEFTLREREGEEDNTCCAEKRRKMLDLEKPNSSVAAKILAI 194
QY 189 TGFFLAIVSVITNVEVPCGTVPCKELPCGERYSVA-----FFCLDTACMIFVEYLL 243
D 195 SIMFVLSTLALNTLP-----ELQSLDEFQSTDNPOLAHEAVCIAMFTMEYLL 246
QY 244 RLFAAPSRRYFRSVMISIDVVAIMPYIGLWMTNN-----EDVSGAFVTLRVFRVFR 296
D 247 RFLSPKWKPFKGPLNAIDLALIPYVITFLTESNKSVLQFQNVRRVYQIFRIMRILR 306
QY 297 IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPA 356
D 307 ILKLARHSTGLQSLGFTLRSYNELGLILFLAMGIMIFSLVFAEKEDBDTKFKSIPA 366
QY 357 SFWYITVMTLGYGDMVPTKIAGKIFGSLGSLGVIALPVPVIVNSRIRYHONORA 416
D 367 SFWATITMTYGYGDIYPKTLGKIYVGLCCIAGVIALPIPIVNNFSEFYKEQKRO 426
QY 417 DKRAQKARLARIRVAKTGSNAVYLSKRNGL-----NEALELTGTPEEHH 464
D 427 EKAIRREA-LER-----AKRNGSIVSNMMDAPARSIEWMDIIVERKNGEN 471
QY 465 MKGTTSLIESQHHHLHLEKTTGILSYLVDDPLSVRTSTIKHEFIDQMEQNCMESS 524
D 472 MGKDKV---QDNHLSPKMKWTKRT-----LS-ETSSKS-----FETK 507
QY 525 MQVNPSTRSPSLSHPLTTCSSRSKKTTHLPNSNLPATRLRSMQELSTIHQSEOP 584
D 508 EQGSPK-----ARSSSSPOHL-----NVQQLMDMYNKMMAKTQSQP 543
QY 585 SLTSSRSSLNKADGRLPNCKTSQITTAISIPTPALTPEGESRPPASPGENNIPS 644
D 544 ILNTKESAAQSKPEEL-----EMESIPSPVAP-----LPT 574
QY 645 ITSNNV 650
D 575 RTEGYI 580

RESULT 12
US-08-464-340A-13
; Sequence 13, Application US/08464340A
; Patent No. 5710019
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CABELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,340A

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; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-464-340A-13

Query Match      21.2%; Score 724; DB 1; Length 539;
Best Local Similarity 33.0%; Pred. No. 1.9e-60;
Matches 163; Conservative 98; Mismatches 165; Indels 68; Gaps 13;

QY 27 MPLAPAD--KMKRQDELIVLVNSGRFQT-WRTTLERYPDITLG-----STEKEFF---- 74
D 15 LPPEMEIVRSACSRVRVNLVGLAHEVLMR-TLDRLPRTLRGLKRDNCNTHDSLLEVC 73
QY 75 -FNEDEKREYFDRDPEVRCVNLNRYRTGKLYPRYECISAYDELAIFYGLPEIGDCY 133
D 74 DYSLDNEYFDRHPGAFTSILNFRYRTGRLHMEEMCALSFQGLDYGWIDEIYLESCCQ 133
QY 134 EBYKDRKRENAERLMDNDSENNOE-----SMPLSFQTMWRAFENPHTSTLALVFYV 189
D 134 ARYHOKKEQNMELKREAEFTLREREGEEDNTCCAEKRRKMLDLEKPNSSVAAKILAI 193
QY 190 GFFLAIVSVITNVEVPCGTVPCKELPCGERYSVA-----FFCLDTACMIFVEYLLR 244
D 194 IMFVLSTLALNTLP-----ELQSLDEFQSTDNPOLAHEAVCIAMFTMEYLLR 245
QY 245 LFAAPSRRYFRSVMISIDVVAIMPYIGLWMTNN-----EDVSGAFVTLRVFRVFR 297
D 246 FLSPKWKPFKGPLNAIDLALIPYVITFLTESNKSVLQFQNVRRVYQIFRIMRILR 305
QY 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPA 357
D 306 ILKLARHSTGLQSLGFTLRSYNELGLILFLAMGIMIFSLVFAEKEDBDTKFKSIPA 365
QY 358 FMYTIVMTLGYGDMVPTKIAGKIFGSLGSLGVIALPVPVIVNSRIRYHONORAD 417
D 366 FWWATITMTYGYGDIYPKTLGKIYVGLCCIAGVIALPIPIVNNFSEFYKEQKROE 425
QY 418 KRAQKARLARIRVAKTGSNAVYLSKRNGL-----NEALELTGTPEEHHM 465
D 426 KAIRREA-LER-----AKRNGSIVSNMMDAPARSIEWMDIIVERKNGENM 470
QY 466 GKTTSLIESQHHHL 479
D 471 GKDKV---QDNHL 481

RESULT 13
US-09-336-643A-4
; Sequence 4, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURRAN, Mark Edward
; APPLICANT: HU, Ping
; APPLICANT: RUTTER, Marc
; APPLICANT: WANG, Jian-Wang
; TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels

```

```

; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 601
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-4

```

Query Match	21.1%;	Score 720.5;	DB 3;	Length 601;
Best Local Similarity	31.8%;	Pred. No. 4.9e-60;		
Matches 192;	Conservative 102;	Mismatches 221;	Indels 89;	Gaps 15

QY	40	ELIVLANSGRFQWRTTLERYPDTLL-----SSTEKEFFENEDTKEYF	83
Db	8	EKIIINVGGRHETRYRSTLTLPGTRLAMLADPDGGREPDGGVWGSOGSGGCGCEFF	67
QY	84	FDRDPEVFCVLNFEYRTGKHLHYPRYECISAYDEDLAFYGLPETIGDCCYEEKDRREN	143
Db	68	FDRHPGVFAVYLNYYRTGKHLCPADVCGPLFEBELAFWGIDETDEPCCWMTY--RQHRD	125
QY	144	AERLM-----DDNSEN-----NOESMPSLS-----FRQTMRAFEN	175
Db	126	ABEALDIFETPDILIGDPPGDEDLAKRLGIEDAAGLGGPDGSGKRWRLQPRMALLFED	185
QY	176	PHSTLALVEYYVTGFFIAVSITNVETVPCGTVPGSXELPCGERYSV-----A	225
Db	186	PYSSRAARFIAPASLFFILVSIITPCLFETHAENIVKNTPEVINGTSVVLQYEIETDPA	245
QY	226	FFCLDTACVMIFTEYELRLFAAPSRXRFIRSMSIIDVAIMPYI-----GLVMTNNE	280
Db	246	LTVEGVCAVMFTEFLVRIVESPKNLEFIKNULNIIDFVAILPEYLEVGSLGSSKAAK	305
QY	281	DVSGAFVTLRVFRVERIFKFSRHSQGLRILGYTLKSCASELGFLFSLTMAIIIPATVMF	340
Db	306	DVLGFLRVVRFVRILRIFKLTRHFVGRLGHTLRASNEFLLLIIFLAGVLIFATMIY	365
QY	341	YAEK-----GSSASKTSIPASFWYITVTMTLGYGDMVPKTIAGKIFGSISLSG	391
Db	366	YAEKVGQPNPSPASSEHTQPKNIPIGFWMAVVTMTTLGYGDMYQPTWSGMLVGALCALAG	425
QY	392	VLVIALPVPVIVSNFSRIYHONORADKRRQAOKKARLARIRVAKTGSSNAYHSKRNLIN	451
Db	426	VLTIAMPPVIVNNFG--MYSLAMAKOLPKRKK--HIPAPQASSPTFCKTELMAACN	482
QY	452	EALBLGTBEEHMGKTTSLIESQHHLHLCKLEKTTGLSYLVDDP--LLSVRTSTIKNHF	510
Db	483	-----STQSDTCLGKDNRLLE--HNRSVLSGDDSTGSRRPLSPERLPIRRSSTRKXR	534
QY	511	IDEQMF-----EQNCMESSMQNYPSTRSPSLSGHGLTTTCCSRRSKTTLPSNULPAT	565
Db	535	RGETCFLLTTGTYCASDGGIRKGYEKSRSLNNIAGLAGN--ALRLSPVTSPPYNSPCPLR	592
QY	566	RLRS	569
Db	593	RSRS	596

RESULT 14
US-09-275-.252A-4
; Sequence 4, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: The Rockefeller University

```

; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-275-252A-4

```

Query Match	21.0%;	Score 715.5;	DB 4;	Length 616;
Best Local Similarity	31.7%;	Pred. No. 1.5e-59;		
Matches 173;	Conservative 105;	Mismatches 153;	Indels 115;	Gaps 15;

[illegible]

RESULT 15
US-09-949-016-8164
; Sequence 8164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8164
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8164

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Query Match      20.9%; Score 713.5; DB 4; Length 552;
Best Local Similarity 33.9%; Pred. No. 2e-59;
Matches 167; Conservative 96; Mismatches 160; Indels 69; Gaps 12;

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QY 18 GMPVANC-----PMP--LAPADKNKRQDELIVNVSGRRFQMTWRTTLERYPDTLL 66
Db 48 GAPPGCGCGGGCGRYERLPPLSLPAAGEQDCGGERVYNISGLRFETQLKLCQFPETLL 107
QY 67 GSTEKEF-FFNEDTKEYFPDRDPEVRCVNFYRT-GKTHYPRYECISAYDDELAFYGL 124
Db 108 GDFKRMRYFDFDLRNEYFEDNRPSFDALYYQSGRIIRPVNPIDIFSEIRFYQ-- 165
QY 125 PEIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMWARFENPHTSTLALV 184
Db 166 --LGEEMEKERE-----DEGLREERPLPRDFQROVWLTPEYPSGPARG 212
QY 185 FYYVTGFFIAVSITNVETVPCGIVPGSKELPC-----GER-----YSV 224
Db 213 IATVSVLVILISIVIFCLETLP--EFREKDYPASTQDSFEAAGNSTGSRAGASSFSD 270
QY 225 AFCLDTACVMIFTVEYLLRLFAAPSRYRFRSVMSIIDVVAIMPYIGLV-----T 277
Db 271 PFFVETLCIIMFSFELLVRFACPSKATFSRNIMLIDIVAIIPYFITGTETELARQGN 330
QY 278 NNEVSGAFV-TLRVFRVRIKFSRHSQGLRILGYTLKSCASELGFLFSLTMAIIIFA 336
Db 331 GQQAMSLAILRVIRLVFRIRFKLSRHSKGLQILGQTLKASMRHLGLIFFLFIVILFS 390
QY 337 TVMEYAEKSSASKFTSTPASFWYTIIVMTTLGYGDMVPKTIAGKIFGSCSLGVLVIA 396
Db 391 SAVYFAEADPTSGFSSIPDAFWAVVTMTVGYGDMHPVTIGKIVGSLCAIAGVLTA 450
QY 397 LPVPVIVSNFGRIVHONQADKRR-----AQKARLARIRVAKTGSSNAYLHAK 445
Db 451 LPVPVIVSNFNFFYHRETEGEEQSQYMHVSCQHLSSAEELRKARSNSTLSKSEYVIE 510
QY 446 RNGLNLEALLET 457
Db 511 EGMNHSAPFQT 522

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Search completed: April 6, 2005, 07:21:28
 Job time : 110.56 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 00:35:45 ; Search time 497.211 Seconds
(without alignments)
509.498 Million cell updates/sec

Title: US-10-062-879-2
Perfect score: 3412
Sequence: 1 MAAGVAAALPFAAAAIIGMM.....PGPNTNIPSTISNVKSVL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3412	100.0	655	5	ABB79584	Abb79584 Human Kv4
2	3403	99.7	655	2	AAW79590	Aaw79590 Human Kv
3	3403	99.7	655	8	ADF91398	Adf91398 Wild-type
4	3396	99.5	655	7	ADD48188	Add48188 Rat Prote
5	3395	99.5	655	8	ADS16294	Ads16294 Human vol
6	3391	99.4	655	4	ABB86321	Abb86321 Human Kv4
7	3300.5	96.7	636	5	ABB79585	Abb79585 Human Kv4
8	3291.5	96.5	636	2	AAW79589	Aaw79589 Human Kv
9	3265.5	95.7	636	2	AAW79591	Aaw79591 Human Kv
10	3035.5	89.0	611	7	ADE61252	Ade61252 Rat Prote
11	2498.5	73.2	630	7	ADM10929	Adm10929 Human O64
12	2498.5	73.2	630	7	ADM10928	Adm10928 Human O64
13	2498.5	73.2	630	7	ADM10930	Adm10930 Human O64
14	2498.5	73.2	630	7	ADM10927	Adm10927 Human O64
15	2498.5	73.2	630	8	ADJ11257	Adj11257 Human ova
16	2498.5	73.2	630	8	ADJ11260	Adj11260 Human ova
17	2498.5	73.2	630	8	ADJ11258	Adj11258 Human ova
18	2498.5	73.2	630	8	ADJ11259	Adj11259 Human ova
19	2498.5	73.2	630	8	ADM43520	Adm43520 Human ova
20	2498.5	73.2	630	8	ADM43519	Adm43519 Human ova
21	2498.5	73.2	630	8	ADM43521	Adm43521 Human ova
22	2498.5	73.2	630	8	ADM43518	Adm43518 Human ova
23	2496.5	73.2	630	2	AAI13523	Aai13523 Amino aci
24	2493.5	73.1	629	4	ABB86319	Abb86319 Human Kv4
25	2113	61.9	647	4	AAm25597	Aam25597 Human pro

26	2108	61.8	646	4	AAB86318	Aab86318 Human Kv4
27	2102	61.6	646	2	AAy34123	Aay34123 Human pot
28	1937.5	56.8	571	4	ABB71722	Abb71722 Drosophil
29	894	26.2	217	4	AAB86320	Aab86320 Human Kv4
30	869	25.5	214	2	AAy13524	Aay13524 Amino aci
31	825	24.2	255	7	ADM10926	Adm10926 Human O64
32	825	24.2	255	8	ADJ11256	Adj11256 Human ova
33	825	24.2	255	8	ADM43517	Adm43517 Human ova
34	767	22.5	806	7	ADJ79875	Adj79875 CIRA_huma
35	755.5	22.1	911	7	ADJ69676	Adj69676 Human hea
36	748.5	21.9	985	8	ADJ30147	Adj30147 Drosophil
37	748.5	21.9	985	8	ADJ30143	Adj30143 Drosophil
38	746	21.9	149	8	ADJ25645	Adj25645 Voltage-g
39	742.5	21.8	854	6	ABP58354	Abp58354 Human pot
40	742.5	21.8	854	7	ADJ79874	Adj79874 CIRA_huma
41	742.5	21.8	858	2	AAy32015	Aay32015 Human cat
42	742.5	21.8	858	5	AAO17058	Aao17058 Human KCN
43	742.5	21.8	858	8	ADJ38328	Adj38328 Human cat
44	742.5	21.8	985	4	ABB57774	Abb57774 Drosophil
45	741	21.7	853	7	ADE63538	Ade63538 Rat Prote

ALIGNMENTS

RESULT 1	
ABB79584	
ID ABB79584 standard; protein; 655 AA.	
XX AC ABB79584;	
XX AC	
DT 01-OCT-2002 (first entry)	
XX	
DE Human Kv4.3 potassium channel (long form).	
XX	
KW Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;	
KW nootropic; neuroprotective; cardiact; gene therapy.	
XX	
OS Homo sapiens.	
XX	
PN US6395477-B1.	
XX	
PD 28-MAY-2002.	
XX	
PF 23-OCT-1998; 98US-00178109.	
XX	
PR 23-OCT-1998; 98US-00178109.	
XX	
PA (AMHP) AMERICAN HOME PROD CORP.	
XX	
PI Cockett MI, Dilks DW, Ling HC, Sokol PT;	
XX	
DR WPI; 2002-556093/59.	
XX	
DR N-PSDB; ABBN84400.	
XX	
PT New isolated polynucleotide encoding human Kv4.3 potassium channel	
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic	
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart	
PT diseases.	
XX	
PS Claim 1; Col 16-20; 19pp; English.	
XX	
CC The present sequence is the protein sequence of the long isoform of novel	
CC human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been	
CC identified: the present full-length form (hKv4.3 long); and a second form	
CC (see ABB79585), which has a deletion of 19 amino acids in the carboxy	
CC domain after the predicted sixth transmembrane domain (hKv4.3 short).	
CC Human heart primarily expresses hKv4.3 long, whereas human brain contains	
CC both forms. The invention provides Kv4.3 polypeptides, polynucleotides,	
CC and methods for producing these polynucleotides. The Kv4.3 polypeptides	
CC and polynucleotides are useful in the diagnosis, treatment and screening	
CC of human diseases relating to an excess or deficiency of hKv4.3 activity,	
CC including Alzheimer's disease and heart disease	


```
XX Sequence 655 AA;
SQ
Query Match 100.0%; Score 3412; DB 5; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPMLAPADKPKRQDELIVLVNSGRRFQRTWRTTLER 60
DB 1 MAGVAAWLPFARAALIGMMPVANCMPMLAPADKPKRQDELIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPREYECISAYDEELAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPREYECISAYDEELAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPTST 180
QY 181 LALVFYVYTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFIVE 240
DB 181 LALVFYVYTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFIVE 240
QY 241 YLRLFAAPSRRYRFRIRSVMSIIDVAIMPYYIGVMTNNEVSGAFVTLRVFRVFRIFKE 300
DB 241 YLRLFAAPSRRYRFRIRSVMSIIDVAIMPYYIGVMTNNEVSGAFVTLRVFRVFRIFKE 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPASFWY 360
QY 361 TIIVMTTLGYGDMVPKTIAGKIFGSIISLGLVLYALPVPVIVSNFSRIYHONQADKRR 420
DB 361 TIIVMTTLGYGDMVPKTIAGKIFGSIISLGLVLYALPVPVIVSNFSRIYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGPREEHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGPREEHMGKTTSLIESQHHL 480
QY 481 HCLEKTTGSLVDDPLLVRSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
DB 481 HCLEKTTGSLVDDPLLVRSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
QY 541 GLTTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEOPSLTSSRSLNLKADG 600
DB 541 GLTTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEOPSLTSSRSLNLKADG 600
QY 601 LRPNCKTSQTTTAIISITPPALTPGEGSRPPASPDPNTNIPISITSNVKVSYL 655
DB 601 LRPNCKTSQTTTAIISITPPALTPGEGSRPPASPDPNTNIPISITSNVKVSYL 655

RESULT 2
AAW79590
ID AAW79590 standard; protein; 655 AA.
XX
AC AAW79590;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hkV4.3 (longer isoform).
XX
KM Potassium channel; Kv; hkV4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 488..506
FT /note="extra residues of longer hkV4.3 isoform"
XX
XX MO9842833-A2.
XX
```

```
PD 01-OCT-1998.
XX
XX 23-MAR-1998; 98WO-EP001901.
XX
PR 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
PA (SMK ) SMITHKLINE BEECHAM LAB PHARM.
PI Bril AMA, Calmels TPG, Faivre USP, Javre J, Rouanet S;
XX
DR WPI; 1998-542277/46.
DR N-PSDB; AAV61572.
XX
PT New potassium channel polypeptides, hkV4.3 - and hkV4.3-encoding
PT polynucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
PS Claim 2; Page 26-27; 47pp; English.
XX
CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hkV4.3. The sequence was deduced from an isolated hkV4.3
CC polynucleotide (see AAV61572), and has 97% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC KV family related proteins. A shorter isoform (see AAW79589) has been
CC identified, which lacks amino acid residues 488-506 of the longer
CC isoform. The invention relates to hkV4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hkV4.3 polypeptides can be used to identify
CC agonists and antagonists of hkV4.3 and to raise specific antibodies. Also
CC claimed are methods for utilizing such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hkV4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hkV4.3 expression or
CC activity
XX
SQ Sequence 655 AA;
Query Match 99.7%; Score 3403; DB 2; Length 655;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPMLAPADKPKRQDELIVLVNSGRRFQRTWRTTLER 60
DB 1 MAGVAAWLPFARAALIGMMPVANCMPMLAPADKPKRQDELIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPREYECISAYDEELAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPREYECISAYDEELAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPTST 180
QY 181 LALVFYVYTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFIVE 240
DB 181 LALVFYVYTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFIVE 240
QY 241 YLRLFAAPSRRYRFRIRSVMSIIDVAIMPYYIGVMTNNEVSGAFVTLRVFRVFRIFKE 300
DB 241 YLRLFAAPSRRYRFRIRSVMSIIDVAIMPYYIGVMTNNEVSGAFVTLRVFRVFRIFKE 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPASFWY 360
QY 361 TIIVMTTLGYGDMVPKTIAGKIFGSIISLGLVLYALPVPVIVSNFSRIYHONQADKRR 420
DB 361 TIIVMTTLGYGDMVPKTIAGKIFGSIISLGLVLYALPVPVIVSNFSRIYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGPREEHMGKTTSLIESQHHL 480
```

|||||
Db 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALLETGTPEEHNKTTSLIESQHHL 480
Qy 481 HCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQNCMESSMONTSTRSPSLSSHP 540
Db 481 HCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQNCMESSMONTSTRSPSLSSHP 540
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSSLNKADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSSLNKADG 600
Qy 601 LRPNCKTSQITTAIISITPPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 655
Db 601 LRPNCKTSQITTAIISITPPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 655
RESULT 3
ADF91398
ID ADF91398 standard; protein; 655 AA.
XX ADF91398;
XX 26-FEB-2004 (first entry)
XX Wild-type hkv4.3 #SEQ ID 5.
XX Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective;
XX tranquiliser; sedative; neuroprotective; nootropic; antiparkinsonian;
XX nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;
XX blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;
XX tachycardia; congestive heart failure; epilepsy; stroke;
XX traumatic brain injury; anxiety; insomnia; Alzheimer's disease;
XX Parkinson's disease.
XX Homo sapiens.
XX WO2003097682-A1.
XX 27-NOV-2003.
XX 14-MAY-2003; 2003WO-IB002453.
XX 15-MAY-2002; 2002GB-00011123.
XX 15-MAY-2002; 2002US-0378076P.
XX 15-MAY-2002; 2002US-0378131P.
XX (DEVG-) DEVGEN NV.
XX Kaletta TJ, Dewulf NE, Plaetinck GKM;
XX MPI; 2004-061981/06.
XX N-PSDB; ADF91397.
XX New nematode worm expressing a heterologous nucleotide sequence encoding
XX a functional voltage-gated potassium channel of the Kv4 family, useful
XX for determining compounds that interact with the voltage-gated potassium
XX channel.
XX Example 1; SEQ ID NO 5; 82pp; English.
XX The invention relates to a nematode worm that expresses a heterologous
XX nucleotide sequence encoding a functional voltage-gated potassium channel
XX of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,
XX part or fragment. The nematode worm is useful in determining whether a
XX compound interacts with the voltage-gated potassium channel of the Kv4
XX family or whether a compound is an agonist, antagonist, opener and/or
XX blocker of the voltage-gated potassium channel expressed by the nematode
XX worm. The methods are used for identifying and developing compounds that
XX interact with voltage-gated potassium channels of the Kv4 family. The
XX compounds may be used in the development and/or preparation of
XX compositions for pharmaceutical, agrochemical and/or veterinary use.
XX These may be used in preparing compositions for preventing or treating
XX diseases or conditions such as arrhythmia, tachycardia, congestive heart

CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,
CC Alzheimer's disease or Parkinson's disease. The current sequence
CC represents wild-type hkv4.3.
XX
SQ Sequence 655 AA;
Query Match 99.7%; Score 3403; DB 8; Length 655;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAAGVAAWLPFAAAATGMPVANCMPPLAPADKNKQDELIVLVNSGRFQWTTLER 60
Db 1 MAAGVAAWLPFAAAATGMPVANCMPPLAPADKNKQDELIVLVNSGRFQWTTLER 60
Qy 61 YPDTLLGSTEKEFFFNEDTKEVFDKDEVRDPEVFCVLFNFRYTGKLAHYPRYECISAYDELA 120
Db 61 YPDTLLGSTEKEFFFNEDTKEVFDKDEVRDPEVFCVLFNFRYTGKLAHYPRYECISAYDELA 120
Qy 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAFENPHST 180
Db 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAFENPHST 180
Qy 181 LALVFYVVTGFPIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIETVE 240
Db 181 LALVFYVVTGFPIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIETVE 240
Qy 241 YLRLFAAPSRHYRFRISVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVERVERIFKE 300
Db 241 YLRLFAAPSRHYRFRISVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVERVERIFKE 300
Qy 301 SRHSGRLILGYTLKSCASELGLFLSLTMAIIFATVMFYAEKGSASKFTSIASFWY 360
Db 301 SRHSGRLILGYTLKSCASELGLFLSLTMAIIFATVMFYAEKGSASKFTSIASFWY 360
Qy 361 TIVMTTLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVSNFSRIYHONQADKRR 420
Db 361 TIVMTTLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVSNFSRIYHONQADKRR 420
Qy 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALLETGTPEEHNKTTSLIESQHHL 480
Db 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALLETGTPEEHNKTTSLIESQHHL 480
Qy 481 HCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQNCMESSMONTSTRSPSLSSHP 540
Db 481 HCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQNCMESSMONTSTRSPSLSSHP 540
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSSLNKADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSSLNKADG 600
Qy 601 LRPNCKTSQITTAIISITPPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 655
Db 601 LRPNCKTSQITTAIISITPPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 655
RESULT 4
ADD48188
ID ADD48188 standard; protein; 655 AA.
XX ADD48188;
XX 02-DEC-2004 (revised)
XX 29-JAN-2004 (first entry)
XX Rat Protein AAB53321, SEQ ID NO 13886.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX Unidentified.
XX WO2003016475-A2.

XX 27-FEB-2003.
PD 14-AUG-2002; 2002MO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urbo D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; AAB53321.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPRO at
CC ftp.wipro.int/pub/published_pct_sequences.
XX
SQ Sequence 655 AA;
Query Match 99.5%; Score 3396; DB 7; Length 655;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 652; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFARAAAI GMPVANCMPPLAPADKNKRQDELIVLVNSGRFQRTTLER 60
DB 1 MAAGVAAWLPFARAAAI GMPVANCMPPLAPADKNKRQDELIVLVNSGRFQRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEXYFDRDPEVFRVCLNFYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKEXYFDRDPEVFRVCLNFYRTGKLHYPRYECISAYDELA 120
QY 121 YGILPEIIGDCCYEYEDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFPENPHST 180
DB 121 YGILPEIIGDCCYEYEDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFPENPHST 180
QY 181 LALVFFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIPTVE 240
DB 181 LALVFFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIPTVE 240
QY 241 YLLRLFAAPSRFRFIRSVMSIIVVAIMPYIIGLVMTNNEVDVSGAFVTLRVFRVRIEKF 300

DB 241 YLLRLFAAPSRFRFIRSVMSIIVVAIMPYIIGLVMTNNEVDVSGAFVTLRVFRVRIEKF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKSSASAKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKSSASAKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIYSNFSRIYHONRADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIYSNFSRIYHONRADKRR 420
QY 421 AOKKARLARIRVAKTGSNAAYLHRSKXNGLNLEAL ELTGTPEEEMGKTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSNAAYLHRSKXNGLNLEAL ELTGTPEEEMGKTSLIESQHHL 480
QY 481 HCLEKTTGLSYLVDDPLLSVTRSTIKNHEFLDEQMEONCMESMONTYSTRSPSLSSHP 540
DB 481 HCLEKTTGLSYLVDDPLLSVTRSTIKNHEFLDEQMEONCMESMONTYSTRSPSLSSHP 540
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLKADDG 600
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLKADDG 600
QY 601 LRPNCKTSQITTAIISIPPPALPREGESRPPASGPNTNIPISITSNVVKSVL 655
DB 601 LRPNCKTSQITTAIISIPPPALPREGESRPPASGPNTNIPISITSNVVKSVL 655

RESULT 5
ADS16294
ID ADS16294 standard; protein; 655 AA.
XX
AC ADS16294;
DT 02-DEC-2004 (first entry)
XX
DB Human voltage-dependent potassium channel (HsapKv4.3) protein.
XX
KW Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region /note= "Hydrophobic region (S1)"
FT Region 225..248
FT /note= "Hydrophobic region (S2)"
FT Region 254..281
FT /note= "Hydrophobic region (S3)"
FT Region 286..305
FT /note= "Hydrophobic region (S4)"
FT Region 315..343
FT /note= "Hydrophobic region (S5)"
FT Region 355..365
FT /note= "Pore region (P)"
FT Region 374..400
FT /note= "Hydrophobic region (S6)"
XX
PN US2004175761-A1.
XX
PD 09-SEP-2004.
XX
PF 01-MAR-2003; 2003US-00377139.
PR 01-MAR-2003; 2003US-00377139.
XX
PA (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX


```

DB 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAVTLRVRVRIKPF 300
QY 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHONQADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALFETGPEEHEMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALFETGPEEHEMGKTTSLIESQHHL 480
QY 481 HCLEKTTGISYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
DB 481 HCLEKTTGISYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 600
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 600
QY 601 LRPNCKTSOITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655
DB 601 LRPNCKTSOITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655

```

RESULT 7

ABB79585
ID ABB79585 standard; protein; 636 AA.

XX ABB79585;

DT 01-OCT-2002 (first entry)

DE Human Kv4.3 potassium channel (short form).

KM Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KW nootropic; neuroprotective; cardiant; gene therapy.

OS Homo sapiens.

XX US6395477-B1.

PN 28-MAY-2002.

PF 23-OCT-1998; 98US-00178109.

PR 23-OCT-1998; 98US-00178109.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Cockett MI, Dilke DW, Ling HC, Sokol PT;

XX WPI; 2002-556093/59.

DR N-PSDB; ABBN84401.

PT New isolated polynucleotide encoding human Kv4.3 potassium channel
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT diseases.

XX Claim 1; Col 23-26; 19pp; English.

XX The present sequence is the protein sequence of the short isoform of
CC novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been
CC identified: a full-length form (hKv4.3 long) (see ABB79584); and the
CC short form, which has a deletion of 19 amino acids in the carboxy domain
CC after the predicted sixth transmembrane domain (hKv4.3 short). Human
CC heart primarily expresses hKv4.3 long, whereas human brain contains both
CC forms. The invention provides Kv4.3 polypeptides, polynucleotides, and
CC methods for producing these polynucleotides. The Kv4.3 polypeptides and

CC polynucleotides are useful in the diagnosis, treatment and screening of
CC human diseases relating to an excess or deficiency of hKv4.3 activity,
CC including Alzheimer's disease and heart disease

XX Sequence 636 AA;

Query Match 96.7%; Score 3300.5; DB 5; Length 636;
Best Local Similarity 97.1%; Pred. No. 1.4e-309;
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

```

QY 1 MAAGVAAWLPFAPAAAIIGMMPVANCMPPLAPADKNKRODELIVNVSGRRPQTWRTTLER 60
DB 1 MAAGVAAWLPFAPAAAIIGMMPVANCMPPLAPADKNKRODELIVNVSGRRPQTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFPDDEPVEFRVCLNFRTGKHYPRYECSAYDDELAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFPDDEPVEFRVCLNFRTGKHYPRYECSAYDDELAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSPROTMMRAFENPHST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSPROTMMRAFENPHST 180
QY 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPGGERYSVAFCLDTACVMITVE 240
DB 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPGGERYSVAFCLDTACVMITVE 240
QY 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPGGERYSVAFCLDTACVMITVE 240
DB 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAVTLRVRVRIKPF 300
QY 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAVTLRVRVRIKPF 300
DB 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAVTLRVRVRIKPF 300
QY 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHONQADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALFETGPEEHEMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALFETGPEEHEMGKTTSLIESQHHL 480
QY 481 HCLEKTTGISYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
DB 481 HCLEKTTGISYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 600
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 600
QY 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 581
DB 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHQSEQPSLTSSRLNLKADG 581
QY 601 LRPNCKTSOITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655
DB 601 LRPNCKTSOITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655

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RESULT 8

AAW79589
ID AAW79589 standard; protein; 636 AA.

XX AAW79589;

DT 11-JAN-1999 (first entry)

DE Human Kv potassium channel hKv4.3 (shorter isoform).

KM Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis.

OS Homo sapiens.

XX WO9842833-A2.

PN 01-OCT-1998.

XX 01-OCT-1998.

XX 23-MAR-1998; 98WO-EP001901.
XX 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX (SMIK) SMITHKLINE BEECHAM LAB PHARM.
PI Bill AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
XX WPI; 1998-542277/46.
DR N-PSDB; AAV61571.
XX
PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
PS Claim 2; Page 25; 47pp; English.
XX
CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3
CC polynucleotide (see AAV61571), and has 99% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC Kv family related proteins. A longer isoform (see AAW79590) has been
CC identified, which has an additional 19 amino acids inserted between amino
CC acids 487 and 488. The invention relates to hKv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hKv4.3 polypeptides can be used to identify
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilising such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hKv4.3 expression or
CC activity
XX
SQ Sequence 636 AA;
Query Match 96.5%; Score 3291.5; DB 2; Length 636;
Best Local Similarity 96.8%; Pred. No. 1e-308;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFAARAAAGMMPVANCMPPLADKKNKQDELIVNVSGRRFQTWRTTLER 60
DB 1 MAAGVAAWLPFAARAAAGMMPVANCMPPLADKKNKQDELIVNVSGRRFQTWRTTLER 60
QY YPDTLLGSTEKERFFENEDTKYFPFRDPEVRCVLFNFRITGKLTHTPRYECSAYDEBLAF 120
DB 61 YPDTLLGSTEKERFFENEDTKYFPFRDPEVRCVLFNFRITGKLTHTPRYECSAYDEBLAF 120
QY YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSISFRQTMWRAFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSISFRQTMWRAFENPHTST 180
QY LALVFFVYTGFTIAVSVITNVVEITVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTV 240
DB 181 LALVFFVYTGFTIAVSVITNVVEITVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTV 240
QY YLRLFEAAPSRRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRIKF 300
DB 241 YLRLFEAAPSRRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRIKF 300
QY YLRLFEAAPSRRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRIKF 300
DB 241 YLRLFEAAPSRRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRIKF 300
QY SRHSGGRLILGTYLKSCASELGLFLSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSGGRLILGTYLKSCASELGLFLSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
QY TIVMTTLIGYGDWVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORADKR 420
DB 361 TIVMTTLIGYGDWVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORADKR 420
QY AOKKARLARIRVAKTGSNAAYLHSGKNGLNLEALLETGTPEEHMGKTTSLIESQHLL 480
DB 421 AOKKARLARIRVAKTGSNAAYLHSGKNGLNLEALLETGTPEEHMGKTTSLIESQHLL 480

DB 421 AOKKARLARIRVAKTGSNAAYLHSGKNGLNLEALLETGTPEEHMGKTTSLIESQHLL 480
QY HCLEKTGLSYLVDPLSVRTSTIKNHEFIDEQMEFONCMESMONTYPSRPSLSHP 540
DB 481 HCLEKT-----NHEFIDEQMEFONCMESMONTYPSRPSLSHP 521
QY GLTTCCSRRSKKTTHLPNSNLPATRLRSQDELSTTHIQGSEOPSLTTSRSSLNLKADG 600
DB 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSQDELSTTHIQGSEOPSLTTSRSSLNLKADG 581
QY LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNITSNVKVSUL 655
DB 582 LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNITSNVKVSUL 636
RESULT 9
AAW79591
ID AAW79591 standard; protein; 636 AA.
XX
AC AAW79591;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hKv4.3.
XX
KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN W09842833-A2.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-EP001901.
XX
PR 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.
XX
PI Bill AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
XX
DR WPI; 1998-542277/46.
DR N-PSDB; AAV61573.
XX
PS Claim 19; Page 28; 47pp; English.
XX
CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3
CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC Kv family related proteins. hKv4.3 isoforms (see AAW79589 and AAW79590)
CC are also claimed. The invention relates to hKv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hKv4.3 polypeptides can be used to identify
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilising such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hKv4.3 expression or
CC activity
XX
SQ Sequence 636 AA;
Query Match 95.7%; Score 3265.5; DB 2; Length 636;
Best Local Similarity 96.2%; Pred. No. 3.4e-306;

```
Matches 630; Conservative 1; Mismatches 5; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFARAAAIIGMPVANCMPMLAPADKNKRQDELIIVLVNSGRRFQRTWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIIGMPVANCMPMLAPADKNKRQDELIIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRVCLNFRYRTGKLMHYPRYECISAYDDEIAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRVCLNFRYRTGKLMHYPRYECISAYDDEIAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPHTST 180
QY 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTYE 240
DB 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTYE 240
QY 241 YLLRLFAAPSRYRFRIRSVMSIIDVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
DB 241 YLLRLFAAPSRYRFRIRSVMSIIDVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
QY 301 SRHSQGLRLIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPASFWY 360
DB 301 SRHSQGLRLIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPASFWY 360
QY 361 TIVTMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVIVSNFRSRIYHONORADKRR 420
DB 361 TIVTMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVIVSNFRSRIYHONORADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYIHSKRNGILNEALELTGPBEEHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYIHSKRNGILNEALELTGPBEEHMGKTTSLIESQHHL 480
QY 481 HCLEKTGSLVDDPLLVSRTSTIKNHFIDEQMFEOQNCMESSMOWYPPSTRPSLSHP 540
DB 481 HCLEKT-----NHFIDEQMFEOQNCMESSMOWYPPSTRPSLSHP 521
QY 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSINLKADGG 600
DB 522 GLTTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSINLKADGG 581
QY 601 LRPNCKTSQTTTAIISITPPALTPGEGSRPPPASPGPNTNIPISITSNVVXVSVL 655
DB 582 LRPNCKTSQTTTAIISITPPALTPGEGSRPPPASPGPNTNIPISITSNVVXVSVL 636
RESULT 10
ADE61252
ID ADE61252 standard; protein; 611 AA.
XX
AC ADE61252;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAA80459, SEQ ID NO 7170.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
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PA (FARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI, 2003-268312/26.
DR GENBANK; AAA80459.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences.
XX
SQ Sequence 611 AA;
Query Match 89.0%; Score 3035.5; DB 7; Length 611;
Best Local Similarity 96.2%; Pred. No. 5.8e-284;
Matches 584; Conservative 2; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFARAAAIIGMPVANCMPMLAPADKNKRQDELIIVLVNSGRRFQRTWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIIGMPVANCMPMLAPADKNKRQDELIIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRVCLNFRYRTGKLMHYPRYECISAYDDEIAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRVCLNFRYRTGKLMHYPRYECISAYDDEIAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEFENPHTST 180
QY 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTYE 240
DB 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTYE 240
QY 241 YLLRLFAAPSRYRFRIRSVMSIIDVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
DB 241 YLLRLFAAPSRYRFRIRSVMSIIDVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
QY 301 SRHSQGLRLIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPASFWY 360
DB 301 SRHSQGLRLIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPASFWY 360
QY 361 TIVTMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVIVSNFRSRIYHONORADKRR 420
DB 361 TIVTMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVIVSNFRSRIYHONORADKRR 420
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```
QY 421 AOKKARLARIRVAKTSSSNAYLHSGKNGLINEALELTGTPEEEMGKTTSLIESQHLL 480
D 421 AOKKARLARIRVAKTSSSNAYLHSGKNGLINEALELTGTPEEEMGKTTSLIESQHLL 480
QY 481 HCLEKTTGLSYLVDDPLLSVTRSTIKNHEFIDEQMFQONCMESMOMNYPTRSPSLSSHP 540
D 481 HCLEKTT-----NHEFIDEQMFQONCMESMOMNYPTRSPSLSSHS 521
QY 541 GLTTTCCSRSSKTTTHLPNSNLPATRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADDG 600
D 522 GLTTTCCSRSSKTTTHLPNSNLPATRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADDG 581
QY 601 LRPNCKT 607
D 582 LRPNCKT 588

RESULT 11
ADM10929
ID ADM10929 standard; protein; 630 AA.
XX
AC ADM10929;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue protein #4.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KM cytosolic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PE 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR MPI; 2003-901037/82.
DR N-PSDB; ADM10923.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 260; 221pp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytosolic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
```

```
XX
SQ Sequence 630 AA;
QY 1 MAGVAAWLPFAAAAGMMPVANCMPPLAPADKNR-QDELIVLVNSGRFQWRTTLE 59
D 1 MAAGVAAWLPFAAAAGMMPVASCMPAPRQERKTQDALIVLVNSGTRFQWQDTLE 60
QY 60 RYPDTLLGSTEKEFEFNEDTKEYEFDPRDPEVRCVINEFYRTGKLHYPRYECISAYDELA 119
D 61 RYPDTLLGSSERDFYHPEEQYFPRDPDIFRHILNFRYRTGKLHYPRHECISAYDELA 120
QY 120 FYGLIPEIIGDCCYEYEDRKRENAERLMDNDSENNOES-MPSLSFRQTMRAFENPHT 178
D 121 FFGIPEIIGDCCYEYEDRRRENAERLQDDADDTGAGESALPTMTARQVWRAFENPHT 180
QY 179 STALVFFYYVTGFFIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
D 181 STMALVFFYYVTGFFIAVSIVANVETVPCGSPGHAKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRYPRIKSVMSIIDVVAIMPYIIGLVMTNNEVDVSGAVTLRVFRVRI 297
D 241 TVEYLRLFAAPSRYPRIKSVMSIIDVVAIMPYIIGLVMTNNEVDVSGAVTLRVFRVRI 300
QY 298 FKFSRHSQGLRILGYTLKSCASEGLFLPSLTMAIIFATVWFYAEKSSASKFTSIPAS 357
D 301 FKFSRHSQGLRILGYTLKSCASEGLFLPSLTMAIIFATVWFYAEKSSASKFTSIPAA 360
QY 358 FWYITVMTTIGYDWPVKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHQNRAD 417
D 361 FWYITVMTTIGYDWPVKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHQNRAD 420
QY 418 KRRACKARLARIRVAKTSSSNAYLHSGKNGLINEALELTGTPEEEMGKTTSLIESQH 477
D 421 KRRACKARLARIRVAKTSSSNAYLHSGKNGLINEALELTGTPEEEMGKTTSLIESQH 479
QY 478 HLHCLEKTTGLSYLVDDPLLSVTRSTIKNHEFIDEQMFQONCMESMOMNYPTRSPSL 537
D 480 HLHCLEKTT-----NHEFIDEQMFQONCMESMOMNYPTRSPSL 520
QY 538 SHPGITTTCCSRSSKTTTHLPNSNLPATRLRSMOELSTIHIQSEOPSLTTSRSSLNLR 597
D 521 SQQGVSTCCSRRHAKTFRIPANVSGSHQSGISQELSTIQICVERTPLSNSRSSLNLR 580
QY 598 DDGLRPNCKTSQITTAIISIPTPALTPGESRP--PPASPEPNTNIPDITSNVYKSVL 655
D 581 EBCVKLNCEQYVTTAIIISIPTPVTPGDDRPSPSPESVSGC-----NIVRVSA 630

RESULT 12
ADM10928
ID ADM10928 standard; protein; 630 AA.
XX
AC ADM10928;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue protein #3.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KM cytosolic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PE 05-FEB-2003; 2003US-00361811.
XX
```

10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
XX
DR WPI: 2003-901037/82.
N-PSDB; ADM10922.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 259; 221bp; English.
XX
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 630 AA;

Query Match 73.2%; Score 2498.5; DB 7; Length 630;
Best Local Similarity 73.6%; Pred. No. 5.5e-232;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

QY 1 MAAVAAWLPFAAALIGMMPVANCMPPLAPADKNKR-QDELIIVANSGRRPQTWRTTLE 59
DB 1 MAAVAAWLPFAAALIGMMPVANCMPPLAPADKNKR-QDELIIVANSGRRPQTWRTTLE 60
QY 60 RYDDTLGSTEKEFFENEDTKKEYFFDRDPEVFRVNLNFRYTGKLAHYRRECIASAYDEELA 119
DB 61 RYDDTLGSSERDPFYHPEYQYFFDRDPDI FRHILNFRYTGKLAHYRRECIASAYDEELA 120
QY 120 FYGLPEITIGDCYEEYKDRKRNARLMDNDSENNQES-MPSLSRQTMRAFENPHT 178
DB 121 FFGILPEITIGDCYEEYKDRRRENAERLQDDADDTAGESALPTMTARQVRWRAFENPHT 180
QY 179 STLALVFYVYTGFFIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
DB 181 STMALVFYVYTGFFIAVSVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRRYRFRIRSVNSIIDVVAIMPYIGLVMTNEDVSGAFVTLRFRVPR 297
DB 241 TVEYLRLFAAPSRRYRFRIRSVNSIIDVVAIMPYIGLVMTNEDVSGAFVTLRFRVPR 300
QY 298 FKFSRHSQGLRIIGYTLKSCASBLGFLFSLTMAIIFATWFFYAEKSSASAKFTSIPAS 357
DB 301 FKFSRHSQGLRIIGYTLKSCASBLGFLFSLTMAIIFATWFFYAEKSSASAKFTSIPAS 360
QY 358 FWYTIIVMTTLGYGDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVNSFRIYHONORAD 417
DB 361 FWYTIIVMTTLGYGDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVNSFRIYHONORAD 420
QY 418 KRAAOKKARLARIRVAKTGSNAVYLHSGKNGLLNEALLETGTPEEEMGKTTSLIESQHA 477
DB 421 KRAAOKKARLARIRVAKTGSNAVYLHSGKNGLLNEALLETGTPEEEMGKTTSLIESQHA 479

QY 478 HLHLCLEKTTGLSYLVDDPLLSVTRSTIKNHEFIDEQMFQONCESSMONTYSTRSPSL 537
DB 480 HLHLCLEKTT-----NHEFVDEQVFEESCEVATVPRPSSHSPSL 520
QY 538 SHPGLTTCCSRRSKTTTHLPNSNLPATRLASMOELSTIHIQSEQPSLTSSRLNLKA 597
DB 521 SQQGVSTCCSRRHKTFRIPNANVSGSHQSIQELSTIQRVETRTPLSNRSSLNAXM 580
QY 598 DDGLRPNCKTSQITTAIISIPTPPALTPGESRP--PPASGPNTNIPSTSNVYKSVL 655
DB 581 EECVKLNCEQPYVTTAIISIPTPPTPEGDDRPESPEYSG-----NIVRVSA 630

RESULT 13

ADM10930
ID ADM10930 standard; protein; 630 AA.
XX
AC ADM10930;
XX
XX 20-MAY-2004 (first entry)
XX
DT Human O64BSgenomicContig_ORF protein.
XX
DE
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cytostatic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX

PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
XX
DR WPI: 2003-901037/82.
DR N-PSDB; ADM10931.

XX
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 261; 221bp; English.
XX
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 630 AA;

Query Match 73.2%; Score 2498.5; DB 7; Length 630;
Best Local Similarity 73.6%; Pred. No. 5.5e-232;

	Matches	486;	Conservative	69;	Mismatches	70;	Indels	35;	Gaps	7;									
Qy	1	MAAGVAAWLP	PARAAAI	GMPVANC	PMPLAD	KNKR-Q	DELI	IVLVNS	GRRFQ	WRTTLE	59								
Db	1	MAGVAAWLP	PARAAAI	GMPVASC	PMPLAD	KNKR-Q	DELI	IVLVNS	GRRFQ	WRTTLE	60								
Qy	60	RYPDILLG	STEKEEFF	FNEDTKE	YFEDR	DEVE	RCV	LNFR	YRTG	KLHYPR	YECISAYDELA	119							
Db	61	RYPDILLG	SSERDFF	FYHPETQ	YFEDR	DPDI	FRHIL	NFYRTG	KLHYPR	HECISAYDELA	120								
Qy	120	FYGLIPEI	IGDCYEE	YKDRKRE	NAERLMD	NDSEN	NOES-M	SLSP	FRQTM	RAFENPHT	178								
Db	121	FYGLIPEI	IGDCYEE	YKDRKRE	NAERLMD	NDSEN	NOES-M	SLSP	FRQTM	RAFENPHT	180								
Qy	179	STLALV	FYYVTG	FFIAVS	VITNV	ETVPC	GTVP	GS-K	ELP	CGERY	SVAF	FCLDTACVMIF	237						
Db	181	STMALV	FYYVTG	FFIAVS	VIANV	ETVPC	GTVP	GS-K	ELP	CGERY	SVAF	FCLDTACVMIF	240						
Qy	238	TVEYLRL	FAAPSR	YRFR	IRSVMS	IIDVVA	IMPYI	GLVMT	NEDV	SGAF	VTLR	RVFRVRI	297						
Db	241	TVEYLRL	FAAPSR	YRFR	IRSVMS	IIDVVA	IMPYI	GLVMT	NEDV	SGAF	VTLR	RVFRVRI	300						
Qy	298	FKFSRH	SOGLRI	LGTYLKS	CASE	LGFLL	FSLTMA	II	FATW	FYA	EKGSS	ASAKFTSIPAS	357						
Db	301	FKFSRH	SOGLRI	LGTYLKS	CASE	LGFLL	FSLTMA	II	FATW	FYA	EKGSS	ASAKFTSIPAA	360						
Qy	358	FWYTI	VTMTL	GYGDM	VPKTI	AGKI	FGS	ICSL	SGVL	VIAL	PVPVI	VSNS	RIYHQ	NO	RAD	417			
Db	361	FWYTI	VTMTL	GYGDM	VPKTI	AGKI	FGS	ICSL	SGVL	VIAL	PVPVI	VSNS	RIYHQ	NO	RAD	420			
Qy	418	KRRAQ	KARLAR	IRVAK	TGSS	SNAYL	SKRNL	NEAL	ELT	GTPE	EEH	MKTSL	IESQ	HH	477				
Db	421	KRRAQ	KARLAR	IRVAK	TGSS	SNAYL	SKRNL	NEAL	ELT	GTPE	EEH	MKTSL	IESQ	HH	479				
Qy	478	HLHCL	EKTG	LSYV	DDPL	LSV	RTST	IKN	HEF	ID	EQM	FEON	CMESS	MONY	PSTR	PSLS	537		
Db	480	HLHCL	EKTG	LSYV	DDPL	LSV	RTST	IKN	HEF	ID	EQM	FEON	CMESS	MONY	PSTR	PSLS	520		
Qy	538	SHPGL	TTTCC	SRRSK	TTTHL	PNSNL	PATRL	RS	MOE	LSTI	HIQ	SE	QPS	LTT	SRSS	SLNLKA	597		
Db	521	SOQGT	STCC	SRRH	KKTFR	IPNAV	SGS	HQ	SIQ	ELSTI	QIR	CV	ERT	PL	SN	RS	SLNLAKM	580	
Qy	598	DDGL	RPNCK	TQIT	TAIS	IPT	PAL	TE	GES	RP--	PPAS	PG	PN	TN	PS	ITS	NV	KVSVL	655
Db	581	EECV	KLNC	EQP	VTTA	ISIP	TP	PVT	T	PEG	DR	PES	BE	YS	GG--	NIV	RVS	AL	630

RESULT 14

ADM10927	ID	ADM10927	standard; protein; 630 AA.
XX	AC	ADM10927;	
XX	DT	20-MAY-2004	(first entry)
XX	DE	Human O647S	genomicContig3 homologue protein #2.
XX	KW	ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;	
XX	KW	cytostatic; gene therapy; human; ds.	
XX	OS	Homo sapiens.	
XX	PN	US2003206918-A1.	
XX	PD	06-NOV-2003.	
XX	PF	05-FEB-2003; 2003US-00361811.	
XX	PR	10-SEP-1999; 99US-00394374.	
XX	PR	01-MAY-2000; 2000US-00561778.	
XX	PR	15-AUG-2000; 2000US-00640173.	
XX	PR	07-SEP-2000; 2000US-00656668.	
XX	PR	14-NOV-2000; 2000US-00713550.	

RESULT 14

ADMI0927	ID	ADMI0927	standard; protein; 630 AA.
XX	AC	ADMI0927;	
XX	DT	20-MAY-2004	(first entry)
XX	DE	Human O647S	genomicContig3 homologue protein #2.
XX	KW	ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;	
XX	OS	cytostatic; gene therapy; human; ds.	
XX	PN	Homo sapiens.	
XX	PD	US2003206918-A1.	
XX	PF	06-NOV-2003.	
XX	PR	05-FEB-2003; 2003US-00361811.	
XX	PR	10-SEP-1999; 99US-00394374.	
XX	PR	01-MAY-2000; 2000US-00561778.	
XX	PR	15-AUG-2000; 2000US-00640173.	
XX	PR	07-SEP-2000; 2000US-00656668.	
XX	PR	14-NOV-2000; 2000US-00713550.	

PR	03-APR-2001; 2001US-00825294.
PR	02-OCT-2001; 2001US-00970966.
PR	02-AUG-2002; 2002US-00212677.
XX	
PA	(CORI-) CORIXA CORP.
PI	Fanger GR, Fling SP;
XX	
DR	WPI; 2003-901037/82.
XX	N-PSDB; ADM10921.
PT	New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
XX	
PS	Example 12; SEQ ID NO 258; 221pp; English.
CC	
CC	This invention describes a novel ovarian tumour protein which can be used to detecting the presence of an ovarian cancer in a patient by
CC	stimulating and/or expanding T cells specific for the tumor protein. The
CC	products of the invention can also be used in a method to inhibit the
CC	development of a cancer in a patient comprising (a) incubating CD4+
CC	and/or CD8+ T cells isolated from a patient with at least one ovarian
CC	tumor protein, such that T cell proliferate and (b) administering to the
CC	patient the proliferated T cells. The cytostatic polynucleotides or
CC	polypeptides described in the invention are useful for treating or
CC	inhibiting the development of cancer, particularly ovarian cancer and for
CC	stimulating and/or expanding T cells specific for a tumour protein or for
CC	gene therapy.
XX	
XX	
XX	Sequence 630 AA;
Qy	Query Match
Db	Best Local Similarity 73.2%; Score 2498.5; DB 7; length 630;
Qy	Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;
1	MAAGVAAWLPFARAAAI
1	MAAGVAAWLPFARAAAI
60	RYPDITLGGSTEKEFFENEDTKEYPFRDPDEVRFCV
61	RYPDITLGGSSERDFFYHPETQYFPRDPDIFRHI
120	FYGLIPEIIGDCYEEYKDRKRENAERLMDNDSEN
121	FYGLIPEIIGDCYEEYKDRKRENAERLMDNDSEN
179	STLALVFFYYVTGFFIAVS
181	STMALVFFYYVTGFFIAVS
238	TVEYLRLFAAPSR
241	TVEYLRLFAAPSR
298	FKFSRHSGGLRIILGYTLKSCASELGFLLFSLTMA
301	FKFSRHSGGLRIILGYTLKSCASELGFLLFSLTMA
358	FWYTIVTMTLGYGDMVPKTIAGKIFG
361	FWYTIVTMTLGYGDMVPKTIAGKIFG
418	KRPAQKKARLARIRVAKTGSSNAYLH
421	KRPAQKKARLARIRVAKTGSSNAYLH
478	HLHCL
480	HLHCL
538	SHPGLTTTCCSRRSKTTTHLPNSNLPATRLRS


```

Db      521  SGGVSTSTCCSRHKKTERIRINANVSGSHQSGIQELSTQIRCVERTPLSNRSSLNAKM 580
QY      598  DDGLRPNCCKTSQITTAIISIPTPPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 655
      581  BECVKLNCEQPYVTTAIISIPTPPVTTPGEDDRPESPEYSGG-----NIVRSAL 630

RESULT 15
ADJ11257
ID      ADJ11257 standard; protein; 630 AA.
XX
AC      ADJ11257;
XX
DT      15-APR-2004 (first entry)
XX
DE      Human ovarian tumour antigen polypeptide SegID 258.
XX
KW      human; ovarian cancer; immunogenic; antibody; antigen presenting cell;
XX      APC; immune system cell; T cell; tumourigenic; cytostatic.
XX      Homo sapiens.
XX      OS
XX      US2003232056-A1.
XX      PD
XX      18-DEC-2003.
XX
PF      14-FEB-2003; 2003US-00369186.
XX
PR      10-SEP-1999; 99US-00394374.
XX      PR
XX      01-MAY-2000; 2000US-00561778.
XX      PR
XX      15-AUG-2000; 2000US-00640173.
XX      PR
XX      07-SEP-2000; 2000US-00656668.
XX      PR
XX      14-NOV-2000; 2000US-00713550.
XX      PR
XX      03-APR-2001; 2001US-00825294.
XX      PR
XX      02-OCT-2001; 2001US-00970966.
XX      PR
XX      02-AUG-2002; 2002US-00212677.
XX      PR
XX      05-FEB-2003; 2003US-00361811.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Fanger GR, Fling SP;
XX
DR      WPI; 2004-178717/17.
XX      DR
XX      N-PSDB; ADJ11251.
XX
XX
PT      Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT      polypeptide, useful as probes of primers for detecting presence of cancer
PT      in a patient.
XX
XX
PS      Example 12; SEQ ID NO 258; 222bp; English.
XX
XX
CC      This invention relates to novel isolated polynucleotides and methods for
CC      the therapy and diagnosis of cancer, particularly ovarian cancer.
CC      Specifically, it refers to these polynucleotides and the encoded
CC      polypeptides thereof, as well as immunogenic peptides, antibodies,
CC      antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC      that are targeted to those cells expressing the proteins of interest. The
CC      present invention describes methods that are useful for stimulating and/
CC      or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC      therapy). Furthermore, compositions can be used for the diagnosis,
CC      treatment and/ or prevention of ovarian cancer by stimulating an immune
CC      response in a patient. Accordingly, these compositions exhibit cytostatic
CC      activity. This polypeptide is a human ovarian tumour antigen protein
CC      sequence given in an exemplification of the invention.
XX
SQ      Sequence 630 AA;

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Query Match      73.2%; Score 2498.5; DB 8; Length 630;
Best Local Similarity 73.6%; Pred. No. 5.5e-232;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

QY 1 MAAGVAAMLFPARAALIGMPPVANCMPMLAPADKNKR-QDELIIVLVSGRRPQTWRTTLE 59

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Db      1  MAAGVAAMLFPARAALIGMPPVASCMPAPRQERKRTQDALIIVLVSGRRPQTWRTTLE 60
QY      60  RYPTLLGSTEKEFEFFNEDTKEYFPDRDPEVRCVLNFRYTGKLYPRYECISAYDELA 119
      61  RYPTLLGSSERDFYHPEYQYFFDRDPDIFRHILNFRYTGKLYPRHBCISAYDELA 120
QY      120  FYGILPEIIGDCCYBEYKDRKRENAERLMDNDSNNQES-MBLSFRQTMRAFENPHT 178
Db      121  FFGILPEIIGDCCYBEYKDRKRENAERLMDNDSNNQES-MBLSFRQTMRAFENPHT 180
QY      179  STLALVFYVTGFFIAVSVTNVTWPCGTVPGS-KELPCGSEYSAVAFPLDTACVMIF 237
Db      181  STMALVFYVTGFFIAVSVTNVTWPCGTVPGS-KELPCGSEYSAVAFPLDTACVMIF 240
QY      238  TVEYLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVGAFTLRVFRVRI 297
Db      241  TVEYLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVGAFTLRVFRVRI 300
QY      298  FKFSRHQGLRIIGYTLKSCASELGFLLFSLTMAIIFPATVMFYAEKGSASKFTSIPAS 357
Db      301  FKFSRHQGLRIIGYTLKSCASELGFLLFSLTMAIIFPATVMFYAEKGSASKFTSIPAS 360
QY      358  FWYTIWMTTLGYGDMVPKTIAGKIFGSGISLGLVLVIALPVPIVSNFSRIYHQNORAD 417
Db      361  FWYTIWMTTLGYGDMVPKTIAGKIFGSGISLGLVLVIALPVPIVSNFSRIYHQNORAD 420
QY      418  KRAQKKARLARIRVAKTSSNAYLHSKRNGLINLEALELTGTPEEHMGKTSLSIESQHH 477
Db      421  KRAQKKARLARIRVAKTSSNAYLHSKRNGLINLEALELTGTPEEHMGKTSLSIESQHH 479
QY      478  HLHCLKEXTGLSYLVDDPLLVSRTSTIKNHEFIDEQMFQONCESSMOMYPSTRSPSL 537
Db      480  HLHCLKEXTGLSYLVDDPLLVSRTSTIKNHEFIDEQMFQONCESSMOMYPSTRSPSL 530
QY      538  SHPGLTTCCSRRSKKTTHLPNSNLPATRLRMQELSTIHIQSEBPSTLTSRSSSLNKA 597
Db      521  SGGVSTSTCCSRHKKTERIRINANVSGSHQSGIQELSTQIRCVERTPLSNRSSLNAKM 580
QY      598  DDGLRPNCCKTSQITTAIISIPTPPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 655
      581  BECVKLNCEQPYVTTAIISIPTPPVTTPGEDDRPESPEYSGG-----NIVRSAL 630

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Search completed: April 6, 2005, 06:53:18
Job time : 501.211 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 07:13:52 ; Search time 455.608 Seconds
(without alignments)
477.292 Million cell updates/sec

Title: US-10-062-879-2
Perfect score: 3412
Sequence: 1 MAAGVAAWLPFARAAGMM.....PGPNTNIPSTSNVXSVL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3412	100.0	655	US-10-062-879-2	Sequence 2, Appli
2	3395	99.5	655	US-10-377-139-6	Sequence 6, Appli
3	3300.5	96.7	636	US-10-062-879-4	Sequence 4, Appli
4	2498.5	73.2	630	US-10-212-677-258	Sequence 258, App
5	2498.5	73.2	630	US-10-212-677-259	Sequence 259, App
6	2498.5	73.2	630	US-10-212-677-260	Sequence 260, App
7	2498.5	73.2	630	US-10-212-677-261	Sequence 261, App
8	2498.5	73.2	630	US-10-361-811-258	Sequence 259, App
9	2498.5	73.2	630	US-10-361-811-259	Sequence 260, App
10	2498.5	73.2	630	US-10-361-811-260	Sequence 261, App
11	2498.5	73.2	630	US-10-361-811-261	Sequence 258, App
12	2498.5	73.2	630	US-10-369-186-258	Sequence 259, App
13	2498.5	73.2	630	US-10-369-186-259	Sequence 259, App

14	2498.5	73.2	630	US-10-369-186-260	Sequence 260, App
15	2498.5	73.2	630	US-10-369-186-261	Sequence 261, App
16	2113	61.9	647	US-10-296-115-1112	Sequence 1112, Ap
17	2102	61.6	646	US-10-121-746-10	Sequence 10, Appli
18	825	24.2	255	US-10-212-677-257	Sequence 257, App
19	825	24.2	255	US-10-361-811-257	Sequence 257, App
20	825	24.2	255	US-10-361-811-257	Sequence 257, App
21	767	22.5	806	US-09-833-466-13	Sequence 13, Appli
22	767	22.5	806	US-10-199-869-6	Sequence 6, Appli
23	767	22.5	806	US-10-815-297-13	Sequence 1482, Ap
24	755.5	22.1	911	US-10-408-765A-1482	Sequence 20, Appli
25	748.5	21.9	985	US-10-154-086-20	Sequence 12, Appli
26	742.5	21.8	854	US-09-833-466-12	Sequence 5, Appli
27	742.5	21.8	854	US-10-199-869-5	Sequence 12, Appli
28	742.5	21.8	854	US-10-815-297-12	Sequence 5, Appli
29	741	21.7	857	US-10-377-139-5	Sequence 4, Appli
30	726.5	21.3	656	US-10-377-139-4	Sequence 13, Appli
31	724	21.2	539	US-10-325-891-13	Sequence 2, Appli
32	721.5	21.1	456	US-09-993-811-2	Sequence 175, App
33	721.5	21.1	456	US-09-974-712-2	Sequence 4, Appli
34	721.5	21.1	456	US-09-989-920-175	Sequence 27, Appli
35	721.5	21.1	456	US-10-254-010-4	Sequence 8, Appli
36	721	21.1	539	US-09-804-014A-27	Sequence 18, Appli
37	721	21.1	539	US-09-804-014A-8	Sequence 766, App
38	720.5	21.1	601	US-10-121-746-4	Sequence 29, Appli
39	718	21.0	599	US-10-403-161-18	Sequence 75, Appli
40	715	21.0	499	US-10-322-281-766	Sequence 33, Appli
41	714.5	20.9	425	US-09-804-014A-29	Sequence 32, Appli
42	714.5	20.9	425	US-09-804-014A-75	Sequence 2015, Ap
43	714	20.9	525	US-09-804-014A-33	
44	713.5	20.9	523	US-09-804-014A-32	
45	713.5	20.9	523	US-10-408-765A-2015	

ALIGNMENTS

RESULT 1
US-10-062-879-2
Sequence 2, Application US/10062879
Publication No. US20020127649A1
GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Hui-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/10/062, 879
PRIOR APPLICATION NUMBER: 2002-01-31
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 655
TYPE: PRT
ORGANISM: human
US-10-062-879-2

Query Match 100.0%; Score 3412; DB 13; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.3e-283;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGVAAWLPFARAAGMMVPVNCMPPLAPADKXKRQDELIVLVNLSGRRFQRTTLER 60
DB 1 MAAGVAAWLPFARAAGMMVPVNCMPPLAPADKXKRQDELIVLVNLSGRRFQRTTLER 60
QY YPDTLLGSTEKEFFFNEDTKEXFFDRDPEVFRVCVNFYRTGKLHYPRYECISAYDDELAF 120
DB YPDTLLGSTEKEFFFNEDTKEXFFDRDPEVFRVCVNFYRTGKLHYPRYECISAYDDELAF 120

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Db 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIFTV 240
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QY 241 YLRLFAAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
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Db 241 YLRLFAAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
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Db 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFRIYHQNRADKRR 420
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QY 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALELGTPEEHEMGKTTSLIESQHHL 480
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Db 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALELGTPEEHEMGKTTSLIESQHHL 480
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QY 481 HCLEKTGSLVLDPLSVRTSTIKNHEFIDEQMFQNCMESSMONTPTSTRPSLSHP 540
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Db 481 HCLEKTGSLVLDPLSVRTSTIKNHEFIDEQMFQNCMESSMONTPTSTRPSLSHP 540
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QY 541 GLTTCCSRRSKKTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTSTRSSINLKADG 600
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Db 541 GLTTCCSRRSKKTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTSTRSSINLKADG 600
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QY 601 LRPNCKTSQITTAIISIPTPPALTPGESRPPASPGPNTNIPSTISNVKSVL 655
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Db 601 LRPNCKTSQITTAIISIPTPPALTPGESRPPASPGPNTNIPSTISNVKSVL 655
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RESULT 2
US-10-377-139-6

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; Sequence 6, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-139-6
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Query Match 99.5%; Score 3395; DB 16; Length 655;
Best Local Similarity 99.7%; Pred. No. 3.7e-282;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MAAGVAAWLPFAAAAIGMPVANCMPPLAPADKNKQDELIVLVNSGRRFQWRTTLER 60
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Db 1 MAAGVAAWLPFAAAAIGMPVANCMPPLAPADKNKQDELIVLVNSGRRFQWRTTLER 60
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QY 61 YPDTLLGSTEKEKFFFNEDTKKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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Db 61 YPDTLLGSTEKEKFFFNEDTKKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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QY 121 YGILPEIIGDCCEEYKDRKRENAERLMDNDSENNOESMPSLSFROTMMRAFENPHTST 180
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Db 121 YGILPEIIGDCCEEYKDRKRENAERLMDNDSENNOESMPSLSFROTMMRAFENPHTST 180
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QY 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIFTV 240
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Db 181 LALVFYVYTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIFTV 240
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QY 241 YLRLFAAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
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Db 241 YLRLFAAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
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Db 301 SRHSQGLRILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSASAKFTSIPASFWY 360
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QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFRIYHQNRADKRR 420
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Db 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFRIYHQNRADKRR 420
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QY 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALELGTPEEHEMGKTTSLIESQHHL 480
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Db 421 AOKKARLARIRVAKTSSNAVYLSKRNGLNEALELGTPEEHEMGKTTSLIESQHHL 480
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|
|
QY 481 HCLEKTGSLVLDPLSVRTSTIKNHEFIDEQMFQNCMESSMONTPTSTRPSLSHP 540
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Db 481 HCLEKTGSLVLDPLSVRTSTIKNHEFIDEQMFQNCMESSMONTPTSTRPSLSHP 540
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QY 541 GLTTCCSRRSKKTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTSTRSSINLKADG 600
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Db 541 GLTTCCSRRSKKTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTSTRSSINLKADG 600
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QY 601 LRPNCKTSQITTAIISIPTPPALTPGESRPPASPGPNTNIPSTISNVKSVL 655
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RESULT 3
US-10-062-879-4

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; Sequence 4, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang, Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-10-062-879-4
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Query Match 96.7%; Score 3300.5; DB 13; Length 636;
Best Local Similarity 97.1%; Pred. No. 4.6e-274;
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

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Db 1 MAAGVAAWLPFAAAAIGMPVANCMPPLAPADKNKQDELIVLVNSGRRFQWRTTLER 60
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|
Db 61 YPDTLLGSTEKEKFFFNEDTKKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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|
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QY 121 YGILPEIIGDCCEEYKDRKRENAERLMDNDSENNOESMPSLSFROTMMRAFENPHTST 180
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|
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Db 121 YGILPEIIGDCCEYKORRENAERLMDNDSENNOESMPSLSFRQTMWRAFENPHST 180
QY 181 LALVEYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIFTE 240
Db 181 LALVEYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIFTE 240
QY 241 YLRLFAAPSRYRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVRFRVRIEKF 300
Db 241 YLRLFAAPSRYRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVRFRVRIEKF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPASFWY 360
Db 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADRR 420
Db 361 TIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADRR 420
QY 421 AOKKARLARIRAKTGSSNAYLHSCRNGLINEALELGTPEEBHMGKTSLSIESQHLL 480
Db 421 AOKKARLARIRAKTGSSNAYLHSCRNGLINEALELGTPEEBHMGKTSLSIESQHLL 480
QY 481 HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSH 540
Db 481 HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSH 540
QY 541 GLTTCCSRRSKKTTHLPNSNLPAIRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPAIRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADG 600
QY 582 GLTTCCSRRSKKTTHLPNSNLPAIRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADG 581
Db 582 GLTTCCSRRSKKTTHLPNSNLPAIRLRSMOELSTIHIQSEOPSLTTSRSSLNLRADG 581
QY 601 LRPNCKTSQITTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 655
Db 601 LRPNCKTSQITTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 655
QY 582 LRPNCKTSQITTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 636
Db 582 LRPNCKTSQITTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 636

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RESULT 4
US-10-212-677-258
; Sequence 258, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; NUMBER OF SEQ ID NOS: 2002-08-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-258

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Query Match 73.2%; Score 2498.5; DB 14; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;
QY 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNKR-ODELIVLVNSGRRFQWRRTTLE 59
Db 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNKR-ODELIVLVNSGRRFQWRRTTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKEYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 60 RYPTLLGSTEKEFFFNEDTKEYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
QY 61 RYPTLLGSEBRDFYHPEETOQYFFDRDPDIFRHILNFRYRTGKLHYPRHECISAYDELA 120
Db 61 RYPTLLGSEBRDFYHPEETOQYFFDRDPDIFRHILNFRYRTGKLHYPRHECISAYDELA 120
QY 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 178
Db 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 178
QY 121 FFGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 180
Db 121 FFGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 180

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QY 179 STLALVEYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STMALVEYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRYRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVRFRVRI 297
Db 241 TVEYLRLFAAPSRYRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVRFRVRI 300
QY 298 FKPSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 357
Db 301 FKPSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 360
QY 358 FWYITVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORAD 417
Db 361 FWYITVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRAOKKARLARIRAKTGSSNAYLHSCRNGLINEALELGTPEEBHMGKTSLSIESQH 477
Db 421 KRAOKKARLARIRAKTGSSNAYLHSCRNGLINEALELGTPEEBHMGKTSLSIESQH 479
QY 478 HLCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSL 537
Db 480 HLCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSL 520
QY 538 SHPGLTTCCSRRSKKTTHLPNSNLPAIRLRSMOELSTIHIQSEOPSLTTSRSSLNLRAD 597
Db 521 SQQGVSTCCSRRHKKTFRIPNANVSGSHOGSIQELSTIQICVERTPLSNSRSSLNLRAD 580
QY 598 DDGLRPNCKTSQITTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 655
Db 581 EECVKNLCEQEPVTTTAIISIPPPALTPGEGSRPPASPGPNTNITSITSNVKVSVL 630

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RESULT 5
US-10-212-677-259
; Sequence 259, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; NUMBER OF SEQ ID NOS: 2002-08-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-259

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Query Match 73.2%; Score 2498.5; DB 14; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;
QY 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNKR-ODELIVLVNSGRRFQWRRTTLE 59
Db 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNKR-ODELIVLVNSGRRFQWRRTTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKEYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 60 RYPTLLGSTEKEFFFNEDTKEYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
QY 61 RYPTLLGSEBRDFYHPEETOQYFFDRDPDIFRHILNFRYRTGKLHYPRHECISAYDELA 120
Db 61 RYPTLLGSEBRDFYHPEETOQYFFDRDPDIFRHILNFRYRTGKLHYPRHECISAYDELA 120
QY 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 178
Db 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 178
QY 121 FFGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 180
Db 121 FFGLPEIIGDCCEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWRAFENPH 180

```

QY	179	STLALVYVVYVGTGFPIAVSVYITNVVEVTPCGIVPGS-KELPCGERYSVAEFLDTRACVMIF	237
Db	181	STMALVFYVYVGTGFPIAVSVIANVVEVTPCGSSPGHIELPCGERYAVAEFLDTRACVMIF	240
QY	238	TVEYLRLFAAPSRRYRFRFIRSVMSIIDVVAIMPYIIGVWMTNNEDEVSGAFVTLRVFRVERI	297
Db	241	TVEYLRLFAAAPSRRYRFRFIRSVMSIIDVVALPYIIGVWMTNNEDEVSGAFVTLRVFRVERI	300
QY	298	EKFSRHSOGRLRIIGYTLKSCASELGPLLPSLTMATIIIFATVMFYAEKGSASAKFTSIPAS	357
Db	301	EKFSRHSOGRLRIIGYTLKSCASELGPLLPSLTMATIIIFATVMFYAEKGSASAKFTSIPAA	360
QY	358	FWYTIWMTTLGYGDMVPKTIAGKIFGSGISLGSGLVIALPVPVIVSNPFRIVHQNORAD	417
Db	361	FWYTIWMTTLGYGDMVPKTIAGKIFGSGISLGSGLVIALPVPVIVSNPFRIVHQNORAD	420
QY	418	KRPAOKARLARIRVAKTSSNAYLHASKRNGLLEALELTGTPEEHHMCKTSLIESQHH	477
Db	421	KRPAOKARLARIRAAKSGSANAYMOSKRNGLLSNQLO-SSEDEQAFVSKSGSSPFTQHH	479
QY	478	HLHLCKEKTGSLVYVDDPLLSVRISTIKAHNEFIDEQMFQONCKESSMONYPSTSPSL	537
Db	480	HLHLCKEKT-----NHEFVDEQYFEESCKEAVATVNRPSHSPSLS	520
QY	538	SHPGLTTCSSRSRKKTTHL PNSNL PATRLRSMQELSTHIGQSEQPSLTLTSSRSSNLKA	597
Db	521	SOQGVTSCTCSSRHHKTFRI PANVANS GHQSGIQELSTIQIRCYERTPLSNRSSSSINAKM	580
QY	598	DDGLRPNCCKTSQITTAIIISIPTPPALTPEGEGRP--PPASPGPNTNIPISITSNVVAVSVL	655
Db	581	EECVKLNCEQPIYTTAIIISIPTPPVTTPTEGDRPESPEVSGG-----NIVAVSAL	630

```

RESULT 6
US-10-212-677-260
; Sequence 260, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-212-677-260

```

Query Match	73.2%;	Score 2498.5;	DB 14;	Length 630;
Best local Similarity	73.6%;	Pred. No. 3.1e-205;		
Matches 486;	Conservative 69;	Mismatches 70;	Indels 35;	Gaps 7;
Qy	1	MAAGVAAMLPFARAAAI	GMPVANCMP	LADKDKR-QDELI
		VLAVNSGR	RFQWR	TTL 59
Db	1	MAAGVAAMLPFARAAAI	GMPVASCMP	PAPBRQERKXTQDALIVLANS
		SGTRFQW	QDTLE	60
Qy	60	RYPDTLIGSTEKEFF	ENEDTKEYFEFDRD	PEVFRCLVNFYRTGKLHYPEYCISAYDDELA
		119		
Db	61	RYPDTLIGSSERDP	FYHPE	TQYFFDRDPDIFRHLNFRYRTGKLHYPHRECISAYDDELA
		120		
Qy	120	FYGLIPETIIGDCCYE	EYKDKRRENAERLMDND	SENNOES-MPSLSFRQTMARAFENPHT
		178		
Db	121	FFGLIPEITIGDCCYE	EYKDKRRENAERLQDDAD	DTDAGESALPTMTARQVRMAFENPHT
		180		
Qy	179	STLALVEYYVTGFFIA	VSIVTNNVETVP	CGTVPGS-KELPCGERYSVAFFCLDTACVMIF
		237		

Db	181	STMALVYYVTGFFIAVSVIANVVEITVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF	240
Qy	238	TVEYLRLEFAABSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNNEDEVSGAFVTLRPRVFR	297
Db	241	TVEYLRLEAABSRRYRFRVRSVMSIIDVALLPYIIGLVMTNNEDEVSGAFVTLRPRVFR	300
Qy	298	FKFSRHSQGLRILGYTLKSCASEIGFLFSLTMAIIFATVMFVFAEKSSASAKFTSIPAS	357
Db	301	FKFSRHSQGLRILGYTLKSCASEIGFLFSLTMAIIFATVMFVFAEKSSASAKFTSIPAA	360
Qy	358	FWYTIYMTTLGYGDMVPKTIAGKIFGSISSLSGVVIALPVPVIVSNFSRIYHONORAD	417
Db	361	FWYTIYMTTLGYGDMVPKTIAGKIFGSISSLSGVVIALPVPVIVSNFSRIYHONORAD	420
Qy	418	KRAOKKARLARIRVAKTGSSNAYLHSHKRNGLNEALIELTGPREEHMGKTTSLIESQHH	477
Db	421	KRAOKKARLARIRAAKSGSANAYMOSKRNGLSNOLO-SSEDEQAFVSKSGSPETOHH	479
Qy	478	HLHLCLEKTTGSLVLDDELLSVRTSTIKHHEFIDEQMEQNCMESSWONYPSTSPSL	537
Db	480	HLHLCLEKTT-----NHEFVDEQVFEESCEMEVATNRPSSHSPSL	520
Qy	538	SHPGLTTCSSRRSKGTHLPLNSNLPATRLSMQOEIITHIQOSEQPSLTTSRSSLINLKA	597
Db	521	SOQGVSTCCSRHKKTFRIPNANVSGSHQSIQEIISTIQIRCVERTPLNSRSSLINAKM	580
Qy	598	DGGLRNCKTSQITTAIISIPTPALTPEGESRP--PPASPGENTNIPISITSNVYKVSVL	655
Db	581	EBCVKLNCEQPYTTAIIISIPTPPTTPEGDRPESEYSG-----NIVRSVAL	630

```

RESULT 7
US-10-212-677-261
; Sequence 261, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenaunt, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-261

```

Query Match	73.2%	Score 2498.5;	DB 14;	Length 630;
Best Local Similarity	73.6%;	Pred. No. 3.1e-205;		
Matches 486;	Conservative 69;	Mismatches 70;	Indels 35;	Gaps 7;
QY	1	MAAGVAAWLPFARAAAIGMMPVANCPMPLAPADKNKR-ODELIVLVNSGRREFQWRTTLE	59	
Db	1	MAAGVAAWLPFARAAAIGMMPVASGMPAPRPRQERKRTQALIVLVNSGTREQTWQDTLE	60	
QY	60	RYPDTLLGSTEKEFFFNEDTKKEYFFEDRDEVEFRCVLFNRYTGKLHYPRYECISAYDDELA	119	
Db	61	RYPDTLLGSSERDFFYHPETQYFFDRDPDI FRHLNFPYTGKLHYPRHECISAYDEELA	120	
QY	120	FYGLIPBELIGDCCYEEYKDKRRENAERLDDNDSENNOES-MPSLSFQRTMWARAFENBHT	178	
Db	121	FFGLIPBELIGDCCYEEYKDKRRRENAERLDDADDTTAGESALPTMTARQRVRAFENBHT	180	
QY	179	STLALVEYVVTGPFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF	237	


```

Db 181 STMALVYVVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACMIF 240
Qy 238 TVEYLRLFAAPSRRYRFRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 297
Db 241 TVEYLRLAAPSRRYRFRSVMSIIDVVAIIPYIIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIYMTTLGVDMPKTIAGKIFGSGISLGVLTALPVPVIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLGVDMPKTIAGKIFGSGISLGVLTALPVPVIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMGKTSLSIESQHH 477
Db 421 KRAQKARLARIRAKSGSANAYMQSKRNGLLSNQOQ-SSDEQAFVSKSGSSFEQHH 479
Qy 478 HLHCKEKTGSLYVDDPLLSVSTSTIKNHEFIDEQMFQONCESSMOMYPPSTRSPSL 537
Db 480 HLHCKEKT-----NHEFVDEQVFEEESCMEVATVNRPPSSHSPSL 520
Qy 538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTIHQSEQPSLTSSSLNKA 597
Db 521 SOQGVSTCCSRHKKTFRIPNANVSGSHQSIQELSTIQRCVERTPLSNRSSLNAM 580
Qy 598 DDGLRPNCKTSQITTAISIPTPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 655
Db 581 EECVKLNCEQPYVTTAISIPTPVTTPGEDRPESEYSGG-----NIVRVSA 630

```

RESULT 8

```

US-10-361-811-258
; Sequence 258, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-258

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy 1 MAAGVAAWLPFARAAAGMMPVANCMPPLAPADKNKR-QDELIYLVNVSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAAAGMMPVAGSMPAPRQERKRTQDALIVLVNVSGRFQWQDTLE 60
Qy 60 RYPTDLLGSTEKEFFENEDTKYFFDRDPEVRCVLANFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLLGSSERDFYHPETQOYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy 120 FYGLIPEIIGCCYEEYKDRKRENAERLMDNSENQES-MPSLSFRQTMWRAFENPHT 178
Db 121 FFGLIPEIIGCCYEEYKDRRENAERLQDDADTDYAGESALPTMTARQVWRAFENPHT 180
Qy 179 STLAIVFYVTGFFIAVSIVTNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMAIVFYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACMIF 240
Qy 238 TVEYLRLFAAPSRRYRFRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 297

```

```

Db 241 TVEYLRLAAPSRRYRFRSVMSIIDVVAIIPYIIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIYMTTLGVDMPKTIAGKIFGSGISLGVLTALPVPVIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLGVDMPKTIAGKIFGSGISLGVLTALPVPVIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMGKTSLSIESQHH 477
Db 421 KRAQKARLARIRAKSGSANAYMQSKRNGLLSNQOQ-SSDEQAFVSKSGSSFEQHH 479
Qy 478 HLHCKEKTGSLYVDDPLLSVSTSTIKNHEFIDEQMFQONCESSMOMYPPSTRSPSL 537
Db 480 HLHCKEKT-----NHEFVDEQVFEEESCMEVATVNRPPSSHSPSL 520
Qy 538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTIHQSEQPSLTSSSLNKA 597
Db 521 SOQGVSTCCSRHKKTFRIPNANVSGSHQSIQELSTIQRCVERTPLSNRSSLNAM 580
Qy 598 DDGLRPNCKTSQITTAISIPTPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 655
Db 581 EECVKLNCEQPYVTTAISIPTPVTTPGEDRPESEYSGG-----NIVRVSA 630

```

RESULT 9

```

US-10-361-811-259
; Sequence 259, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-259

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy 1 MAAGVAAWLPFARAAAGMMPVANCMPPLAPADKNKR-QDELIYLVNVSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAAAGMMPVAGSMPAPRQERKRTQDALIVLVNVSGRFQWQDTLE 60
Qy 60 RYPTDLLGSTEKEFFENEDTKYFFDRDPEVRCVLANFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLLGSSERDFYHPETQOYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy 120 FYGLIPEIIGCCYEEYKDRKRENAERLMDNSENQES-MPSLSFRQTMWRAFENPHT 178
Db 121 FFGLIPEIIGCCYEEYKDRRENAERLQDDADTDYAGESALPTMTARQVWRAFENPHT 180
Qy 179 STLAIVFYVTGFFIAVSIVTNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMAIVFYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACMIF 240
Qy 238 TVEYLRLFAAPSRRYRFRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 297
Db 241 TVEYLRLAAPSRRYRFRSVMSIIDVVAIIPYIIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357

```

```
Db      301 EKFSRHSQGLRILGYTLKSCASELGFLLSLTMAIIIFATVMFYAEKSSASAKFTSIPAA 360
Qy      358 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 417
        |||||
Db      361 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 420
Qy      418 KRAQOKARLARIRVAKTSSNAYLHRSKRNGLINEALELTGTPEEHEMGKTSLSIESOH 477
        |||||
Db      421 KRAQOKARLARIRAKSGSANAYMQSKRNGLSNOLQ-SEDEQAFVSKSGSSFETOHH 479
Qy      478 HLHCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMEONCMESMONTSTRSPSL 537
        |||||
Db      480 HLHCLEKTT-----NHEFVDEQVEESCMEVATVNRSSHSPSL 520
Qy      538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEQPSLTSSSLNLKA 597
        |||||
Db      521 SOQGVSTCCSRHKKTFRIPNANVSGSHQSGIOELSTIQIRCVERTPLSNRSRLNAKM 580
Qy      598 DGLRPNCCKTSQITTAIISIPPPALPREGESRP--PPASPGPNTNIPSTSNVVKVSVL 655
        ::::
Db      581 BECVKLNCEQPYVTTAIISIPTPVTTPEDDRPESPEYSGG-----NIVRSAL 630
```

RESULT 10

```
US-10-361-811-260
; Sequence 260, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-260
```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;

Best Local Similarity 73.6%; Pred. No. 3.1e-205;

Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```
Qy      1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNKR-ODELIIVNVSGRRPQTWRTTLE 59
        |||||
Db      1 MAAGVAAWLPFARAALIGMMPVAGMPAPRQERKRTQDALIVNVSGTRFQTWDTLE 60
Qy      60 RYPDTLGSTEKEFFENEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 119
        |||||
Db      61 RYPDTLGSSSERDFYHPETQOYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy      120 FYGLLPEITGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFAFENPHT 178
        |||||
Db      121 FFGILPEITGDCCYEYKDRRENAERLQDDADTDTAGESALPTMTARQVRWRAFAFENPHT 180
Qy      179 STLALVFYYVTGFFIAVSITNVVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
        |||||
Db      181 STMALVFYYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
Qy      238 TVEYLRLPAAPSRIRFIRSVMSIIDVVAIMPYIIGLWMTNNEDEVGAFVTLRVFRVERI 297
        |||||
Db      241 TVEYLRLPAAPSRIRFIRSVMSIIDVVAIIPYIIGLWMTNNEDEVGAFVTLRVFRVERI 300
Qy      298 FKFSRHSQGLRIIGYTLKSCASELGFLLSLTMAIIIFATVMFYAEKSSASAKFTSIPAS 357
        |||||
Db      301 FKFSRHSQGLRIIGYTLKSCASELGFLLSLTMAIIIFATVMFYAEKSSASAKFTSIPAA 360
Qy      358 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 417
        |||||
```

```
Db      361 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 420
Qy      418 KRAQOKARLARIRVAKTSSNAYLHRSKRNGLINEALELTGTPEEHEMGKTSLSIESOH 477
        |||||
Db      421 KRAQOKARLARIRAKSGSANAYMQSKRNGLSNOLQ-SEDEQAFVSKSGSSFETOHH 479
Qy      478 HLHCLEKTTGLSYLVDPLLSVTRSTIKNHEFIDEQMEONCMESMONTSTRSPSL 537
        |||||
Db      480 HLHCLEKTT-----NHEFVDEQVEESCMEVATVNRSSHSPSL 520
Qy      538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEQPSLTSSSLNLKA 597
        |||||
Db      521 SOQGVSTCCSRHKKTFRIPNANVSGSHQSGIOELSTIQIRCVERTPLSNRSRLNAKM 580
Qy      598 DGLRPNCCKTSQITTAIISIPPPALPREGESRP--PPASPGPNTNIPSTSNVVKVSVL 655
        ::::
Db      581 BECVKLNCEQPYVTTAIISIPTPVTTPEDDRPESPEYSGG-----NIVRSAL 630
```

RESULT 11

```
US-10-361-811-261
; Sequence 261, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-261
```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;

Best Local Similarity 73.6%; Pred. No. 3.1e-205;

Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```
Qy      1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNKR-ODELIIVNVSGRRPQTWRTTLE 59
        |||||
Db      1 MAAGVAAWLPFARAALIGMMPVAGMPAPRQERKRTQDALIVNVSGTRFQTWDTLE 60
Qy      60 RYPDTLGSTEKEFFENEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 119
        |||||
Db      61 RYPDTLGSSSERDFYHPETQOYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy      120 FYGLLPEITGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFAFENPHT 178
        |||||
Db      121 FFGILPEITGDCCYEYKDRRENAERLQDDADTDTAGESALPTMTARQVRWRAFAFENPHT 180
Qy      179 STLALVFYYVTGFFIAVSITNVVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
        |||||
Db      181 STMALVFYYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
Qy      238 TVEYLRLPAAPSRIRFIRSVMSIIDVVAIMPYIIGLWMTNNEDEVGAFVTLRVFRVERI 297
        |||||
Db      241 TVEYLRLPAAPSRIRFIRSVMSIIDVVAIIPYIIGLWMTNNEDEVGAFVTLRVFRVERI 300
Qy      298 FKFSRHSQGLRIIGYTLKSCASELGFLLSLTMAIIIFATVMFYAEKSSASAKFTSIPAS 357
        |||||
Db      301 FKFSRHSQGLRIIGYTLKSCASELGFLLSLTMAIIIFATVMFYAEKSSASAKFTSIPAA 360
Qy      358 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 417
        |||||
Db      361 FWYTIWMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 420
Qy      418 KRAQOKARLARIRVAKTSSNAYLHRSKRNGLINEALELTGTPEEHEMGKTSLSIESOH 477
        |||||
```

```

Db 421 KRAQKARLARIIRAKSGSANAYMOSKRNGLISNOLO-SSDEQAFVSKSGSSFEQOH 479
Qy 478 HLHCKEKTGLSYLVDDPLSVTRSTIKNHEFIDEQMFQONCMESSMONYPSTRSPSL 537
Db 480 HLHCKEKT-----NHEFVDEQVFEEESCMEVATVNRPSHSPSL 520
Qy 538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLKA 597
Db 521 SQQGVSTCCSRHKKTFRIPNANVSGSHQSIQELSTIQRCVETPLSNRSSSLNAKM 580
Qy 598 DDGLRPNCKTSQITTAISIPTPPALTPGESRP--PPASPGPNTNIPSTSNVAVSVL 655
Db 581 BECVKNCQEPYVTTAISIPTPPTTPEGDDRPESPEYSGG-----NIVRVSL 630

```

RESULT 12

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US-10-369-186-258
; Sequence 258, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-258

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

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Qy 1 MAAGVAAWLPARAAGMMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPARAAGMMPVASCMPMPAPRQERKTQDALIVLVNSGTRFQWQDTLE 60
Qy 60 RYPTDILGSTEKEFFFNEDTKEYFEFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDILGSSERDFYHPEBTOQYFFDRDPDIFRHLNFRYRTGKLHYPRHICISAYDELA 120
Qy 120 FYGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCYEEYKDRRENAERLQDDADTDGAGESALPTMTARQVWRAFENPHT 180
Qy 179 STLALVFYVYVGFPIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVYVGFPIAVSVIANVETVPCGSSPGHIXELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLLRLFAAPSRRYRFRSVMSIIDVVAIMPYYIGLVMTNNEVDVSGAFVTLRVERVRI 297
Db 241 TVEYLLRLAAPSRRYRFRSVMSIIDVVALIPYYIGLVMTNNEVDVSGAFVTLRVERVRI 300
Qy 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPAA 360
Qy 358 FWYTIYMTTLLGYGDMVPKTIAGKIFGSGISLGVLVIALPVPVIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLLGYGDMVPKTIAGKIFGSGISLGVLVIALPVPVIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIIRAVAGTSSNAVYLSKRNGLNLEALJGTPEEHNKGTSLIESQHH 477
Db 421 KRAQKARLARIIRAKSGSANAYMOSKRNGLISNOLO-SSDEQAFVSKSGSSFEQOH 479
Qy 478 HLHCKEKTGLSYLVDDPLSVTRSTIKNHEFIDEQMFQONCMESSMONYPSTRSPSL 537

```

```

Db 480 HLHCKEKT-----NHEFVDEQVFEEESCMEVATVNRPSHSPSL 520
Qy 538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLKA 597
Db 521 SQQGVSTCCSRHKKTFRIPNANVSGSHQSIQELSTIQRCVETPLSNRSSSLNAKM 580
Qy 598 DDGLRPNCKTSQITTAISIPTPPALTPGESRP--PPASPGPNTNIPSTSNVAVSVL 655
Db 581 BECVKNCQEPYVTTAISIPTPPTTPEGDDRPESPEYSGG-----NIVRVSL 630

```

RESULT 13

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US-10-369-186-259
; Sequence 259, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-259

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy 1 MAAGVAAWLPARAAGMMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPARAAGMMPVASCMPMPAPRQERKTQDALIVLVNSGTRFQWQDTLE 60
Qy 60 RYPTDILGSTEKEFFFNEDTKEYFEFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDILGSSERDFYHPEBTOQYFFDRDPDIFRHLNFRYRTGKLHYPRHICISAYDELA 120
Qy 120 FYGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCYEEYKDRRENAERLQDDADTDGAGESALPTMTARQVWRAFENPHT 180
Qy 179 STLALVFYVYVGFPIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVYVGFPIAVSVIANVETVPCGSSPGHIXELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLLRLFAAPSRRYRFRSVMSIIDVVAIMPYYIGLVMTNNEVDVSGAFVTLRVERVRI 297
Db 241 TVEYLLRLAAPSRRYRFRSVMSIIDVVALIPYYIGLVMTNNEVDVSGAFVTLRVERVRI 300
Qy 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGSASKFTSIPAA 360
Qy 358 FWYTIYMTTLLGYGDMVPKTIAGKIFGSGISLGVLVIALPVPVIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLLGYGDMVPKTIAGKIFGSGISLGVLVIALPVPVIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIIRAVAGTSSNAVYLSKRNGLNLEALJGTPEEHNKGTSLIESQHH 477
Db 421 KRAQKARLARIIRAKSGSANAYMOSKRNGLISNOLO-SSDEQAFVSKSGSSFEQOH 479
Qy 478 HLHCKEKTGLSYLVDDPLSVTRSTIKNHEFIDEQMFQONCMESSMONYPSTRSPSL 537
Db 480 HLHCKEKT-----NHEFVDEQVFEEESCMEVATVNRPSHSPSL 520
Qy 538 SHPGLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLKA 597

```

```
Db 521 SQQGVSTSCSRHKKTERIPANVSGSHQSIGELSTIQIRCVERTPLSNRSLSNAKM 580
Qy 598 DDGIRPNCKTSQITTAIISIPPPALPEGESRP--PPASGPNTNIPSTSNVVKSVL 655
Db 581 BECVKLNCEQPYVTTAIISIPPPVTTEGGDRPESPESYSGG-----NIVRVSL 630

RESULT 14
US-10-369-186-260
; Sequence 260, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-369-186-260

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

Qy 1 MAAGVAAWLPFARAAGMMPVANCMPPLAPADKNR--ODELIVLVNSGRFRQTWRTTLE 59
Db 1 MAAGVAAWLPFARAAGMMPVASCMPAPRQERKRTQDALIVLVNSGTRFQWQDTLE 60
Qy 60 RYDPTLLGSTEKEFEFFNEDTKYFFDRDPEVFCVINFYRTGKLHYPRYECISAYDELA 119
Db 61 RYDPTLLGSSERDFYHPETQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy 120 FYGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQES--MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDKRRENAERLQDDADDTAGESALPTMTARQVWRAFENPHT 180
Qy 179 STTALVFYVYTGFFIAVSVTNNVETVPCGTVPGS--KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVYTGFFIAVSIVANVETVPCGSSPGHIELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLLRLFAAPSRIRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFVTLRVFRVRI 297
Db 241 TVEYLLRLAAPSRRIRFIRSVMSIIDVAIIPYIIGLVMTNNEDEVGAFVTLRVFRVRI 300
Qy 298 FKFSRHSQGLRIIGTLKSCASELGLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGTLKSCASELGLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIIVMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVSNFSRIYHQNORAD 417
Db 361 FWYTIIVMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVSNFSRIYHQNORAD 420
Qy 418 KRAOKKARLARIRVAKTSSNAYLHRSKNGLNLEALBELTGTPEEHMGKTSLSIESQHN 477
Db 421 KRAOKKARLARIRAKSGSANAYMQSKRNGLNSQLQ--SSEDEQAFVSKSSSFETQHN 479
Qy 478 HLHGLEKTGSLYVDDPLSVRTSTIKNHEFIDEQMEQNCMESSMONTYSTRSPSLIS 537
Db 480 HLHGLEKTT-----NHEFVDEQVFEESCMEEVATVNRPSHSPSLIS 520
Qy 538 SHPGLTTCCSRSKKTHLPLNSLPAIRLRSMQELSTIHQSEQPSLITSRSLNLKA 597
Db 521 SQQGVSTSCSRHKKTERIPANVSGSHQSIGELSTIQIRCVERTPLSNRSLSNAKM 580
Qy 598 DDGIRPNCKTSQITTAIISIPPPALPEGESRP--PPASGPNTNIPSTSNVVKSVL 655
Db 581 BECVKLNCEQPYVTTAIISIPPPVTTEGGDRPESPESYSGG-----NIVRVSL 630
```

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Db 581 BECVKLNCEQPYVTTAIISIPPPVTTEGGDRPESPESYSGG-----NIVRVSL 630

RESULT 15
US-10-369-186-261
; Sequence 261, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-369-186-261

Query Match 73.2%; Score 2498.5; DB 15; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

Qy 1 MAAGVAAWLPFARAAGMMPVANCMPPLAPADKNR--ODELIVLVNSGRFRQTWRTTLE 59
Db 1 MAAGVAAWLPFARAAGMMPVASCMPAPRQERKRTQDALIVLVNSGTRFQWQDTLE 60
Qy 60 RYDPTLLGSTEKEFEFFNEDTKYFFDRDPEVFCVINFYRTGKLHYPRYECISAYDELA 119
Db 61 RYDPTLLGSSERDFYHPETQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
Qy 120 FYGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQES--MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDKRRENAERLQDDADDTAGESALPTMTARQVWRAFENPHT 180
Qy 179 STTALVFYVYTGFFIAVSVTNNVETVPCGTVPGS--KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVYTGFFIAVSIVANVETVPCGSSPGHIELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLLRLFAAPSRIRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFVTLRVFRVRI 297
Db 241 TVEYLLRLAAPSRRIRFIRSVMSIIDVAIIPYIIGLVMTNNEDEVGAFVTLRVFRVRI 300
Qy 298 FKFSRHSQGLRIIGTLKSCASELGLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGTLKSCASELGLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIIVMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVSNFSRIYHQNORAD 417
Db 361 FWYTIIVMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVSNFSRIYHQNORAD 420
Qy 418 KRAOKKARLARIRVAKTSSNAYLHRSKNGLNLEALBELTGTPEEHMGKTSLSIESQHN 477
Db 421 KRAOKKARLARIRAKSGSANAYMQSKRNGLNSQLQ--SSEDEQAFVSKSSSFETQHN 479
Qy 478 HLHGLEKTGSLYVDDPLSVRTSTIKNHEFIDEQMEQNCMESSMONTYSTRSPSLIS 537
Db 480 HLHGLEKTT-----NHEFVDEQVFEESCMEEVATVNRPSHSPSLIS 520
Qy 538 SHPGLTTCCSRSKKTHLPLNSLPAIRLRSMQELSTIHQSEQPSLITSRSLNLKA 597
Db 521 SQQGVSTSCSRHKKTERIPANVSGSHQSIGELSTIQIRCVERTPLSNRSLSNAKM 580
Qy 598 DDGIRPNCKTSQITTAIISIPPPALPEGESRP--PPASGPNTNIPSTSNVVKSVL 655
Db 581 BECVKLNCEQPYVTTAIISIPPPVTTEGGDRPESPESYSGG-----NIVRVSL 630

Search completed: April 6, 2005, 08:33:59
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Thu Apr 7 08:08:04 2005

us-10-062-879-2.apr5.rapb

Page 9

Job time : 457.608 secs

mis ruge blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 04:45:50 ; Search time 118.215 Seconds
(without alignments)
533.115 Million cell updates/sec

Title: US-10-062-879-2
Perfect score: 3412
Sequence: 1 MAAGVAAWLFPARAALIGWM.....PGENTNIPITSNVKVSVL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2499.5	73.3	630	2	JU0271	voltage-sensitive potassium channel
2	2122	62.2	651	2	A39372	potassium channel
3	1915.5	56.1	490	2	A35312	potassium channel
4	1103	32.3	236	2	I57681	potassium channel
5	766.5	22.5	802	2	JH0595	potassium channel
6	742.5	21.8	858	2	S31761	potassium channel
7	741	21.7	853	1	CHRTD1	potassium channel
8	736	21.6	602	2	JH0166	potassium voltage-sensitive potassium channel
9	735	21.5	857	2	I56529	potassium channel
10	728	21.3	643	2	S00480	potassium channel
11	727.5	21.3	656	2	JH0193	potassium channel
12	726	21.3	924	2	S12746	potassium channel
13	719	21.1	598	2	S66669	potassium channel
14	719	21.1	602	2	A49507	potassium channel
15	715	21.0	499	2	I77466	potassium channel
16	714	20.9	525	2	A43531	potassium channel
17	713	20.9	499	2	I84204	potassium channel
18	713	20.9	499	2	A33814	potassium channel
19	712.5	20.9	523	2	A38101	potassium channel
20	712	20.9	585	2	A39395	potassium channel
21	709.5	20.8	489	2	I51532	potassium channel
22	709	20.8	528	2	I84205	potassium channel
23	709	20.8	924	2	B41359	potassium channel
24	708	20.8	613	2	A39402	potassium channel
25	707.5	20.7	511	2	A46020	potassium channel
26	707	20.7	460	2	T27759	hypothetical prote
27	706.5	20.7	511	2	S07095	potassium channel
28	706.5	20.7	769	2	I56546	Shaw type potassiu
29	706	20.7	495	2	A40090	potassium channel

30	706	20.7	495	2	B39113	potassium channel
31	705	20.7	476	2	S21144	potassium channel
32	705	20.7	597	2	S51212	BAXS protein - bov
33	704	20.6	495	2	I57680	potassium channel
34	701.5	20.6	498	2	A41359	potassium channel
35	700	20.5	679	2	A42073	potassium channel
36	699.5	20.5	489	2	JC4787	Shaw protein - Cal
37	699	20.5	499	2	JH0313	potassium channel
38	699	20.5	624	2	S22703	voltage-gated pota
39	697.5	20.4	625	2	S13919	potassium channel
40	697	20.4	499	2	A48672	delayed rectifier
41	694.5	20.4	660	2	S24125	potassium channel
42	692.5	20.3	581	2	S17150	potassium channel
43	692.5	20.3	653	2	A39922	potassium channel
44	692.5	20.3	654	2	S11049	potassium channel
45	690	20.2	558	2	T23991	hypothetical prote

ALIGNMENTS

RESULT 1						
JU0271						
voltage-sensitive potassium channel protein [validated] - rat						
N;Alternate names: rat sha/1						
C;Species: Rattus norvegicus (Norway rat)						
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004						
C;Accession: JU0271; A39113						
R;Baldwin, T.J.; Tsaour, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.						
Neuron 7, 471-483, 1991						
A;Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K+ c						
A;Reference number: JU0271; MUID:92000693; PMID:1840649						
A;Accession: JU0271						
A;Molecule type: mRNA						
A;Residues: 1-630 <BAL>						
A;Cross-references: UNIPROT:Q63881; GB:S64320; NID:g236196; PIDN:AB19939.1; PID:g236197						
R;Experimental source: hippocampus						
R;Roberts, S.L.; Tamkun, M.M.						
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991						
A;Title: Cloning and tissue-specific expression of five voltage-gated potassium channel						
A;Reference number: A39113; MUID:91156694; PMID:1705709						
A;Accession: A39113						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>						
A;Cross-references: GB:M59980; NID:g203467; PIDN:AAA40929.1; PID:g203468						
C;Function:						
A;Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [valida						
C;Superfamily: potassium channel protein dkt1						
C;Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel						
F;38/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #sta						
F;54,280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status						
F;70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta						
F;101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta						
F;113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase						
F;592/Binding site: phosphate (Tyr) (covalent) #status predicted						
Query Match						
Best Local Similarity 73.3%; Score 2499.5; DB 2; Length 630;						
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;						
QY	1	MAAGVAAWLFPARAALIGMPVYANCPMPLAPADKXKR-QDEILIVNVSGRRFQTRWTTLE	59			
DB	1	MAAGVAAWLFPARAALIGMPVYASGMPAPPROEKRTQDALLIVNVSGTRFQTWQDTLE	60			
QY	60	RYPTLLGSTEKEFFENEDTKYFFEDRDEVFRCVLFYRFGKTHYRYECISAYDDELA	119			
DB	61	RYPTLLGSSERRDFYHAPETQYFFDRDDIFRHLINFYRFGKTHYRHECISAYDEELA	120			
QY	120	FYGLPEIIDDCCYEYKDKRKENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT	178			
DB	121	FFGLPEIITGDCYEYKDKRRENAERLQDDADITNTGESALPTMTARQRVMAAFENPHT	180			

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QY 179 STLALVYVYVTFIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACWIF 237
||:|||||
DB 181 STMALVFYVYVTFIAVSVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACWIF 240
QY 238 TVEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 297
||:|||||
DB 241 TVEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSGOGLRIIGYTLKSCASELGFLLSLTMAIIIPATVMFYAEKSSASKFTSIPAS 357
||:|||||
DB 301 FKFSRHSGOGLRIIGYTLKSCASELGFLLSLTMAIIIPATVMFYAEKSSASKFTSIPAA 360
QY 358 FWTIVTMVTLTGGMVPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONQPAD 417
||:|||||
DB 361 FWTIVTMVTLTGGMVPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONQPAD 420
QY 418 KRAOKKARLARIRVAKTGSNAVLHSKRNGLNLEALGTPEEHMGKTSLSIESQNH 477
||:|||||
DB 421 KRAOKKARLARIRAKSGSANAVMQSKRNGLSNQLQ-SEDEPAFVSKSGSSFETQHH 479
QY 478 HLHCLKTKTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFQNCMESSMONTYSTRSPSL 537
||:|||||
DB 480 HLHCLKTKT-----NHEFVDEQVFESCEVAVTNRPSSHSPLS 520
QY 538 SHPGLTTCSSRSRKKTHLPNSNLPATRLRSMOELSTIHIOGSEQSLTTSRSLNKA 597
||:|||||
DB 521 SGGVTSSTCSRRHKKSFRIPANVSGSHRGVQELSTIQRCVERTPLSNRSSLNKA 580
QY 598 DDGLRPNCCKTSQITTAIISIPTPALPPEGESRP--PPASPGPNTNIPSTSNVVKVSVL 655
||:|||||
DB 581 EECVKLNCQRPYVTAIISIPPTPTTEGDDRPESPEYSGG-----NIVRSAL 630
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RESULT 2

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A39372
potassium channel protein Shal1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C/Accession: A39372
R/Pak, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salcoff, L.
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A/Title: mshal, a subfamily of A-type K(+) channel cloned from mammalian brain.
A/Reference number: A39372; MUID:91239573; PMID:2034678
A/Accession: A39372
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-651 <PAK>
A/Cross-references: UNIPROT:Q03719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813
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Query Match 62.2%; Score 2122; DB 2; Length 651;
Best Local Similarity 63.8%; Pred. No. 7.3e-154;
Matches 434; Conservative 76; Mismatches 116; Indels 54; Gaps 14;
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QY 1 MAAGVAAWLPFAARAAIGMMPVANCMPPLAPADKNKRODELIVLNVSGRRFQTRTTLER 60
||:|||||
DB 1 MAAGVATWLPFAARAAVGMPLAQPLPPAPEVKASRGDEVLVVNVSGRRFETWKNITLDR 60
QY 61 YPDTLLGSTEKEFFENEDTKYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDEELAF 120
||:|||||
DB 61 YPDTLLGSSSEKFFYDAESGEYFFDRDPDMFRHVLNFYRTGRLHCPQECIOAFDEELAF 120
QY 121 YGILPEIIGDCCYEYKDKRKRENAERLMDNDSENNOESMPSL----SFRQTMWRAFENP 176
||:|||||
DB 121 YGILPELVGDCCLLEERYDRKRENAERLAEDEAEQAGEG-PALPAGSSLRQRLWRAFENP 179
QY 177 HTSTLALVFYVYVTFIAVSVITNVETVPCGTVP--GSKELPCGERYSVAFFCLDTACV 234
||:|||||
DB 180 HTSTALVFYVYVTFIAVSVIANVETIPCRGTPRMPSKEQSCGDRHPTAFECMDTACV 239
QY 235 MFTVEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRV 294
||:|||||
DB 240 LIFTGEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRV 299
```

```
QY 295 FRIFKFSRHSGOGLRIIGYTLKSCASELGFLLSLTMAIIIPATVMFYAEKSSASKFTSI 354
||:|||||
DB 300 FRIFKFSRHSGOGLRIIGYTLKSCASELGFLLSLTMAIIIPATVMFYAEKSTSKINFTSI 359
QY 355 PASFWITIVTMVTLTGGMVPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONQ 414
||:|||||
DB 360 PAFWITIVTMVTLTGGMVPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONQ 419
QY 415 RADKRRAROKKARLARIRVAKTGSNAVLHSKRNGLNLEALGTPEEHMGKTSLSIESQ 473
||:|||||
DB 420 RADKRRAROKKARLARIRLAKSGTNAFLQYKONG---GLEDSGSGDGMCLVRSRSAFE 475
QY 474 SOHHHLHCLKTKTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFQNCMESSMONTYSTRS 533
||:|||||
DB 476 QOHHHLHCLKTKT-----CHEFTDELTPSEALGAVSLGGRS-RS 515
QY 534 PLSLSP-----GLTTCSSRR-SKKTTHLPNSNLPATRLRSMOELSTIHIOGSEQSLT 588
||:|||||
DB 516 TSVSSQPMGPGSLFSSCCSRRVNRRAIRLANSTASVSR-GSMQELDT--LAGLRSPAPQ 572
QY 589 SRSLNLKADGRLPNCKTSQITTAIISIPTPALPPEGESRPPEPASPG-----PNTNI 642
||:|||||
DB 573 TRSLNLAKPHDSLNLDCSRDFAVAIISIPTPANTPD-ESQPSPSGGSGGTPTNTTL 631
QY 643 -----PSITSNVVKVSVL 655
||:|||||
DB 632 RNSSLGTPCLLPETVTKISL 651
```

RESULT 3

```
A35312
potassium channel protein Shal2 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C/Accession: A35312; S12747
R/Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salcoff, L.
Science 248, 599-603, 1990
A/Title: K+ current diversity is produced by an extended gene family conserved in Drosophila.
A/Reference number: A35312; MUID:90239553; PMID:2333511
A/Accession: S12747
A/Molecule type: mRNA
A/Residues: 1-490 <WEI>
A/Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-490 <BUT>
A/Cross-references: EMBL:M32660; NID:g158456; PID:g158457
A/Genetics:
A/Gene: shal2
A/Cross-references: FlyBase:FBgn0005564
C/Superfamily: potassium channel protein drk1
C/Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein
```

```
Query Match 56.1%; Score 1915.5; DB 2; Length 490;
Best Local Similarity 73.6%; Pred. No. 2.8e-138;
Matches 360; Conservative 61; Mismatches 63; Indels 5; Gaps 4;
```

```
QY 3 AGVAAWLPFAARAAIGMMPVANCMPPLAPADKNKRO--DELIVLNVSGRRFQTRTTLER 60
||:|||||
DB 2 ASVAAWLPFAARAAIGWVPIATHTPLPPPMKDRKRTDEKLLINVSGRRFETWKNITLTK 61
QY 61 YPDTLLGSTEKEFFENEDTKYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDEELAF 120
||:|||||
DB 62 YPDTLLGNSNEREFFYDEDECKEYFFDRDPDIFRHILNYRTGKLHYPKHECLTSYDEELAF 121
QY 121 YGILPEIIGDCCYEYKDKRKRENAERLMDNDSENNOESMPSL--SFRQTMWRAFENPHTS 179
||:|||||
DB 122 FGIMPVIGDCCYEYDRDKRKRENAERLMDNKLSENQDNLQQLTNWRQKMRFAFENPHTS 181
```

[illegible]

RESULT 4
157681
potassium channel protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000
C:Accession: 157681
R:Rudy, B.; Kentros, C.; Vega-Saenz de Miera, E.C.
Mol. Cell. Neurosci. 2, 89-102, 1991
A>Title: Families of potassium channel genes in mammals: Toward an understanding of the
A:Reference number: 157681
A:Accession: 157681
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: GB:M74898; NID:g205040; PIDN:AAA41468.1; PID:g205041
C:Superfamily: potassium channel protein drk1

Query Match 32.3%; Score 1103; DB 2; Length 236;
Best Local Similarity 93.2%; Pred. No. 1.1e-76;
Matches 219; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 170 WRAFENPHTSTLALVFYYVTGFFIAVSVITNVETVPCCGTPGSGELPCGGRYSVAFFCL 229
|||||
1 WRAFENPHTSTLALVFYYVTGFFIAVSVITNVETVPCCGTPGSGELPCGGRYSVAFFCL 60
DB 230 DTACVMIFTEVEYLRLFAAPSRYSRFSVMSIIDVVAIMPYYIGIVMTNNEVSGAFVTL 289
||||| : |||||
61 DTACVMIFTEVEYLRLFGHPAGYRFRSVMSIIDVVAIMPYYIGIVMTNNEVSGAFVTL 120
QY 290 RVERVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWMEYAEKSSAS 349
|||||
121 RVERVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWMEYAEKSSAS 180
QY 350 KFTSIPASFWYITVMTTLGYGDMVPKTIAGKIFGSGICSLGVLVIALPVPVIVS 404
|||||
181 KFTSIPASFWYITVMTTLGYGDMVPKTIAGKIFGSGICSLGVLVIALPVPVIVS 235
DB

RESULT 5
JH0595
potassium channel protein cdRk - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 20-Aug-1999
C:Accession: JH0595
R:Rhwang, P.M.; Glatz, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H.
Neuron 8, 473-481, 1992
A>Title: A novel K+ channel with unique localizations in mammalian brain: molecular cloning

A;Accession: JH0595
A;Molecule type: mRNA
A;Residues: 1-802 <HMA>
A;Cross-references: GB:M77482; NID:G203395; PIDN:AAA40905.1; PID:G203396
A;Experimental source: Circumvallate papillae
C;Superfamily: potassium channel protein dkl1
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;191-212/Domain: transmembrane #status predicted <TM1>
F;233-254/Domain: transmembrane #status predicted <TM2>
F;265-286/Domain: transmembrane #status predicted <TM3>
F;299-320/Domain: transmembrane #status predicted <TM4>
F;335-356/Domain: transmembrane #status predicted <TM5>
F;397-418/Domain: transmembrane #status predicted <TM6>
F;187, 287, 419, 446/Binding site: carboxylate (Asn) (covalent) #status predicted
F;446, 500/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match	22.5%	Score 766.5	DB 2	Length 802	
Best Local Similarity	29.3%	Pred. No. 2.9e-50			
Matches	210	Conservative 123	Mismatches 263	Indels 121	Gaps 23
Qy	27	ME LAPAD--KMKRQDELYLVNLSGRFRQT-WRTTLERYPDTLG-----STEKEFF----	74		
Db	20	LPPEPVDIIRSKTCSRKVKINVGNGLHNEVLMR-TLDRLLPRTLGLRDCNTHESLLEVC	78		
Qy	75	-FNEDTKEVFFDRDPEVERFCVLNFRYTGKLYHPRYECISAYDDELAFYGLPEIIGDCCY	133		
Db	79	DYNLNENEYFFDRHPGAFTSLNERYTGKLMMEENCALSFGQELDWGIDELYLESCCQ	138		
Qy	134	BEYKDR-----RENARLMDNDSENNOESMBLSFRQTMRAEENPHTSLALVF	186		
Db	139	ARYHQKEQMNEELRREALTRDRGEEFNTCCPER--RKLMDLEKPNSSVAAKILA	196		
Qy	187	YVTGFIAVSVLTNVEVETPCGTVBSKELPCGERY-----SVAFFCJDTACVMIFTVEY	241		
Db	197	IVSILFIVLSTIALSLNTLP-----ELQENDERGQSPDRKLAAHEAVCIAMFTMEY	248		
Qy	242	LRLFAAPSRRYRFRSVMSIIDVVAIMPHYIIGLVMTNN-----EDVSGAFVTLRVFRV	294		
Db	249	LRLFLSSPNKMKRFPKGPLNVIDLAILPYVVTIFLTESNKSVLQFQNRVRVVOIFRIMRI	308		
Qy	295	FRIFKSRHSQGLRILGYTLKSCASELGFLLPSLMAIIIPATVMFAEKSSASKFTSI	354		
Db	309	LRIKLARHSTGQSLGFTLRSRNEIGLILFLAMGIMIFSSLVFRAKEDBATKFTSI	368		
Qy	355	PASFMYITVMTTLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVSNFSRIYHONQ	414		
Db	369	PASFMYATITMTVGYGDIYPKTLIGKIVGLCCIAGLVLTALPIPIVNNFSEFYKEOK	428		
Qy	415	RADK---RRAOKKAR-----LARIYAKTGS-----NAYLH	443		
Db	429	ROEKALKREALERAKNGSIVSMNLKDAFARSMELIDVAEKAGESANIKSDVDDNHL	488		
Qy	444	SKRNGLNEAL-----ELTGPBEENHNGKTSLIESQHHLHLCLEKTG	489		
Db	489	PSRWKMARAKALSETSSNKS YENKQYQEVSOQDSHQDLNNTSS--SSPGLHSAQKLE----	541		
Qy	490	SYLVDDPLLVSPTSTIKNHEFIDE-----QMEFQNCMESSM--QNYPTRSPS	535		
Db	542	--MLYNEITKTQTHSHPNPDQOEOPERSAYEEIEEMEYVCPQEOQLAVALQTEVIVDKMS	599		
Qy	536	LSHSGELTTCCSRRSKKTTHLPNSNLPATRLRSQOELSTHIQGSQPSLTSRSSLNL	595		
Db	600	TSSIDSTS--CATDFTETERSP---LPPPSASHLQMKFPDDLPGMBEHQRYAAPPFLTL	654		
Qy	596	KADDLGRPNCKTSQITTAIISIPTR-PALTRPEGSESRPPASRGENTNIPISITSNVVK	651		
Db	655	SRDKG--PAAREALDYAPRIDITVNLDAAGSHGRLQOPDASDSPKSLKG--SNPLK	707		

RESULT 6
S31761
potassium channel protein DRK1 - human
C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S31761
R/Albrecht, B.; Llorca, C.; Stocker, K.; Pongs, O.
submitted to the EMBL Data Library, September 1992
A/Description: Cloning, expression and chromosomal localization of the delayed rectifier
A/Reference number: S31761
A/Accession: S31761
A/Molecule type: DNA
A/Residues: 1-858 <ALB>
A/Cross-references: UNIPROT:Q14721; EMBL:X68302; NID:g30892; PIDN:CAA48374.1; PID:g30893
C/Genetics:
A/Gene: GDB:KCNB1; KV2.1; DRK1
A/Cross-references: GDB:128081; OMIM:600397
A/Map position: 20q13.2-20q13.2
C/Superfamily: potassium channel protein drkl

Query Match 21.8%; Score 742.5; DB 2; Length 858;
Best Local Similarity 29.1%; Pred. No. 2.1e-48;
Matches 194; Conservative 116; Mismatches 213; Indels 143; Gaps 20;

QY 27 MFLPAD--KNKQDELIVNVSGRRFQT-WRTTLERYDPTLLG-----STEKEFF---- 74
DB 16 LPPEPMEIVRSKACSRVRVNVGGLAHEVLMR-TLDRLPRTRLGKLRDCNTHDSLQVCD 74
QY 75 -FNEDTKEVFEFRDEVEFRVCVNFYRTGKLHYPRYECTISAYDELAFYGLPEIIGDCCY 133
DB 75 DYSLEDNEYFFDRHGAFTSILNFYRTGRLHMEEMCALSFQSELDYWGIDIEYLSGCCQ 134
QY 134 BEYKDRKRENAERLMDNDSENNOE-----SMPSLSFRQTMWRAFPENPHTSTLALVEYVV 188
DB 135 ARYHQQKEQNMEEELKREAEITREREGEEFDNTCCAEKRKKLMDLEKPNSSVAAKITAI 194
QY 189 TGEFFIAVSVITNVETVPCGTVPGSKELPCGERYSVA-----FFCLDTACVMIFTVEYLL 243
DB 195 SIMETIVSTIALSLNTLP-----ELQSLDEFGQSTDPQLAHEAVCIAMFTMEYLL 246
QY 244 RLFAAPSRVYRFRSVMISIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVFRYER 296
DB 247 RFLSSPKWKMKFKGDLNALDIALILPYVTIIFLTESNKSVALQFQVRRRVQIFRIMRLR 306
QY 297 IFKFSRHSQGLRIGYTLKSCASELGLFLSLTMAIIFATVMFYAEKSSASKFTSIPA 356
DB 307 ILKLARHSTGLQSLGFTLRRSYNELGLLILFLAMGIMIFSSLVFAEKDEDDTKFKSIPA 366
QY 357 SFWYTIWMTTGLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVVSFRIYHONORA 416
DB 367 SFWMATITMTTVGVDIYPKTLIGKIVGGLCCIAGVLVIALPIPIIVNFSFYEKQKQ 426
QY 417 DKRAQKARLARIRVAKTSSNAYLHSCRNGLI-----NEALEITGTPEEHH 464
DB 427 EKAIKRREARLER-----AKRNGSIVSMNMKDAFARSIEMMDIVEKNGEN 471
QY 465 MGKTTSLIESQHHLLHCLEKTGSLVLDPLLSVRTSTIKNHEFTIDEQMEQNCMESS 524
DB 472 MGKKDKV---QDNHLSPNKMKWTKRT-----LS-ETSSKS-----FETK 507
QY 525 MONYPSTRSPSLSSHGLTTCCSRRSKKTTHLPNSNLPATRLSRMOELSTIHQSGEOP 584
DB 508 EQGSPEK-----ARSSSSPOHL-----NVQOLEDMYMKAKTQGO 543
QY 585 SLTTSRSSNLKADDGLRPNCKTSQITTAIISITPPALTPEGESRPPASGPNNTIPS 644
DB 544 ILNTKESAASKPEEL-----EMESIPSPVAP-----LPT 574
QY 645 ITSNVV 650
DB 575 RTEGVI 580

RESULT 7
CHRTD1
potassium channel protein drkl - rat
C/Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S05448; A44838
R/Frech, G.C.; Vandongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A/Title: A novel potassium channel with delayed rectifier properties isolated from rat b
A/Reference number: S05448; MUID:89365157; PMID:2770868
A/Accession: S05448
A/Molecule type: mRNA
A/Residues: 1-853 <PRE>
A/Cross-references: UNIPROT:P15387; EMBL:X16476; NID:g57785; PIDN:CAA34497.1; PID:g57786
A/Note: It is uncertain whether Met-1 or Met-17 is the initiator
R/Drewe, J.A.; Verma, S.; Frech, G.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A/Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from diffe
A/Reference number: A44838; MUID:92156897; PMID:1740690
A/Accession: A44838
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 'MPAG', 1-571 <DRE>
A/Cross-references: GB:M81783; NID:g205038
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:P:81768)
C/Genetics:
A/Gene: drkl
C/Superfamily: potassium channel protein drkl
C/Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane f
F:1-182/Domain: intracellular #status predicted <INT1>
F:183-204/Domain: transmembrane #status predicted <TM1>
F:225-245/Domain: transmembrane #status predicted <TM2>
F:256-276/Domain: transmembrane #status predicted <TM3>
F:291-312/Domain: transmembrane #status predicted <TM4>
F:327-348/Domain: transmembrane #status predicted <TM5>
F:389-410/Domain: transmembrane #status predicted <TM6>
F:411-853/Domain: intracellular #status predicted <INT2>
F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.7%; Score 741; DB 1; Length 853;
Best Local Similarity 27.8%; Pred. No. 2.8e-48;
Matches 207; Conservative 126; Mismatches 266; Indels 146; Gaps 22;

QY 27 MFLPAD--KNKQDELIVNVSGRRFQT-WRTTLERYDPTLLG-----STEKEFF---- 74
DB 12 LPPEPMEIVRSKACSRVRVNVGGLAHEVLMR-TLDRLPRTRLGKLRDCNTHDSLQVCD 70
QY 75 -FNEDTKEVFEFRDEVEFRVCVNFYRTGKLHYPRYECTISAYDELAFYGLPEIIGDCCY 133
DB 71 DYSLEDNEYFFDRHGAFTSILNFYRTGRLHMEEMCALSFQSELDYWGIDIEYLSGCCQ 130
QY 134 BEYKDRKRENAERLMDNDSENNOE-----SMPSLSFRQTMWRAFPENPHTSTLALVEYVV 188
DB 131 ARYHQQKEQNMEEELKREAEITREREGEEFDNTCCAEKRKKLMDLEKPNSSVAAKITAI 190
QY 189 TGEFFIAVSVITNVETVPCGTVPGSKELPCGERYSVA-----FFCLDTACVMIFTVEYLL 243
DB 191 SIMETIVSTIALSLNTLP-----ELQSLDEFGQSTDPQLAHEAVCIAMFTMEYLL 242
QY 244 RLFAAPSRVYRFRSVMISIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVFRYER 296
DB 243 RFLSSPKWKMKFKGDLNALDIALILPYVTIIFLTESNKSVALQFQVRRRVQIFRIMRLR 302
QY 297 IFKFSRHSQGLRIGYTLKSCASELGLFLSLTMAIIFATVMFYAEKSSASKFTSIPA 356
DB 303 ILKLARHSTGLQSLGFTLRRSYNELGLLILFLAMGIMIFSSLVFAEKDEDDTKFKSIPA 362
QY 357 SFWYTIWMTTGLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVVSFRIYHONORA 416
DB 363 SFWMATITMTTVGVDIYPKTLIGKIVGGLCCIAGVLVIALPIPIIVNFSFYEKQKQ 422
QY 417 DK---RAQKAR-----LARIRVAKTSSNA-----YLHSH 445
DB 423 EKAIKRREALERAKRNGSIVSMNMKDAFARSIEMMDIVEKNGESIAKKDKYQDNHLSPN 482
QY 446 RNLGLNEALBLTG-----TPBEHNGKTTSLIESQHHLLHCLEKTGSLVLDPLLS 499


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Db      483 KWKTKRALSETSSKSFETEOGSPFKARSSSPQHIANVOQLEDMYSKMAKTQSOGIILN 542
               ||| | | : | | | | : : : : : | : | :
Oy      500 VRTSTIKNHFIDEQMFEQNCMESSMONYPS----- 530
               : : : | : | : | :
Db      543 TKEMAPQSk--PPEELEMSSMPSPVAPLPARTEGVIDMRSMSSIDSFISCATDFPEATR 599
               : : : : : : : : :
Oy      531 -TRSP-SLSHPGLITTT-----CCSRRSKKTTHL-----PNSNIIPAT 565
               : | | | | | : | : | : | : | : | :
Db      600 FSHSPLASLSSKAGSSTAPEVGWRGALGASGGRLTETNPDPETSRSGFFVESPRSSMKTN 659
               : : | | | | : | : | : | : | :
Oy      566 RLRSMOELSTHIOGSEQSPSTTSRSSLNKKADDLGRPNCKTSQTITAI--ISIPTPAL 623
               : : : : : | | | | : : : : :
Db      660 NPLKLRAALKVNFEVDPTPLL---PSLGL-YHDPLRNCGAALAAYAGLEGASLDLRFL 714
               : : : : : | | | | : : : : :
Oy      624 TPE-----GESRPPASPENNTNI 642
               : | | : | | | | : |
Db      715 SPESSIYTITASARTPPRPSPKHTAI 739

```

RESULT 8

potassium voltage-gated channel - rat
 N:Alternate names: potassium channel KV1; potassium channel RK4; shaker-related potassium
 C:Species: Rattus norvegicus (Norway rat)
 C:date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text_change 09-Jul-2004
 C:Accession: JH0166; D39113; I55392
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunn
 Neuron 4, 929-939, 1990
 A>Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectifi
 A:Reference number: JH0166; MUID:90297965; PMID:2361015
 A:Accession: JH0166
 A:Molecule type: mRNA
 A:Residues: 1-602 <SWA>
 A:Cross-references: UNIPROT:P19024; GB:M27158; NID:g205100; PID:AAA41498.1; PID:g205100
 A:Experimental source: brain
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A>Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
 A:Reference number: A39113; MUID:91156694; PMID:1705709
 A:Accession: D39113
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-552, 'S', 554-602 <ROB>
 R:Morl, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
 J. Biol. Chem. 268, 26482-26493, 1993
 A>Title: The transcription of a mammalian voltage-gated potassium channel is regulated b
 A:Reference number: I55392; MUID:94075338; PMID:8253777
 A:Accession: I55392
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-15 <RES>
 A:Cross-references: GB:L23434; NID:g443766; PID:AAA42337.1; PID:g443767
 A:Experimental source: Sprague-Dawley
 C:Genetics:
 A:Gene: KV1.5
 C:Superfamily: potassium channel protein drk1
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt
 F:242-260/Domain: transmembrane #status predicted <TW1>
 F:316-336/Domain: transmembrane #status predicted <TW2>
 F:347-368/Domain: transmembrane #status predicted <TW3>
 F:387-408/Domain: transmembrane #status predicted <TW4>
 F:423-444/Domain: transmembrane #status predicted <TW5>
 F:484-505/Domain: transmembrane #status predicted <TW6>
 F:10, 44, 116, 181, 290/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:81, 535, 546, 569/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match

Query Match	21.6%;	Score 736;	DB 2;	Length 602;
Best Local Similarity	34.0%;	Pred. No. 4.1e-48;		
Matches 177;	Conservative 90;	Mismatches 162;	Indels 92;	Gaps 11;

```

0x 30 APADKKRQDELIVLWNGRRFQWRTTLERYPTLLGSTEKEF-FENEDTKEYFPDRDP 88
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db	101	APDAGSLHQRVLINISGRFETQIGTLAOFNTLLGDPAKRHLHYFDPRLNEYFFDRNR	160
Qy	89	EYFRCVINFYRT-GKLIHPYECIAVDDELAFYGLIPEIIGCCYEYKDRKRENAERL	147
Db	161	PSFDGILYYQSGGRLRRPNVNSLDVFADEIRFYQ-----LGDAMERERE-----	206
Qy	148	MDDNDSENNQESMPSLSFRQTMRAENPHSTLALVYVYVTFGEFIAVSITNVVETVP-	206
Db	207	-DEGFICEEKPLPRNEFOQVWLFEYPESGSAARAIAVSVLISITITPCLETLPE	265
Qy	207	-----CGTVPGSKE-----LPCGERYSVAFFCLDTACV	234
Db	266	FDERELLRHPVPQPPAPAPGINGSVSGALSSGPTVAPLLP--RTLADPFFIVETTCV	323
Qy	235	MIPTVEYLRLFAAPSRRYREIRSVMSIIDVAIMPYYIGLWMTNEDVSGA-----	285
Db	324	IMPTFELLVRFACPSKAERSRNIMNIIDVAIIPYPTITGLTEIAEQPQGGGQNGQAM	383
Qy	286	----FVTLRVFRVRIFKFSRHSQGLRILGYTLKSCSELGFLFSLTMAIIFATVMFY	341
Db	384	SLAILRVRLRVFRRIFKLSRHSKGIQILGTLQASMBELGLLIFFLFIGVILFSSAVYF	443
Qy	342	AEKGSSASKETSI PASFWYITVTMTLLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVV	401
Db	444	AEADNHGSHFSSSIDAFMWAVVTMTVTGYGDMRPITVYGKIVGSLCAlAGVLTIALPVV	503
Qy	402	IYSNFSRIYH-----QNRADKRR-----AQKARLARIRAVTGSSNAYLH	443
Db	504	IYSNFNYFYHRETDHEQALKEEQONQRRESGLDTGGQKRVKSCSASFCKTGSLSSD	563
Qy	444	SKRNGLNEALELTGTPEEBHMGKTTSLIESQHHLHGLE 484	
Db	564	STRG-----SCPLEKCHLKAKSNVDLRSLYALCLD 595	

RESULT 9

potassium channel protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56529
R/Pak, M.D.; Covarrubias, M.; Ratcliffe, A.; Salkoff, L.
J. Neurosci. 11, 869-880, 1991
A>Title: A mouse brain homolog of the Drosophila Shab K⁺ channel with conserved delayed-
A/Reference number: I56529; MUID:91162315; PMID:2002364
A/Accession: I56529
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-857 <RES>
A/Cross-references: UNIPROT:Q03717; GB:M64228; NID:g200975; PIDN:AAA40112.1; PID:g200976
C/Genetics:
A/Gene: Shab
C/Superfamily: potassium channel protein drkl

Query Match

Query Match 21.5%; Score 735, DB 2, Length 857;
 Best Local Similarity 27.3%; Pred. No. 8e-48;
 Matches 205; Conservative 131; Mismatches 258; Indels 156; Gaps 23

```
Qy      27 MELAPAD--KNKQODELIVLVNSGRFRQT-WRTTLERYPDITLG----STEKEFF-----   74
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     16 LPEBPEMLVRSKACSRVRVLNVGGLAHEVLMR-TLDLRLPRTRGKLRCDCNTHDSLQVCD   74
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      75 -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECSAYDELAFYGILPEIIGDCCY 133
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      75 DYSLEDNEYFFDRHFGAFSTSLNFRTTGRLMHMEEMCALSFSEOLDYMGIDETYLESQQ   134
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy     134 EEYXDKRKRENAERLMDNDSENNOE-----SMPSLFROTMMRAFEINPHSTLTALVFYVV 188
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     135 ARHQKQEOMNEELKREAFTLRERGEEFPDNTCCAERRKKJMDLEKPNSVVAAKILAIT   194
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy     189 TGFPIAAVSITNVETPCGTVPGEKELPCGERYSVA-----FFCLDTFACVMIFTEVEYL 243
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     195 SIMFIIVSTITALSINTLP-----ELQSIDIEFGOSTDNPOLAHVAENCIAWFMEYLL    246
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
```

QY	244	KLFAABSRRYRFRBSVMSIIDVVAIMPYYITGLVMTN-----EDVSGAFVTLLAVRVR	296
	:	: : : : : : : : : : : : : : : : : :	:
Db	247	RFLSSPKMKWFKFPGPLNADIDLALIPYVVITFLTESKSVLGQNVRARVQIFRIMRLR	306
	:	: : : : : : : : : : : : : : : : : :	:
QY	297	IEKFSRHSOGLRIILGYTLKS CASDELGELLPSLTMAIIIFATVNFYAEKGSASKPTSIPA	356
	:	: : : : : : : : : : : : : : : : : :	:
Db	307	ILKLARSTGLQSGLFTLRSYNEGLLILFLAMGINIFFSLVFPAEKDEDDTKEKSIPA	366
	:	: : : : : : : : : : : : : : : : : :	:
QY	357	SFWYTIYMTTGVDGMVKTIAGKIEGSTCSLSGVIVIALPVPIVSNFSRIHQNORA	416
	:	: : : : : : : : : : : : : : : : : :	:
Db	367	SFWMATITMTVGDIYBKTLKGIVGLCCIAGVLVIALPIPIIANNFSEFYEEKROQ	426
	:	: : : : : : : : : : : : : : : : : :	:
QY	417	DK--RAOKKAR-----LARIRVAKTG-----SSN	439
	:	: : : : : : : : : : : : : : : : : :	:
Db	427	EKAIKREALERAKNGSIVSMNMKDAFARSIEMDIIVEKXGEVAKKDQVODHNLSPN	486
	:	: : : : : : : : : : : : : : : : : :	:
QY	440	AYLHSKRGNLNEALELTG-----TPREEHMKTTSLESQHHLHLEKTTGLSYLV	493
	:	: : : : : : : : : : : : : : : : : :	:
Db	487	KWKWTKR-----ALSETSSKSFEETKEQGPBEKARSSSPQHINVQOLQDMYSKWAKTQ	540
	:	: : : : : : : : : : : : : : : : : :	:
QY	494	DDPLSVRTSTIKNHEFIOMEPEONCMESSMONYP-----	530
	:	: : : : : : : : : : : : : : : : : :	:
Db	541	SQPILNTRKEMAPSQ---PQBELENGSMPSVPAPLPRTTEGVIDMRSMSSIDSFISCATD	597
	:	: : : : : : : : : : : : : : : : : :	:
QY	531	-TRSP-SLSHPQLT-----CCGRRSKUTHTLPNSN-----LPA	564
	:	: : : : : : : : : : : : : : : : : :	:
Db	598	PPEATRFESHSPLASLGGKSGASTAPEVGMWGALGASGRLMETNPPIPEASRGPFVESPR	657
	:	: : : : : : : : : : : : : : : : : :	:
QY	565	TRLRS----MOELSTIHOGSEOBSLTTSRSSJLNLKADD-GLRPNCCKSQITTALISIP	618
	:	: : : : : : : : : : : : : : : : : :	:
Db	658	SMKTHNMKLRALKVNPLEGDPTPL---PALGLVHDPLRNNGGARAAVAGLEGASL	713
	:	: : : : : : : : : : : : : : : : : :	:
QY	619	TTPALTPE-----GESRPPASPENTNI	642
	:	: : : : : : : : : : : : : : : : : :	:
Db	714	DKPVLSPRESSIYTASARTPPRSPKHTAI	743

RESULT 10
S00480
potassium channel protein A (clone Sh-beta) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
C:Accession: S00480; S01111
R:Pongs, O.; Keeskemethy, N.; Mueller, R.; Krah-Jentgens, I.; Baumann, A.; Kiltz, H.H.;
EMBO J. 7, 1087-1096, 1988
A:Title: Shaker encodes a family of putative potassium channel proteins in the nervous s
A:Reference number: S00479; MUID:88296413; PMID:2456921
A:Accession: S00480
A:Molecule type: DNA
A:Residues: 1-643 <PON>
A:Cross-references: EMBL:X07132; NID:g8602; PIDN:CAA30144.1; PID:g8603
A:Note: the clone is designated as Sh-beta
R:Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nucleur 331, 137-142, 1988
A:Title: Multiple potassium-channel components are produced by alternative splicing at t
A:Reference number: S00508; MUID:88122563; PMID:2448635
A:Accession: S01111
A:Molecule type: mRNA
A:Residues: 1-643 <SCH>
A:Note: the clone is designated as Shd1
R:Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nucleur 332, 740, 1988
A:Reference number: S01113
A:Contents: annotation; erratum
C:Genetics:
A:Gene: Shaker
A:Cross-references: FlyBase:FBgn0003380
C:Superfamily: potassium channel protein drk1
C:Keywords: alternative splicing; transmembrane protein

Query Match 21.3%; Score 728; DB 2; Length 643;
Best Local Similarity 31.8%; Pred. No.1.8e-47;

	Matches	182;	Conservative	107;	Mismatches	186;	Indels	98;	Gaps	14;
QY	40	ELIVLVNGRRFQWRTTLERXPDTLLGSTEKEE-FPNEDTKEYFDRDRPEVRCVLFY	98							
Db	85	ERVVINVSGLRFETQLRTLLNGFPDITLLGDPARLRVYFDPLRNEYFDRSRPSFDALYY	144							
QY	99	RT-GKLHYPRYECISAYDDELAFYGLPEIIGDCYEEYKDRKRENAERLMDNDSENNQ	157							
Db	145	QSGRLRRPVNPPLDVFSSEIKFYE-----LGDQAINKPRE-----DEGFIKEE	189							
QY	158	ESMPSLSRQTMRAFENPHSTLALVYVYTGFFIAVSITNVETVP-----	206							
Db	190	RLPDPNEKQKRWLLFEYPESQARVAIIISVFILLSTVIFCLETLPEFKHYKVFNT	249							
QY	207	-CGTVPSKELPCGGRYSVAFCLDPACVMIFTVEYLRPLFAAPSRXYRISVMSIIDV	265							
Db	250	TNGTKIEDEVP---DITDPFLIETLCIIMWTFELTVRELA CPNKLNFCRDVNNVIDI	306							
QY	266	AIMPYIIGLV-----MTNNEVSGAFV-TLRVFRVERIFKFSRH	303							
Db	307	AIIPFYITLATVVAEEDTILNLPKAPVSPQDKSSNQAMSLAIRVLRVRFRIKLSRH	366							
QY	304	SGGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWYTI	363							
Db	367	SKGLQILKRTLKASWRELGLIIFLFLIGVLLFSSAVYFAEAGSENSFPKSIIPAFWMAV	426							
QY	364	TMTTLGYGDMVPKTIAGKIFGSGISCSGLVLIAPVPVIVSNFSRIYHONORADKRAOK	423							
Db	427	TMTTVGYGDMTPVGWGWKIVGSLCAIAGVLTIALPVPVIVSNFNFYHRETDOEEMQSON	486							
QY	424	KARLARIRVAKTGSSNAYL-----HSKRNGL-----LNBALELTGTPEEHMGKT	468							
Db	487	FHHV-----TSCPYLRPGLGQHMKKSSLSSESSDMMDLDDGVESTPGLTETHPGRS	537							
QY	469	-----TSLIBSQHHLLHCLKTTGLS-YLVDPPLSVRTSTIKNHEF	510							
Db	538	AVAPFLGAQQQQQPEVASSLSMSIDKQLHPLQLTQTGYYQQQQQQQQQQGFGKQQQ	597							
QY	511	IDQWFEQNCMESSMONTYPTSPSLSGHPGLT	543							
Db	598	QTQQQLQQ--QQSHITINASAAAATSGSGSSGLT	628							

RESULT 11
JH0193
potassium channel shaker form epsilon - fruit fly (Drosophila melanogaster)
N;Alternate names: potassium channel protein A
C/Species: Drosophila melanogaster
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: JH0193; S00508; S0110; S00479; S00482; S02822; S01674
R;Kamb, A.; Tseng-Crank, J.; Tanouye, M.A.
Neuron 1, 421-430, 1988
A;Title: Multiple products of the Drosophila Shaker gene may contribute to potassium char
A;Reference number: JH0193; MUID:90166523; PMID:3272175
A;Accession: JH0193
A;Molecule type: mRNA
A;Residues: 1-656 <KAM>
A;Cross-references: UNIPROT:P08510
A;Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in the putative G prot
R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1988
A;Title: Multiple potassium-channel components are produced by alternative splicing at th
A;Reference number: S00508; MUID:88122563; PMID:2448635
A;Accession: S00508
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-512, 514-564, 'Q', 565-583, 'HV', 586-656 <SCH>
A;Cross-references: GB:X06742; NID:g288441; PIDN:CAA29917.1; PID:g288442
A;Accession: S0110
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'MQMT', 57, 'VAG', 61-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-5
, 'QT', 577-579, 'LQ', 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS',

R;Pongs, O.; Kecskenethy, N.; Mueller, R.; Krah-Jentgens, I.; Baumann, A.; Kiltz, H.H.; EMBL J. 7, 1087-1096, 1988

A;Title: Shaker encodes a family of putative potassium channel proteins in the nervous system

A;Reference number: S00479; MUID:88296413; PMID:2456921

A;Accession: S00479

A;Molecule type: DNA

A;Residues: 1-452, 'F', 454-462, 'V', 464-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-515, 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QL', 643-647, 'V'

A;Cross-references: EMBL:X07131

A;Accession: S00482

A;Molecule type: DNA

A;Residues: 1-348, 'V', <P03>

A;Cross-references: EMBL:X07134; NID:g8606; PIDN:CAA30146.1; PID:g8607

R;Pongs, O.

submitted to the EMBL Data Library, March 1988

A;Reference number: S02822

A;Accession: S02822

A;Molecule type: mRNA

A;Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-515, 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QL', 643-647

A;Cross-references: EMBL:X07131; NID:g8600; PID:g8601

R;Tempel, B.L.; Papazian, D.M.; Schwarz, T.L.; Jan, Y.N.; Jan, L.Y.

Science 237, 770-775, 1987

A;Title: Sequence of a probable potassium channel component encoded at Shaker locus of Drosophila

A;Reference number: S01674; MUID:87292096; PMID:2441471

A;Accession: S01674

A;Molecule type: mRNA

A;Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-515, 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QL', 643-647

A;Cross-references: EMBL:M17211; NID:g157063; PIDN:AAA28417.1; PID:g157064

A;Note: 360-Met and 464-Ile were also found

C;Comment: This protein is a component of a fast, transient, voltage-dependent, or A-type potassium current

C;Genetics:

A;Gene: Shaker

A;Cross-references: FlyBase:FBgn0003380

A;Intons: 61/2; 102/3; 159/1; 191/2; 256/3; 297/2; 348/3; 406/1; 449/2; 514/1

C;Superfamily: potassium channel protein drk1

C;Keywords: alternative splicing; glycoprotein; phosphoprotein; potassium channel; transmembrane

F;228-246/Domain: transmembrane #status predicted <TM1>

F;279-300/Domain: transmembrane #status predicted <TM2>

F;311-332/Domain: transmembrane #status predicted <TM3>

F;358-382/Domain: S4-like region #status predicted <S4L>

F;396-417/Domain: transmembrane #status predicted <TM4>

F;432-453/Domain: transmembrane #status predicted <TM5>

F;457-478/Domain: transmembrane #status predicted <TM6>

F;102,259,263/Binding site: carboxylate (Asn) (covalent) #status predicted

F;521/Binding site: phosphate (Ser) (covalent) #status predicted

	Query Match	21.3%;	Score 727.5;	DB 2;	Length 656;	
	Best Local Similarity	31.7%;	Pred. No. 2.1e-47;			
	Matches	182;	Conservative	107;	Mismatches	186; Indels 99; Gaps 14;
Qy	40 ELIVLVNSGRRFQTWRITLERYPDILLGSTKEKF-FVNETDKYFFPDRDPVFRCLVNFY	98				
Dd	97 ERVINVSGLRFETQLRLNQFPDILLGGPARLRLRYFDLRNEFFDRSRPSFDAILYY	156				
Qy	99 RT-GKLHYPRYCISAYDDDLAFYGILPEIIGDCCYEEXKDRKENAERLMDNDSENNO	157				
Dd	157 QSGRLRPPVNPPLDVFSSEIKFYE----LGDAQINKFRE-----DEGFIKERE	201				
Qy	158 ESMSLSFRQTMWRAFENPHSTLLALVFYYVTGFFIAVSVITNVEVP-----	206				
Dd	202 RPLPDNEKQRKVMLFEYBESSQAARVAISVFVILLISIVICLETLPPEPKHYKVENTT	261				
Qy	207 -CGTVPGSKELPCGERYSVAFPCLDTACVMIFTEVEYLRLFAAPBSRYRPFIRSVMSIIDVV	265				
Dd	262 TNGTKIEEDVP---DIIDPFFLIETLCIMFTFELTYRFLACPKNLTFCRDVMNVIDI	318				
Qy	266 AIMNYIIGLV-----MTNNEDVSGAFV-TLRVRVERIRFKFSRH	303				
Dd	319 AIIIFYFITLATVAEEEDTLNLPAKAVSPQDKSSNQAMSLAIRLVRIQLRVVERIFKLSRH	378				
Qy	304 SQGRILGYTLKSCASEGFLFSLTMAIIPATMVFVAEKGSASAKFTSIPASFMYTIV	363				

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Db      379 SKGLQILGRTLLKASMRRELILLIFLPIGVVLFSSAVYFAEAGSENSFFXSIIPDAFWMAVV 438
Qy      364 TMTTLGYDMPKTIAGKIFGSICLSGLVIALPVPIVSNFSRITHONORADKRRAOK 423
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      439 TMTTVGSDMTPVGWKGKIVGSLCAIAGVLITALLPVPVIVSNFNRYFYHNETDOEBMOSON 498
Qy      424 KARLARIRVAKTSSNAYL-----HSKRNGL-----LNELBELGTPEEBHM GK 467
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      499 FNHV-----TSCPYLPGLTVQGHHMKKSLSSESSDDMDDDGVESFPGLTEHPGR 549
Qy      468 T-----TSLIESQHHLHLCHLEKTTGLS-YLVDDPLLSVRTSTIKNE 509
        -----
Db      550 SAVAPFLGAQQQQQQPFVASLSMSIDKOLHPQLLTQTQLYQQQQQQQQQQONGFKQQO 609
Qy      510 FIDEQMFEQNCMESSMONYPSTRSPSLSHPGLT 543
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      610 QOTQOOLOQ--QOSHNTINASAAAATSGSGSGGLT 641

```

RESULT 12
S12746
potassium channel protein shab11 - fruit fly (*Drosophila melanogaster*)
C,Species: *Drosophila melanogaster*
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C,Accession: S12746; S15058
R,Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990
A,Title: Shal, Shab, and Shaw: three genes encoding potassium channels in *Drosophila*.
A,Reference number: S12746; MUID:90245668; PMID:2336395
A,Accession: S12746
A,Molecule type: mRNA
A,Residues: 1-924 <BUT>
A,Cross-references: UNIPROT:P17970; EMBL:M32659
R,Butler, A.; Wei, A.; Salkoff, L.
submitted to the EMBL Data Library, March 1990
A,Description: Shal, Shab, and Shaw: Three genes encoding potassium channels in *Drosophila*.
A,Reference number: S15058
A,Accession: S15058
A,Molecule type: mRNA
A,Residues: 1-625, 'YG', 628-924 <BU2>
A,Cross-references: EMBL:M32659; NID:g158458; PIDN:AAA28896.1; PID:g158459
C,Genetics:
A,Gene: shab11
A,Cross-references: FlyBase:FBgn0003383
C,Superfamily: potassium channel protein dkl1
C,Keywords: ion channel; potassium channel; transmembrane protein

	Query Match	21.3%;	Score 726;	DB 2;	Length 924;	
	Best Local Similarity	-30.8%;	Pred. No. 4.3e-47;			
	Matches 179;	Conservative 110;	Mismatches 214;	Indels 78;	Gaps 17	
Qy	26 PMPLPADKDKRQDELIVLVNSGRRFQT-WRTTLERYPTDLTG-----STEKEFF-----	74				
Dd	264 PEPFMIA-QSKAVNSRVISINVGVRHEVLMR-TLEBLLPHTRIGRLGECTTHEALVELCDD	321				
Qy	75 FNEDTKEYFFORDPEVFRCVLNFYRTGKLHYPRYECSAYDDELAFYGLLPEIIGDCCYE	134				
Dd	322 YSLADNEYFDFDRHPKSFSSILNIFYRTGKLHIVDEMVCVLAFGDDLVEYMGVDELYESSCCQH	381				
Qy	135 EYDKRK-----RENARLMDDDNDSENNQESMPSLSFRQTMRAFENPHTSTLALVFYY	187				
Dd	382 KYHQREKNVHEMRKEAKESLRQRDEEFGEKGFS--EYQXYIMELLEKPNTSPARVIAY	439				
Qy	188 VTGFPAVSVINNVETVP-----CGIYPGSKELPCGERISVAFFCLDTACWMIFTVEY	241				
Dd	440 ISILFIYLSTALTINTLPQLQHIIDNGTPODNPOLA-----WEAVCITWFTLEY	489				
Qy	242 LLRLFAAPSRYRPIRSVMSIIDVVAIMPYYIGLVW--TTNN-----EDVSGAFVTLRVFR	293				
Dd	490 ILRFSSSPDKWRPFKGGINIIDLAILPYFVSLFLGETNKNAATDQFOVRRVVGVFRIMR	549				
Qy	294 VRIIFKFSRHSGCLRILGYTLKSCASELGILLFSLTMAIIIFATVMFYAEKGSASKFTS	353				

[illegible]

RESULT 13
S66669
potassium channel (Kv1.5) - rabbit
C.Species: *Oryctolagus cuniculus* (domestic rabbit)
C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: S66669
R.Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A1.Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit
A1.Reference number: S66669; MUID:96032538; PMID:7556635
A1.Accession: S66669
A1.Status: preliminary; nucleic acid sequence not shown
A1.Molecule type: mRNA
A1.Residues: 1-598 <SAS>
A1.Cross-references: UNIPROT:P50638; EMBL:D45025; NID:g1060972; PIDN:BAAB08082.1; PID:d1000
C1.Superfamily: potassium channel protein drk1

Query Match	21.1%	Score 719;	DB 2;	Length 598;
Best Local Similarity	35.0%;	Pred. No. 8e-47;		
Matches 166;	Conservative 85;	Mismatches 141;	Indels 82;	Gaps 9;

[illegible]

RESULT 14
A49507
potassium channel Kv1.5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A49507; B49507
R:Altali, B.; Lesage, F.; Ziliiani, P.; Guillemare, E.; Honore, E.; Waldmann, R.; Hugnot, J. Biol. Chem. 268, 24283-24289, 1993
A:Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+) A:Reference number: A49507; MUID:94043264; PMID:8226976
A:Accession: A49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-602 <ATT>
A:Cross-references: UNIPROT:Q61762; GB:L22218; NID:g435603; PIDN:AAA39365.1; PID:g435604
A:Accession: B49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 201-602 <AT2>
A:Cross-references: GB:L22218
C:Superfamily: potassium channel protein drk1
C:Keywords: alternative splicing

Query Match	21.1%;	Score 719;	DB 2;	Length 602;
Best Local Similarity	34.3%;	Pred. No. 8.1e-47;		
Matches 176;	Conservative 93;	Mismatches 168;	Indels 76;	Gaps 12;

[illegible]

RESULT 15
I77466
potassium channel - human
C/Species: Homo sapiens (man)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I77466
R/Ramashami, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990

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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:33:59 ; Search time 612.889 Seconds
(without alignments)
547.263 Million cell updates/sec

Title: US-10-062-879-2

Perfect score: 3412

Sequence: 1 MAGVAAHLFPAFAAIGMM.....PGPNTNIPSTISNVKSVL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3407	99.9	655	1 KCD3_HUMAN	Q9UK17 homo sapien
2	3400	99.6	655	1 KCD3_RAT	Q62897 rattus norv
3	3390	99.4	655	1 KCD3_MOUSE	Q9Z0V1 mus musculu
4	3381	99.1	655	1 KCD3_RABIT	Q9T55 oryctolagus
5	3378	99.0	655	2 Q8WN02	Q8WN02 mustela put
6	3237.5	94.9	658	2 Q9PTD3	Q9PTD3 gallus gall
7	2925	85.7	659	2 O57662	O57662 xenopus lae
8	2570.5	75.3	638	2 Q7ZW36	Q7ZW36 brachydano
9	2510.5	73.6	630	2 Q8HYZ1	Q8HYZ1 mustela put
10	2504.5	73.4	630	1 KCD2_RABIT	P59995 oryctolagus
11	2503.5	73.4	630	1 KCD2_MOUSE	Q9Z0V2 mus musculu
12	2499.5	73.3	630	1 KCD2_RAT	Q63881 rattus norv
13	2498.5	73.2	630	1 KCD2_HUMAN	Q9NZV8 homo sapien
14	2497.5	73.2	632	2 Q8UW33	Q8UW33 gallus gall
15	2122	62.2	651	1 KCD1_MOUSE	Q03719 mus musculu
16	2113	61.9	647	1 KCD1_HUMAN	Q9NAE2 homo sapien
17	2013	59.0	660	2 Q95PC8	Q95PC8 panulirus i
18	2007	58.8	660	2 Q95PC7	Q95PC7 panulirus i
19	2004	58.7	680	2 Q95PC6	Q95PC6 panulirus i
20	1967	57.6	579	2 Q95PC5	Q95PC5 panulirus i
21	1965	57.6	585	2 Q95PC4	Q95PC4 panulirus i
22	1961.5	57.5	546	2 Q26040	Q26040 panulirus i
23	1961.5	57.5	551	2 Q95PD0	Q95PD0 panulirus i
24	1946.5	57.0	561	2 Q95PC9	Q95PC9 panulirus i
25	1944	57.0	608	2 Q95PC3	Q95PC3 panulirus i
26	1915.5	56.1	490	1 C1KL_DROME	P17971 drosophila
27	1908.5	55.9	490	2 Q7Q157	Q7Q157 anopheles g
28	1885.5	55.3	800	2 Q6R4N6	Q6R4N6 clona intes
29	1842	54.0	633	2 Q8IAD3	Q8IAD3 halocynthia
30	1786	52.3	471	2 Q8IAD2	Q8IAD2 halocynthia
31	1750.5	51.3	609	2 Q95XD1	Q95XD1 caenorhabdi

ALIGNMENTS

32	1654.5	48.5	372	2	Q75LS7	Q75LS7 homo sapien
33	1328.5	38.9	478	2	P91784	P91784 polyorchis
34	1103	32.3	236	2	Q6I9B6	Q6I9B6 rattus norv
35	837	24.5	409	2	P91783	P91783 polyorchis
36	767	22.5	908	2	O18476	O18476 loligo peal
37	766.5	22.5	907	1	KCB2_RAT	Q63099 rattus norv
38	761	22.3	911	2	Q7Z7D0	Q7Z7D0 homo sapien
39	756	22.2	816	2	Q98SV4	Q98SV4 ictalurus p
40	755.5	22.1	911	1	KCB2_HUMAN	Q92953 homo sapien
41	754.5	22.1	898	2	Q91592	Q91592 xenopus lae
42	750	22.0	911	1	KCB2_RABIT	Q95111 oryctolagus
43	748.5	21.9	985	1	C1KB_DROME	P17970 drosophila
44	746	21.9	858	1	KCB1_RABIT	Q9MZ19 oryctolagus
45	745	21.8	494	2	Q91830	Q91830 oncorhynch

RESULT 1

KCD3_HUMAN STANDARD; PRT; 655 AA.
AC Q9UK17; O60576; O60577; Q9UH85; Q9UH86; Q9UK16;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
potassium channel subunit Kv4.3).
GN Name=KCND3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND
RP FUNCTION.
RC TISSUE=Heart;
RC MEDLINE=99061682; PubMed=9843794;
RA Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.,
RT "Isolation and characterization of the human gene encoding Ito:
RT further diversity by alternative mRNA splicing.";
RL Am. J. Physiol. 275:R1963-R1970(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Brain, and Heart;
RC MEDLINE=99218223; PubMed=10200233;
RA Dilks D., Ling H.-P., Cockett M., Sokol P., Numann R.,
RT "Cloning and expression of the human Kv4.3 potassium channel.";
RL J. Neurophysiol. 81:1974-1977(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RC Camels T.P.G., Fatyre J.-F., Javre J.-L., Cheval B., Rouanet S.,
RA Bril A.,
RT "Long and short human isoforms of the Kv4.3 channel: cloning,
RT expression, electrophysiology, pharmacology and phosphorylation by
RT protein kinase C.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain cortex;
RC MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;
RA Isbrandt D., Leicher T., Waldschuetz R., Zhu X.-R., Luhmann U.,
RA Michel U., Sauter K., Pongs O.,
RT "Gene structures and expression profiles of three human KCND (Kv4)
RT potassium channels mediating A-type currents I(TO) and I(SA).";
RL Genomics 64:144-154(2000).
RN [5]
RP INTERACTION WITH KCNIP2; KCNE1; KCNE2; SCN1B AND KCNA1.
RP MEDLINE=22233757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9;
RA Deschenes I., Tomaselli G.F.,
RT "Modulation of Kv4.3 current by accessory subunits.";

RL FEBS Lett. 528:183-188(2002).
CC - FUNCTION: pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC - SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4 (By similarity). Interacts with KCNE1, KCNE2, SCN1B and
CC KCNAB1.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=KCND3L, Long;
CC IsoId=Q9UK17-1; Sequence=Displayed;
CC Name=2; Synonyms=KCND3S, Short;
CC IsoId=Q9UK17-2; Sequence=VSP_008826;
CC - TISSUE SPECIFICITY: Highly expressed in heart and brain, in
CC particular in cortex, cerebellum, amygdala and caudate nucleus.
CC Detected at lower levels in liver, skeletal muscle, kidney and
CC pancreas. Isoform 1 predominates in most tissues. Isoform 1 and
CC isoform 2 are detected at similar levels in brain, skeletal muscle
CC and pancreas.
CC - DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC - SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.

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DR EMBL; AF048712; AAC05121.1; -;
DR EMBL; AF048713; AAC05122.1; -;
DR EMBL; AF187963; AAF01044.1; -;
DR EMBL; AF187964; AAF01045.1; -;
DR EMBL; AF205856; AAF20924.1; -;
DR EMBL; AF205857; AAF20925.1; -;
DR EMBL; AF120491; AAD38898.1; -;
DR EMBL; AF166011; AAF68177.1; -;
DR EMBL; AF166009; AAF68177.1; JOINED.
DR EMBL; AF166010; AAF68177.1; JOINED.
DR EMBL; AF166011; AAF68178.1; -;
DR EMBL; AF166009; AAF68178.1; JOINED.
DR EMBL; AF166010; AAF68178.1; JOINED.
DR HSSP; Q16968; 1A68.
DR Genew: HGNC:6239; KCND3.
DR MIM; 605411; -;
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR pfam; PF00520; Ion_trans.1.
DR pfam; PF02214; K_tetra.1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KM Alternative splicing; Ion transport; Ionic channel; Multigene family;
KM Potassium; Potassium channel; Potassium transport; Transmembrane;
KM Transport; Voltage-gated channel.
FT DOMAIN 1 181 Cytoplasmic (Potential).
FT TRANSMEM 182 202 Segment S1 (Potential).
FT TRANSMEM 222 242 Segment S2 (Potential).
FT

FT DOMAIN 243 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Segment S3 (Potential).
FT TRANSMEM 287 307 Segment S4 (Potential).
FT DOMAIN 308 320 Cytoplasmic (Potential).
FT TRANSMEM 321 341 Segment S5 (Potential).
FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).
FT DOMAIN 403 655 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPLIC 488 506 Missing (in isoform 2).
FT FTId=VSP_008826.
FT CONFLICT 239 239 V -> G (in Ref. 1).
FT CONFLICT 375 375 P -> L (in Ref. 1).
FT CONFLICT 408 408 R -> G (in Ref. 2).
FT CONFLICT 452 452 E -> G (in Ref. 2).
FT CONFLICT 531 531 T -> Q (in Ref. 2).
FT CONFLICT 564 564 A -> D (in Ref. 2).
FT CONFLICT 646 646 A -> T (in Ref. 1).
FT CONFLICT 654 654 V -> A (in Ref. 3 and 4).
SQ SEQUENCE 655 AA; 73479 MW; ADC8502A97204764 CRC64;
Query Match 99.9%; Score 3407; DB 1; Length 655;
Best Local Similarity 99.8%; Pred. No. 3.6e-205;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAGVAAWLPAPAAAIGWNPVANCMPPLAPADKNKQDELIVNVSGRRPQTWRTTLER 60
DB 1 MAAGVAAWLPAPAAAIGWNPVANCMPPLAPADKNKQDELIVNVSGRRPQTWRTTLER 60
QY YEDTLTGSTEKEFFPNEDTKEYFPDDEPVEFRVCLNFRYTGKLAHYPRYECISAYDDELA 120
DB YEDTLTGSTEKEFFPNEDTKEYFPDDEPVEFRVCLNFRYTGKLAHYPRYECISAYDDELA 120
QY YGILPEITGDCCEYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAFENPHTST 180
DB YGILPEITGDCCEYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAFENPHTST 180
QY LALVFYVYTGFFIAVSVITNVETVPCGTVPSSKELPCGERYSVAFCLDPAACVMIFVE 240
DB LALVFYVYTGFFIAVSVITNVETVPCGTVPSSKELPCGERYSVAFCLDPAACVMIFVE 240
QY YLLRLFAAPSRRYRFRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRYRVFRIFKE 300
DB YLLRLFAAPSRRYRFRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRYRVFRIFKE 300
QY SRRSOGRLILGYTIKSCASELGLFLSLTMAIIPATWVFYAEKSSASAKTSPASWY 360
DB SRRSOGRLILGYTIKSCASELGLFLSLTMAIIPATWVFYAEKSSASAKTSPASWY 360
QY TIVTMTLGYGDMVPKTIACKIFGSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
DB TIVTMTLGYGDMVPKTIACKIFGSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
QY AOKKARLARIRVAKTGSSNAYLHASKNGLNLEALELTGPPEEHNGKTTSLIESQHHL 480
DB AOKKARLARIRVAKTGSSNAYLHASKNGLNLEALELTGPPEEHNGKTTSLIESQHHL 480
QY HCLEKTGLSYLVDDPLSLVSTSTIKGHEFIDEQMEQCMSSMONTPTSPSLSSHP 540
DB HCLEKTGLSYLVDDPLSLVSTSTIKGHEFIDEQMEQCMSSMONTPTSPSLSSHP 540
QY GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNKADG 600
DB GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNKADG 600
QY LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVVKVSVL 655
DB LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGPNTNIPSTSNVVKVSVL 655
RESULT 2
KCD3 RAT
ID KCD3_RAT STANDARD; PRT; 655 AA.

AC Q62897; Q08723; P70622; Q63286; Q99P42;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
GN Name=Kcnd3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=96428386; PubMed=8831489;
RA Dixon J.E., Shi W., Wang H.-S., McDonald C., Yu H., Wymore R.S.,
RA Cohen I.S., McKinnon D.;
RT "Role of the Kv4.3 K+ channel in ventricular muscle. A molecular
RT correlate for the transient outward current.";
RL Circ. Res. 79:659-668(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=96317227; PubMed=8734615;
RA Serodio P., Vega-Saenz de Miera E., Rudy B.;
RT "Cloning of a novel component of A-type K+ channels operating at
RT subthreshold potentials with unique expression in heart and brain.";
RL J. Neurophysiol. 75:2174-2179(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hippocampus;
RX MEDLINE=97154683; PubMed=9001401; DOI=10.1016/S0014-5793(96)01388-9;
RA Tsaur M.-L., Chou C.-C., Shih Y.-H., Wang H.-L.;
RT "Cloning, expression and CNS distribution of Kv4.3, an A-type K+
RT channel alpha subunit.";
RL FEBS Lett. 400:215-220(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=smooth muscle, and Vas deferens;
RX MEDLINE=98111009; PubMed=9450548; DOI=10.1016/S0014-5793(97)01483-X;
RA Ohya S., Tanaka M., Oku T., Asai Y., Watanabe M., Giles W.R.,
RA Imaizumi Y.;
RT "Molecular cloning and tissue distribution of an alternatively spliced
RT variant of an A-type K+ channel alpha-subunit, Kv4.3 in the rat.";
RL FEBS Lett. 420:47-53(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=21402960; PubMed=11427525; DOI=10.1074/jbc.M101058200;
RA Song M., Helguera G., Eghbali M., Zhu N., Zarek M.M., Olcese R.,
RA Toro L., Stefani E.;
RT "Remodeling of Kv4.3 potassium channel gene expression under the
RT control of sex hormones.";
RL J. Biol. Chem. 276:31883-31890(2001).
RN [6]
RP SEQUENCE OF 455-606 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97460452; PubMed=93114834;
RA Takimoto K., Li D., Hershan K.M., Li P., Jackson E.K., Levitan E.S.;
RT "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel subunit
RT mRNAs in ventricles of renovascular hypertensive rats.";
RL Circ. Res. 81:533-539(1997).
RN [7]
RP INTERACTION WITH KCNIP1; KCNIP2 AND KCNIP3.
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
RA An W.F., Bowldy M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
RA Hinson J.W., Mattsson K.I., Straasle B.W., Trimmer J.S., Rhodes K.J.;
RT "Modulation of A-type potassium channels by a family of calcium
RT sensors.";
RL Nature 403:553-556(2000).
RN [8]
RP SUBCELLULAR LOCATION.
RX MEDLINE=2212857; PubMed=12006572; DOI=10.1074/jbc.M203651200;
RA Takimoto K., Yang E.-K., Conforti L.;

RT "Palmitoylation of Kchp splicing variants is required for efficient
RT cell surface expression of Kv4.3 channels.";
RL J. Biol. Chem. 277:26904-26911(2002).
RN [9]
RP INTERACTION WITH KCNIP4.
RX MEDLINE=21664433; PubMed=11805342; DOI=10.1073/pnas.022509299;
RA Holmqvist M.H., Cao J., Hernandez-Pineda R., Jacobson M.D.,
RA Carroll K.I., Sung M.A., Betty M., Ge P., Gilbride K.J., Brown M.E.,
RA Jurman M.E., Lawson D., Slos-Santiago I., Xie Y., Covarrubias M.,
RA Rhodes K.J., Distefano P.S., An W.F.;
RT "Elimination of fast inactivation in Kv4 A-type potassium channels by
RT an auxiliary subunit domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:1035-1040(2002).
CC -I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(fro)
CC current in heart and I(fsa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC -I- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNAB1 (by
CC similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Interaction with
CC palmitoylated KCNIP2 and KCNIP3 enhances cell surface expression.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Kv4.3 long form;
CC IsoId=Q62897-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q62897-2; Sequence=VSP_008831;
CC Name=3;
CC IsoId=Q62897-3; Sequence=VSP_008831, VSP_008832;
CC -I- TISSUE SPECIFICITY: Highly expressed in brain, in particular in
CC the retrosplenial cortex, medial habenula, anterior thalamus,
CC hippocampus, cerebellum and lateral geniculate and superior
CC colliculus. Highly expressed in heart atrium and throughout the
CC ventricle wall, in lung and vas deferens.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -I- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -----
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CC EMBL; U42975; AAC52695.1; -;
CC EMBL; U75448; AAB18337.1; -;
CC EMBL; U48619; AAA80459.1; -;
CC EMBL; AF334791; AAK07651.1; -;
CC EMBL; AB003587; BAA24525.1; -;
CC HSSP; U92897; AAB53321.1; -;
CC HSSP; Q16968; IAG8.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003091; K+channel.
CC InterPro; IPR003131; K tetra.
CC InterPro; IPR004056; KV43channel.
CC InterPro; IPR003968; Kv_channel.
CC InterPro; IPR005820; M+channel_nlg.
CC InterPro; IPR003975; Shal_channel.
CC Pfam; PF00520; Ion_trans; 1.
CC Pfam; PF02214; K tetra; 1.
CC PRINTS; PR00169; KCHANNEL.
CC PRINTS; PR01518; KV43CHANNEL.
CC PRINTS; PR01491; KVCHANNEL.
CC PRINTS; PR01497; SHALCHANNEL.
CC Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW

```
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181 Cytoplasmic (Potential).
FT TRANSMEM 182 202 Segment S1 (Potential).
FT TRANSMEM 222 242 Segment S2 (Potential).
FT TRANSMEM 243 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Segment S3 (Potential).
FT TRANSMEM 287 307 Segment S4 (Potential).
FT TRANSMEM 308 320 Cytoplasmic (Potential).
FT TRANSMEM 321 341 Segment S5 (Potential).
FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).
FT DOMAIN 403 655 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPPLIC 488 506 Missing (in isoform 2 and isoform 3).
FT VARSPPLIC 608 655 /FTid=VSP_008831.
FT VARSPPLIC 608 655 SQTITATISIPTRPALTPGEGSRPPASPGPNTNIPSTNS
VVKVSVL -> QDEQPRGRVVTCKQEEITLICI (in
isoform 3).
FT FTid=VSP_008832.
FT L -> H (in Ref. 3).
FT S -> T (in Ref. 2 and 5).
FT S -> T (in Ref. 3).
FT P -> A (in Ref. 2).
FT V -> A (in Ref. 1 and 4).
SQ SEQUENCE 655 AA; 73513 MW; 26BC512BDE069C09 CRC64;

Query Match 99.6%; Score 3400; DB 1; Length 655;
Best Local Similarity 99.7%; Pred. No. 9.8e-205;
Matches 653; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAGVAAMPFARAAAGMPVANCMPMLAPADKNKRODELIVLANSGRFPQWRTTLER 60
DB 1 MAGVAAMPFARAAAGMPVANCMPMLAPADKNKRODELIVLANSGRFPQWRTTLER 60
QY 61 YPDTLGSTEKEFEFNEDETKYFFDRDEVEFRVYINFTGKLHYPRYECISAYDELA 120
DB 61 YPDTLGSTEKEFEFNEDETKYFFDRDEVEFRVYINFTGKLHYPRYECISAYDELA 120
QY 121 YGILPEITGDCYEEYKDKRKNRANERLMDNDSENQESMPSLSFQOTMRAFENPHST 180
DB 121 YGILPEITGDCYEEYKDKRKNRANERLMDNDSENQESMPSLSFQOTMRAFENPHST 180
QY 121 YGILPEITGDCYEEYKDKRKNRANERLMDNDSENQESMPSLSFQOTMRAFENPHST 180
DB 121 YGILPEITGDCYEEYKDKRKNRANERLMDNDSENQESMPSLSFQOTMRAFENPHST 180
QY 181 LALVEYVYVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCCLDTACVMIFVE 240
DB 181 LALVEYVYVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCCLDTACVMIFVE 240
QY 241 YLLRLFAASRRYRFRSVMSIIDVVAIMPYIIGVMTNEDVSGAFYTLRVFRVRIKFE 300
DB 241 YLLRLFAASRRYRFRSVMSIIDVVAIMPYIIGVMTNEDVSGAFYTLRVFRVRIKFE 300
QY 241 YLLRLFAASRRYRFRSVMSIIDVVAIMPYIIGVMTNEDVSGAFYTLRVFRVRIKFE 300
DB 241 YLLRLFAASRRYRFRSVMSIIDVVAIMPYIIGVMTNEDVSGAFYTLRVFRVRIKFE 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGASKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGASKFTSIPASFWY 360
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGASKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSGASKFTSIPASFWY 360
QY 361 TIVMTTIGYGDMPKTIAGKIFGSGISLGVLYIALPVPIVSNFSRIYHONQADKRR 420
DB 361 TIVMTTIGYGDMPKTIAGKIFGSGISLGVLYIALPVPIVSNFSRIYHONQADKRR 420
QY 361 TIVMTTIGYGDMPKTIAGKIFGSGISLGVLYIALPVPIVSNFSRIYHONQADKRR 420
DB 361 TIVMTTIGYGDMPKTIAGKIFGSGISLGVLYIALPVPIVSNFSRIYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYHSKRNGLNEALELTGTPEEHEMGTSTLSIQHHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYHSKRNGLNEALELTGTPEEHEMGTSTLSIQHHHL 480
QY 421 AOKKARLARIRVAKTGSSNAYHSKRNGLNEALELTGTPEEHEMGTSTLSIQHHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYHSKRNGLNEALELTGTPEEHEMGTSTLSIQHHHL 480
QY 481 HCLEKTTGSLVLDPELLSVRTSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
DB 481 HCLEKTTGSLVLDPELLSVRTSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
QY 481 HCLEKTTGSLVLDPELLSVRTSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
DB 481 HCLEKTTGSLVLDPELLSVRTSTIKNHEFIDEQMFQONCESSMOMYPTSTRPSLSHP 540
QY 541 GLTTTCCSRSKKTHLPNSNLPATRLASMOELSTIHIGSEQPSLTSSSLNLKADG 600
DB 541 GLTTTCCSRSKKTHLPNSNLPATRLASMOELSTIHIGSEQPSLTSSSLNLKADG 600
QY 541 GLTTTCCSRSKKTHLPNSNLPATRLASMOELSTIHIGSEQPSLTSSSLNLKADG 600
DB 541 GLTTTCCSRSKKTHLPNSNLPATRLASMOELSTIHIGSEQPSLTSSSLNLKADG 600
QY 601 LRPNCKTSQITTAISIPTRPALTPGEGSRPPASPGPNTNIPSTNSVVKVSVL 655
DB 601 LRPNCKTSQITTAISIPTRPALTPGEGSRPPASPGPNTNIPSTNSVVKVSVL 655
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DB 601 LRPNCKTSQITTAISIPTRPALTPGEGSRPPASPGPNTNIPSTNSVVKVSVL 655
RESULT 3
KCD3_MOUSE STANDARD; PRT; 655 AA.
AC Q9Z0V1; Q8CC44; Q9Z0V0;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
potassium channel subunit Kv4.3).
GN Name=Kcnd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkfein R.J., Fleet C., Clark R.B., Giles W.R.;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldeirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriani L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guericchini S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pallai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [3]
RP INTERACTION WITH KCND2 AND KCNIP2.
RX MEDLINE=21481767; PubMed=11598014; DOI=10.1093/emboj/20.20.5715;
RA Liles B., Franz O., Sewing S., Bruns R., Neuhoef H., Roeper J.;
RT "Tuning pacemaker frequency of individual dopaminergic neurons by
RT Kv4.3L and KChIP3.1 transcription."
RL EMBO J. 20:5715-5724 (2001).
RN [4]
RP INTERACTION WITH KCND2 AND KCNIP2.
RX MEDLINE=21906624; PubMed=11909823;
RA DOI=10.1161/01.RES.0000012664.05949.B0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RA Nerbonne J.M.;
RT "Role of heteromultimers in the generation of myocardial transient
RT outward K+ currents."
RL Circ. Res. 90:586-593 (2002).
```


CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(TO)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC
CC -!- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNAB1 (By
CC similarity).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Kv4.3L;
CC IsoId=Q9Z0V1-1; Sequence=Displayed;
CC Name=2; Synonyms=Kv4.3M;
CC IsoId=Q9Z0V1-2; Sequence=VSP_008827;
CC Name=3;
CC IsoId=Q9Z0V1-3; Sequence=VSP_008828, VSP_008829;
CC Note=May be due to intron retention. No experimental
CC confirmation available;
CC
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC
CC -!- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AF107781; AAD16973.1; -.
DR EMBL; AF107782; AAD16974.1; -.
DR EMBL; AK033962; BAC28529.1; -.
DR HSSP; Q16968; 1A68.
DR MGD; MGI:1928743; Kcnd3.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004056; Kv43channel.
DR InterPro; IPR003968; Kv channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181
FT TRANSMEM 182 202 Cytoplasmic (Potential).
FT TRANSMEM 222 242 Segment S1 (Potential).
FT DOMAIN 243 256 Segment S2 (Potential).
FT TRANSMEM 257 277 Cytoplasmic (Potential).
FT TRANSMEM 287 307 Segment S3 (Potential).
FT DOMAIN 308 320 Segment S4 (Potential).
FT TRANSMEM 321 341 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Segment S5 (Potential).
FT TRANSMEM 382 402 Segment H5 (pore-forming) (Potential).
FT DOMAIN 403 455 Segment S6 (Potential).
FT SITE 367 372 Cytoplasmic (Potential).
FT VARSPLIC 488 531 Selectivity filter (By similarity).
FT GLSYVDDPLSVRTSTIKNHEPDEQMEQNCMESSMONY
FT SKTIVSLPIG (in isoform 3).
FT /FTId=VSP_008828.
FT Missing (in isoform 2).
FT VARSPLIC 488 506

FT FT VARSPLIC 532 655 /FTId=VSP_008827.
FT Missing (in isoform 3).
FT /FTId=VSP_008829.
SQ SEQUENCE 655 AA; 73462 MW; 17FCE5AE2868B33 CRC64;
Query Match 99.4%; Score 3390; DB 1; Length 655;
Best Local Similarity 99.4%; Pred. No. 4.2e-204;
Matches 651; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MAAGVAAWLPFAAAATGMPVANCMPMLAPADKNRQDELIVLVNSGRRFQWTPTLLR 60
DB 1 MAAGVAAWLPFAAAATGMPVANCMPMLAPADKNRQDELIVLVNSGRRFQWTPTLLR 60
QY YPDTLLGSTEKEFFFNEDTKYFEDRDPEVFCVILNFRYTGKLIHYPRYECISAYDELA 120
DB YPDTLLGSTEKEFFFNEDTKYFEDRDPEVFCVILNFRYTGKLIHYPRYECISAYDELA 120
QY YGILPEIIGDCYEEYKDRKRENERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180
DB YGILPEIIGDCYEEYKDRKRENERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180
QY LALVEYVVTGFEIIVSVITNVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIPTVE 240
DB LALVEYVVTGFEIIVSVITNVETVPCGTVPGSKELPCGERYSVAFCLDTACVMIPTVE 240
QY YLRLFAAPSRKRFIRGVSIIIDVVAIMPEYIIGLVMTNNEVSGAFVTLRVERVRIK 300
DB YLRLFAAPSRKRFIRGVSIIIDVVAIMPEYIIGLVMTNNEVSGAFVTLRVERVRIK 300
QY SRHSGRLRLGTLKSCASELGFLLSTMAIIFATVMFYAEKSSASAKFTSIIPASFWY 360
DB SRHSGRLRLGTLKSCASELGFLLSTMAIIFATVMFYAEKSSASAKFTSIIPASFWY 360
QY TIVMTTLGYGDMVPKTIAGKIFGSIISGLVLYALPVPIVSNFSRIYHONGRADKRR 420
DB TIVMTTLGYGDMVPKTIAGKIFGSIISGLVLYALPVPIVSNFSRIYHONGRADKRR 420
QY AOKKARLARIIVAKTGSSNAYLHSHKNGLINEALELTGTPEEHMGKTSLIESQHHL 480
DB AOKKARLARIIVAKTGSSNAYLHSHKNGLINEALELTGTPEEHMGKTSLIESQHHL 480
QY HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
DB HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONYPSTRSPSLSSHP 540
QY GLTTCCSRRSKKTHLPNSNLPAIRLRSMQELSTLHIGSQSPSLTSSSLNLKADG 600
DB GLTTCCSRRSKKTHLPNSNLPAIRLRSMQELSTLHIGSQSPSLTSSSLNLKADG 600
QY LRPNCKTSQITTAIISIPTPPALTPGESRPPAPSGPNTNIPISITSNVVKSVL 655
DB LRPNCKTSQITTAIISIPTPPALTPGESRPPAPSGPNTNIPISITSNVVKSVL 655
RESULT 4
KCD3_RABIT STANDARD; PRT; 655 AA.
ID KCD3_RABIT
AC Q9TTT5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=New Zealand white; TISSUE=Corneal endothelium;
RA Rae J.L.;
RT "Ion channels in cornea endothelium.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 73-645 FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=22117972; PubMed=12122138;
 RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G., Obeso A., Ganfornina M.D., Gonzalez C.;
 RT "Molecular identification of Kv alpha subunits that contribute to the oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit carotid body."
 RT J. Physiol. (Lond.) 542:369-382(2002).
 CC -1- FUNCTION: pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.
 CC -1- SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNA1 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q9TTS-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=Q9TTS-2; Sequence=YSP_008830;
 CC -1- TISSUE SPECIFICITY: Detected in carotid body chemoreceptor cells and in frontal cortex.
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.
 CC -----
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 CC -----
 DR EMBL; AF198445; AAF06021.1; -;
 DR EMBL; AF493549; AAM46843.1; -;
 DR HSSP; Q16968; 1A68.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR004056; KV43channel.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR003975; Shal channel.
 DR Pfam; PF00520; Ion_trans_1.
 DR Pfam; PF02214; K_tetra_1.
 DR PRINTS; PRO0169; KCHANNEL.
 DR PRINTS; PRO1518; KV43CHANNEL.
 DR PRINTS; PRO1491; KVCHANNEL.
 DR PRINTS; PRO1497; SHALCHANNEL.
 KW Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane; Transport; Voltage-gated channel.
 KW DOMAIN 1 181 Cytoplasmic (Potential).
 FT TRANSMEM 182 202 Segment S1 (Potential).
 FT TRANSMEM 222 242 Segment S2 (Potential).
 FT DOMAIN 243 256 Cytoplasmic (Potential).
 FT TRANSMEM 257 277 Segment S3 (Potential).
 FT TRANSMEM 287 307 Segment S4 (Potential).
 FT DOMAIN 308 320 Cytoplasmic (Potential).
 FT TRANSMEM 321 341 Segment S5 (Potential).
 FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
 FT TRANSMEM 382 402 Segment S6 (Potential).

FT DOMAIN 403 655 Cytoplasmic (Potential).
 FT SITE 367 372 Selectivity filter (By similarity).
 FT VARSPLIC 488 506 Missing (in isoform 2).
 FT FTId=VSP_008830.
 SQ SEQUENCE 655 AA; 73380 MW; C6AE9E855415FAF9 CRC64;
 Query Match 99.1%; Score 3381; DB 1; Length 655;
 Best Local Similarity 99.1%; Pred. No. 1.5e-203;
 Matches 649; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MAAGVAAWLPFAFAAAIGWMPVANCMPPLAPADKNKRODELIVNVSGRRFQRTWRTLER 60
 DB 1 MAAGVAAWLPFAFAAAIGWMPVANCMPPLAPADKSKRODELIVNVSGRRFQRTWRTLER 60
 QY YPDTLLGSTEKEFFFNEDTKEYFFPDDEVEFRVCVLPFRYTGKLYPRYECTSAYDELA 120
 DB 61 YPDTLLGSTEKEFFFNEDTKEYFFPDDEVEFRVCVLPFRYTGKLYPRYECTSAYDELA 120
 QY YGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQESMPSLFRQTMWRAFENPTST 180
 DB 121 YGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQESMPSLFRQTMWRAFENPTST 180
 QY LALVIFYVTGFFIAVSVITNVETVPCGTVPKSKELPGGERYSVAFCLDTACMITVE 240
 DB 181 LALVIFYVTGFFIAVSVITNVETVPCGTVPKSKELPGGERYSVAFCLDTACMITVE 240
 QY LALVIFYVTGFFIAVSVITNVETVPCGTVPKSKELPGGERYSVAFCLDTACMITVE 240
 DB 181 LALVIFYVTGFFIAVSVITNVETVPCGTVPKSKELPGGERYSVAFCLDTACMITVE 240
 QY YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVFRIFKF 300
 DB 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVFRIFKF 300
 QY YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVFRIFKF 300
 DB 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVFRIFKF 300
 QY SRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVWFYAEKSSASAKFTSIPASFWY 360
 DB 301 SRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVWFYAEKSSASAKFTSIPASFWY 360
 QY SRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVWFYAEKSSASAKFTSIPASFWY 360
 DB 301 SRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVWFYAEKSSASAKFTSIPASFWY 360
 QY TIVTMTTIGYGDWPKTIAGKIFGSLCSLGVIALPVPVIVSFSRIYQNOBARKR 420
 DB 361 TIVTMTTIGYGDWPKTIAGKIFGSLCSLGVIALPVPVIVSFSRIYQNOBARKR 420
 QY AOKKARLARIRVAKTGSSNAYLHRSKNGLNLEALGTPEEHEHMGKTTSHIESQHHL 480
 DB 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLNLEALGTPEEHEHMGKTTSHIESQHHL 480
 QY HCLEKTGSLVDDPLSVRTSTIKNHEFIDQMFQNCMESSMNYPTSTRPSLSHP 540
 DB 481 HCLEKTGSLVDDPLSVRTSTIKNHEFIDQMFQNCMESSMNYPTSTRPSLSHP 540
 QY GLTTCCSRSSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEOPSLTSTRSLNKADDDG 600
 DB 541 GLTTCCSRSSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEOPSLTSTRSLNKADDDG 600
 QY LRPNCSTQITTAIISIPTPPALTPGESRPPASPNTNIPSTSNVAVSVL 655
 DB 601 LRPNCSTQITTAIISIPTPPALTPGESRPPASPNTNIPSTSNVAVSVL 655
 RESULT 5
 ID Q8WN02 PRELIMINARY; PRT; 655 AA.
 AC Q8WN02;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Voltage-gated potassium channel Kv4.3 long form.
 OS Muscivora putorius furo (Ferret).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae; Mustela.
 OC NCBI_TaxID=9669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=21896086; PubMed=11897837;
 RA Patel S.P., Campbell D.L., Morales M.J., Strauss H.C.;

RT "Heterogeneous expression of Kchir2 isoforms in the ferret heart."
RL J. Physiol. 539:649-656 (2002).
DR EMBL; AF454388; AAL51038.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 655 AA; 73375 MW; 3DD3E94819FEF6C1 CRC64;

Query Match 99.0%; Score 3378; DB 2; Length 655;
Best Local Similarity 98.8%; Pred. No. 2.3e-203;
Matches 647; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFARAAAIGWMPVANCMPPLAPADKNKRQDELIVLVNSGRGFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIGWMPVANCMPPLAPADKNKRQDELIVLVNSGRGFQWRTTLER 60

QY 61 YPDTLLGSTEKEFFFNEDTKKEYFDRDPEVFRVCVLFNFRYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKKEYFDRDPEVFRVCVLFNFRYRTGKLHYPRYECISAYDELA 120

QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180

QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHST 180

QY 181 LALVEYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMIFTV 240
DB 181 LALVEYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMIFTV 240

QY 241 YLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFKF 300
DB 241 YLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFKF 300

QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFW 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFW 360

QY 361 TIVMTTLLGSDMPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONRADKR 420
DB 361 TIVMTTLLGSDMPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONRADKR 420

QY 421 AOKKARLARIRIVAKTSSNAYLHSGRNGLLNEALELGTPEEEMGKTSLSIESQHHL 480
DB 421 AOKKARLARIRIVAKTSSNAYLHSGRNGLLNEALELGTPEEEMGKTSLSIESQHHL 480

QY 481 HCLEKTGTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQONCMESMONTYPSTRSPSLSH 540
DB 481 HCLEKTGTGLSYLVDPLLSVTRSTIKNHEFIDEQMFQONCMESMONTYPSTRSPSLSH 540

QY 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIQGSSEPSLTSSSLNKADG 600
DB 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIQGSSEPSLTSSSLNKADG 600

QY 601 LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGPNTNIPITSINVKVSVL 655
DB 601 LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGPNTNIPITSINVKVSVL 655

RESULT 6
Q9PTD3 PRELIMINARY; PRT; 658 AA.
ID Q9PTD3
AC Q9PTD3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Potassium channel Kv4.3.
GN Name=KCND3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bred White Leghorn; TISSUE=lens epithelium;
RA Rae J.L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209722; AAF22832.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 658 AA; 73896 MW; 0F8743D4AF8B12A8 CRC64;

Query Match 94.9%; Score 3237.5; DB 2; Length 658;
Best Local Similarity 94.8%; Pred. No. 1.5e-194;
Matches 624; Conservative 19; Mismatches 12; Indels 3; Gaps 3;

QY 1 MAAGVAAWLPFARAAAIGWMPVANCMPPLAPADKNKRQDELIVLVNSGRGFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIGWMPVANCMPPLAPADKNKRQDELIVLVNSGRGFQWRTTLER 60

QY 61 YPDTLLGSTEKEFFFNEDTKKEYFDRDPEVFRVCVLFNFRYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKKEYFDRDPEVFRVCVLFNFRYRTGKLHYPRYECISAYDELA 120

QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOE-SMPSLSFRQTMRAFENPHST 179
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOE-SMPSLSFRQTMRAFENPHST 179

QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOE-SMPSLSFRQTMRAFENPHST 179
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOE-SMPSLSFRQTMRAFENPHST 179

QY 180 TLALVFFYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMIFTV 239
DB 180 TLALVFFYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMIFTV 239

QY 240 EYLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFK 299
DB 240 EYLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFK 299

QY 241 EYLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFK 300
DB 241 EYLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEDEVGAFTLRFVFRIRIFK 300

QY 300 FSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFW 359
DB 300 FSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFW 359

QY 361 YTIYMTTLLGSDMPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONRADKR 420
DB 361 YTIYMTTLLGSDMPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONRADKR 420

QY	420	RAQKKARLARIRVAKTGGSNAYLH\$KRNGLNLEALBETG-TPEEHMGKTTSLIESQHH	478
Db	421	RAQKKARLARIRVAKTGGSNAYLH\$KRNGLNLEALBETGSTEDEQHTTKGTLIESQHH	480
QY	479	LIHCKEKTGLSYLVDPLLSVRTSTIKNHEFIDEQMEQNCMESSMONTSTRSPBLS	538
Db	481	LIHCKEKTGLSYLVDPLLSVRTSTIKNHEFIDEQLEQNCMESSMONTSTRSPBLS	540
QY	539	HPELTTCCSR\$SKTTHLEPNSNLPATRLRSMOELSTHIOGSEOPSLT\$RSSLN\$KAD	598
Db	541	HHGLTTSCC\$RHHKKTTHLEPNS\$VPATRLRSMOELSTHIOQSEOPSLT\$RSSLN\$KAD	600
QY	599	DGLRPNCT\$QITTAIISIP\$PALTEGESR\$PPASIP\$PNTNI-\$P\$ITSNVV\$K\$V\$L	655
Db	601	DGLRPNCT\$QITTAIISIP\$PALTEGESR\$PP\$SPH\$STNISTTT\$SNV\$K\$V\$L	658

RESULT 7
057662
ID 057662 PRELIMINARY; PRT; 659 AA

DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Potassium channel xKv4.3.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. Lautermilch N.U., Spitzer N.C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U89265; AAB94379.1; -.
DR HSP; Q63881; 1S6C.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO: GO:000515; F:protein binding; IEA.
DR GO: GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR GO: GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 659 AA; 74515 MW; 735CF339C6A0F47 CRC64;

Query Match	85.7%	Score 2925;	DB 2;	Length 659;
Best Local Similarity	86.3%	Pred. No. 5.7e-175;		
Matches 573;	Conservative 37;	Mismatches 40;	Indels 14;	Gaps 7

[illegible]

Db	61	YPDNLGRPEKEFFNEETKEYFFDRDPEVFRSLNFRTGKLYHPRIEYISAYDEELSF	120
QY	121	YGI LPEIIGDCCYEEYKDKRKNEMARLMDNDNSENNQESMPSLSFROTMMRAFENPHST	180
Db	121	YGI LPEIIGDCCYEEYKDKRKNEMARLMDNDNEFENNQEAMPSSLNRETWMRAFENPHST	180
QY	181	LALVFYVYTGFFIAVSVITNVETVPCGTVGSGKEJPCGERYSVAFCLDTACVMI FVE	240
Db	181	LALVFYVYTGFFIAVSVIANVETVPCGTVPGNKEJPCGERYQVAFCLDTACVMI FVE	240
QY	241	YLRLFPAPSRRYRFRISVW--SIIDVVAIMPYYIGLVMTN-NEVDSGAFVTLRFRVFR	296
Db	241	YLRLFPAPSRRYRFRMSVMSLIDVVAIMPYYIGLVMTNINEDVSGAFVTLRFRVFR	300
QY	297	IFKFSRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVMFYAEKSSASKFTSIPA	356
Db	301	IFKFSRHSQGLRILGYTLKSCASELGFLLPSLTMAIIFATVMFYAEKSTSKFTSIPA	360
QY	357	SFWYTIIVMTTLGYGDMVPKTIAGKIFG-SISLSGLVLIALPVPVIVANSFSRIYHONOR	415
Db	361	SFWYTIIVMTTLGYGDMVPKTIAGKIFEFHILTSLSGLVLIALPDPVWVMSFSRIYHONOR	420
QY	416	ADKRRRAQKKARLARIRVAKTGSSNAYLHRSKNGLLNLALELTGPBEEHNGKTSILIESQ	475
Db	421	ADKRRRAQKKARLARIRVAKTGSSNAYLHRSKNGLLNLALELMSTEEPHIGKSASLIESQ	480
QY	476	HHHLHLEKTTGLSYLVDDPLLSVRTSTIKNE----FIDEQMFQONCMESSMONYPST	531
Db	481	HHHLHLEKTTGLSYLVDDPLLSVRTS--DHEEPCLMSQMFEQONCRENSCKNYPST	537
QY	532	RSPSLSHPLGLTTCCSRSKKTHLPNSNLPATRLBSMOELSTIHIOGSEQPSLTSRS	591
Db	538	ATASLSHSHGLTSCSRNKKTHLPNSNVPATRLRMOELSTIHIOGSDQPSLTSASRS	597
QY	592	SLNLKADGGLRPNCCKTSQITTAIISIPTPALTPPEGSRPPASPGPNTNIPSTISNVVK	651
Db	598	SLNLKSEDEMRSNCKASQITTAIISIPTPALTPPEGETR-PCGPPGRSTNIHS-TSNIVK	655
QY	652	VSUVL 655	
Db	656	VSAL 659	

RESULT 8
Q7ZW36
ID Q7ZW36 PRELIMINARY; PRT; 638 AA

DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Potassium voltage-gated channel, Shal-related family, member 3.
GN ORFNames=zgc:55306;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feinsgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohitsuiki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045304; AAB45304.1; -.
DR HSSP; O6381; 1S6C.
DR ZFIN; ZDB-GENE-030131-5626; zgc:55306.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005155; F:Protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 638 AA; 72053 MW; 038645FB28947F47 CRC64;

Query Match 75.3%; Score 2570.5; DB 2; Length 638;
Best Local Similarity 75.6%; Pred. No. 8.8e-153;
Matches 501; Conservative 71; Mismatches 58; Indels 33; Gaps 11;

QY 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNGKODELIVLVNSGRRFQWTWTLER 60
DB 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNGKODELIVLVNSGRRFQWTWTLDR 60
QY 61 YPDTLLGSTKEKFFNEDTKCYFPDRDPEVRCVLFNFYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSSEKKEFFNEDTKCYFPDRDPEVRCVLFNFYRTGKLHYPRYECISAYDELA 120
QY 121 YGILPEIIGDCCYEYKDKRKRENAERLMDNDSENNOESMPSISFRQTMWRAFPENPH 180
DB 121 YGILPEIISDCCYEYKDKRKRENTERLMDIE-DNKDSKLPNNTFREIMWRAFPENPH 179
QY 181 LALVFYVTVGFFIIVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTACVMTF 240
DB 181 MALVFYVTVGFFIALSVITNVVETVPCGYMNDQDVCGERYEAFQMDTACVMTF 239
QY 241 YLRLFAAPSRFRFIRSVSIIDVAIMPYIIGLVMTNEDVSGAFVTLRFRVFRIFKF 300
DB 241 YLRLFAAPSRFRFIRSVSIIDVAIMPYIIGLVMTNEDVSGAFVTLRFRVFRIFKF 299
QY 301 SRHSGGLRIIGTLKSCASELGFILSLTMAIIFATVMFYAEKSSASKFTSIPASFW 360
DB 301 SRHSGGLRIIGTLKSCASELGFILSLTMAIIFATVMFYAEKSSASKFTSIPASFW 359
QY 361 TIVMTTLLGYGMVPKTIAGKIFGSIICSLGVLVIALVPVIVSNFSRIYHONRADK 420
DB 361 TIVMTTLLGYGMVPKTIAGKIFGSIICSLGVLVIALVPVIVSNFSRIYHONRADK 419

QY 421 AOK--KARLARIVAKTGSSNAYLHSKRNLNLEALTLGTBPBE-EHMKTTSLIESQ 477
DB 420 AOKVOKARLARIVAKTGSSNAYLHSKRNLNLEALTLGTSLIEDQOLKTTSLIESQ 478
QY 478 HLHCLKTKTGLSYLVDDPLSVRTSTIKNHEFIDECMFQONCMSSMONTPTSPSL 537
DB 479 HLHCLKTKT-----NHEFVDERLYEQGYLQYALONFPS-QSPSL 518
QY 538 SHPGLITTCGSRRSKKTTHLPNSNLPATRLRSMOELSTIHIGSEOPSLTSSSLNKA 597
DB 519 SEEGITGTCRRPKKNIQPLNATHTSHNLOELSAHIOCGEQPLNTSRSSSLNLS 578
QY 598 DDGLRPNCKTS-QITTAIISIPPPA-----LTPEGSRPPAPSPGPNTPISITSNVKV 652
DB 579 DESGLNCKSSGLVTTAIIISIPPPSNRGRASPDPAPPPNPAP-PLIN-PSST-DVVKI 635
QY 653 SVL 655
DB 636 SAL 638

RESULT 9
ID Q8HYZ1 PRELIMINARY; PRT; 630 AA.
AC Q8HYZ1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Voltage-gated potassium channel Kv4.2.
OS Mustela putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9669;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Patel S.P., Straus H.C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY147192; AAN39878.1; -.
DR HSSP; O6381; 1S6C.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005155; F:Protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 630 AA; 70565 MW; DA4CFD16998A9842 CRC64;

Query Match 73.9%; Score 2510.5; DB 2; Length 630;
Best Local Similarity 73.9%; Pred. No. 5e-149;
Matches 488; Conservative 68; Mismatches 69; Indels 35; Gaps 7;

QY 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNGKODELIVLVNSGRRFQWTWTL 59
DB 1 MAAGVAAWLPARAAGMMPVANCMPMLAPADKNGKODELIVLVNSGRRFQWTWTL 60

QY	60	RYPDTLGSTEKEFFENEDKXYFFPRDPPEVRCVLNFRRTGKJHYPRYECISAYDELA	119
Db	61	RYPDTLGSSSERDFYHPEYQYFFPRDPDIFRHILNFYRTGKJHYPRHETISAYDELA	120
QY	120	FYGLPEIIGDCCYEEYKDKRENARLMDNDSENNOOS-MPSLSFRQTMRAFENPHT	178
Db	121	FFGLPEIIGDCCYEEYKDKRENARLQDDADDTDNTEGSALPTWTARQVWRAFENPHT	180
QY	179	STLALVFFYVTGFFIAVSVTINVEFVPCGTVPGS-KELPCGERYSVAFFCLDTACMIF	237
Db	181	STMALVFFYVTGFFIAVSIVIANVEFVPCGSSPGHIKELPCGERYAAVAFCLDTACMIF	240
QY	238	TVEYLLRLEAPSRRYRFRIRVMSIIDVAIMPYYIGLVMTNNEVSGAFYTLRVFVRIRI	297
Db	241	TVEYLLRLAAPSRRYRFRVRSMSIIDVAIIIPYYIGLVMTDNEDVSGAFYTLRVFVRIRI	300
QY	298	EKFSRHSOGLRIIGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKGSSASKFTSIPAS	357
Db	301	FKFSRHSOGLRIIGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKGSSASKFTSIPAA	360
QY	358	FWYTIIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHQNORAD	417
Db	361	FWYTIIVMTTLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHQNORAD	420
QY	418	KRAAQKARLARIRIVAKTGSNAYLHKKRNGLLNEALELTGTPEEHMGKTTSLISSQH	477
Db	421	KRAAQKARLARIRIAKTGSANAYMGSKRNGLLSNOLQ-SSDEDEQAFVSGSSSFFEQHH	479
QY	478	HLHCLKETTGLSYLVDDPLLSVRTSTIIKNHEFIDEQMFQNCMESSMÖNYPSTRPSLS	537
Db	480	HLHCLKEXT-----NHEFVDEQYFEBESCHEVATGNRPSSHSPLS	520
QY	538	SHPGLTTCSSRSRCKTTHLPNSNLPATRLRSMOELSTIIQGSQPSLTTSSSLNLKA	597
Db	521	SOQGVSTSCSRRHKKTFRIPNANVSGHSGVQELSTIQIRCVERTPLSSRSSSLNAKM	580
QY	598	DDGLRPNCKTSQITTAIISLPTPALTPGESRP-PPAASPGPNTNIPSTISNVKXSVL	655
Db	581	EECVKLNKEQPYVTAAIISLPTPVITPTEGDDRPESPEVSG-----NIVRYSAL	630

```

RESULT 10
KCD2_RABIT
ID KCD2_RABIT STANDARD; PRT; 630 AA.
AC P59955;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
DE potassium channel subunit Kv4.2).
GN Name=KCND2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Cornea;
RA Rae J.L.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 15-614 FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=22117972; PubMed=12122138;
RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G.,
RA Obeso A., Ganfornina M.D., Gonzalez C.;
RT "Molecular identification of Kv alpha subunits that contribute to the
RT oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit
RT carotid body.";
RL J. Physiol. (Lond.) 542:369-382(2002).
CC -I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Isa) current in neurons. Channel properties

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[illegible]

```
Db 181 STMALVYVYVGTGFFIAVSIVANVETVPCGSSPGHIKELPCGERVAVAFCDTACWIF 240
Cy 238 TVEYLRLFAAPSRYPFRISVMSIIVVAIMPIYIGLWMTNEDVSGAFVTLRVFRFRI 297
Db 241 TVEYLRLAABPSRYPFRVSVMSIIVVAILEFYIGLWMTNEDVSGAFVTLRVFRFRI 300
Cy 298 FKFSRHSQGLRIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSI PAS 357
Db 301 FKFSRHSQGLRIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSI PA 360
Cy 358 FWYITVMTTLGYGDMVPKTIAGKIFGSCISGLVIALPVPIVSNFSRIYHQNORAD 417
Db 361 FWYITVMTTLGYGDMVPKTIAGKIFGSCISGLVIALPVPIVSNFSRIYHQNORAD 420
Cy 418 KRRACKKARLARIRVAKTSSNAVHLSKRNGLNEALELTGTPERE--HMKTTSLIESQ 475
Db 421 KRRACKKARLARIRVAKTSSNAVHLSKRNGLNSQLQ---SSEEPAPFVSKSSGSETQ 477
Cy 476 HHHLHLEKKTGSLVYVDDPLLSYRTSTIKNHEFIDEQMEQONCMSSMONTPTSRSPS 535
Db 478 HHHLHLEKKTGSLVYVDDPLLSYRTSTIKNHEFIDEQMEQONCMSSMONTPTSRSPS 518
Cy 536 LSHHPGLITTCSSRRSKTTHLPNSNLPATRLRSMOELSTIHIGSEOPSLTTSRSLNL 595
Db 519 LSSQCGVSTCCSRHKTFRIPNANVSGSGVQELSTIQICVERTPLSNRSLSLA 578
Cy 596 KADGRLPNCKTSQITTAIISIPFPALTPEGESRP--PPASPGPNTNIPSTSNVYKVS 653
Db 579 KMEECVTLNCEQPVVTTAISIPFPVPTTPGEDDRPESPEYSG-----NIYRVS 628
Cy 654 VL 655
Db 629 AL 630
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RESULT 11
KCD2_MOUSE STANDARD; PRT; 630 AA.
ID KCD2_MOUSE STANDARD; PRT; 630 AA.
AC Q920V2; Q8BSK3; Q8CHB7; Q9JU60;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
potassium channel subunit Kv4.2).
GN Name=Kcnd2; Synonyms=Kiaa1044;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark R.B., Giles W.R.;
RT "Cloning and functional characterization of mouse heart K+ channel
alpha subunits, Kv1.5, Kv4.2 and Kv4.3."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RT Hashimoto K.;
RL "Isolation of full-length cDNA clones from mouse brain cDNA library.";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=22353125; PubMed=12465718;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RT Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT I. The complete nucleotide sequences of 100 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
```

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RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 9:179-188 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros, and Olfactory bulb;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi Y., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Savelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [5]
RP PHOSPHORYLATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20497051; PubMed=11040264;
RA Varga A.W., Anderson A.E., Adams J.P., Vogel H., Sweatt J.D.;
RT "Input-specific immunolocalization of differentially phosphorylated
RT Kv4.2 in the mouse brain."
RL Learn. Memory 7:321-332 (2000).
RN [6]
RP INTERACTION WITH KCNIP3, MUTAGENESIS OF SER-552, AND PHOSPHORYLATION.
RX MEDLINE=22338839; PubMed=12451113;
RA Schrader L.A., Anderson A.E., Mayne A., Pfaffinger P.J., Sweatt J.D.;
RT "PKA modulation of Kv4.2-encoded A-type potassium channels requires
RT formation of a supramolecular complex."
RL J. Neurosci. 22:10123-10133 (2002).
RN [7]
RP INTERACTION WITH KCND3 AND KCNIP2.
RX MEDLINE=21906624; PubMed=11909823;
RX DOI=10.1161/01.RES.0000012664.05949.E0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RA Nerbonne J.M.;
RT "Role of heteromultimers in the generation of myocardial transient
RT outward K+ currents."
RL Circ. Res. 90:586-593 (2002).
RN [8]
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
inactivating A-type potassium channels. May contribute to I(TO)
current in heart and I(Sa) current in neurons. Channel properties
are modulated by interactions with other alpha subunits and with
regulatory subunits.
RN [9]
RP SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
KCNIP4. Interacts with DPP6, DLG4 and FROO. Interacts with FLNA
and FLNC (by similarity).
RN [10]
RP SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in brain, especially in hippocampus,
medial habenular nucleus, striatum, amygdala, cortex and
cerebellum.
RN [11]
RP DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
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CC every third position.
CC -I- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -I- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 520.
CC -----
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CC -----
DR EMBL; AF107780; AAD16972.1; -.
DR EMBL; AB045326; BAA97986.1; ALT_FRAME.
DR EMBL; AB093280; BAC41464.1; ALT_INIT.
DR EMBL; AK032268; BAC27787.1; -.
DR EMBL; AK032772; BAC28015.1; -.
DR PIR; P10675; P10675.
DR HSSP; Q16968; 1A68.
DR MGD; MGI:102663; Kcnd2.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KM Ion transport; Ionic channel; Multigene family; Phosphorylation;
KM Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 183 Cytoplasmic (Potential).
FT TRANSMEM 184 204 Segment S1 (Potential).
FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 630 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphothreonine.
FT MOD_RES 552 552 Phosphoserine.
FT MOD_RES 602 602 Phosphothreonine.
FT MOD_RES 607 607 Phosphothreonine.
FT MOD_RES 616 616 Phosphoserine.
FT MUTAGEN 552 552 S->A: Abolishes PKA-mediated modulation
of channel activity.
FT CONFLICT 22 22 V -> A (in Ref. 2).
FT CONFLICT 516 516 S -> R (in Ref. 3).
SQ SEQUENCE 630 AA; 70576 MW; 7FB9427429E7683 CRC64;
```

```
Query Match 73.4%; Score 2503.5; DB 1; Length 630;
Best Local Similarity 73.8%; Pred. No. 1.4e-148;
Matches 487; Conservative 68; Mismatches 70; Indels 35; Gaps 7;
```

```
QY 1 MAAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
DB 1 MAGVAAWLPFARAALIGMPVANSMPAPPRQERKRTQDALIVLVNSGTRFQWQDTLE 60
QY 60 RYDDTLGSTEKEFFENEDTKYFFEDRDPEVFRCLVNFRTGKLHYPRYECISAYDDELA 119
DB 61 RYDDTLGSSERDFYHPETQGYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDDELA 120
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QY 120 FYGILPEIIGDCCEYEYKDKRENARLMDNDSENNOES-MPSLSFRQTMWRAFENPHT 178
DB 121 FFGILPEIIGDCCEYEYKDKRENARLQDDADTDNTGESALPTMTARQWRARAFENPHT 180
QY 179 STLAVFYVVTGFIYAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFPCLDTACWIF 237
DB 181 STMALVFYVVTGFIYAVSVIANVETVPCGSGPHIKELPCGERYAVAFPCLDTACWIF 240
QY 238 TVEYLLRLFAAPSRYRFRKSVMSIIDVAIMPYIIGLVMTNNEVSGAFVTLRVFRVRI 297
DB 241 TVEYLLRLAAAPSRFRVRSVMSIIDVAILEPYIIGLVMTNNEVSGAFVTLRVFRVRI 300
QY 298 FKESRHSQGLRIIGYTLKSGASELGFLLSLTMAIIFATVMFYAEKGSASKFTSI PAS 357
DB 301 FKFSRHSQGLRIIGYTLKSGASELGFLLSLTMAIIFATVMFYAEKGSASKFTSI PAA 360
QY 358 FMYTIVMTTLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVSNFSRIYHONRAD 417
DB 361 FMYTIVMTTLGYGDMVPKTIAGKIFGSGISGLVLTALPVPIVSNFSRIYHONRAD 420
QY 418 KRAQKARLARIFVAKTGSNAYLHRSKNGLLNEALELGTPEREHMGKTSLSIESQH 477
DB 421 KRAQKARLARIFVAKTGSNAYLHRSKNGLLNEALELGTPEREHMGKTSLSIESQH 479
QY 478 HLHCLKETTGLSYLVDDPLSVRTSTIKHBEFIDEQMEQONCESSMONTSTRSPSL 537
DB 480 HLHCLKETT-----NHEFVDEQVFEESCEVATVNRPSHSPLS 520
QY 538 SHPGLTTCSSRSRKTTHLPNSNLPAIRLSMOELSTHIQSGRQPSLTSSSLNKA 597
DB 521 SGGVTSRCCSRHKKTFRIPNANVSGSHRGVQELSTQIRCVERTPLSNRSSLNKA 580
QY 598 DDGLRPNCQTQTAAIISIPTPALTPEGESRP--PPASGPPTNIPSTSNVVKSVL 655
DB 581 BECVKNCQEPYVTTAIIISIPTPVTTPEGDRPESPEYSG-----NIVRSAL 630
```

RESULT 12

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KCD2 RAT STANDARD; PRT; 630 AA.
ID KCD2 RAT Q00090; Q99249;
AC Q63861; Q00090; Q99249;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
DE potassium channel subunit Kv4.2) (Shall) (RK5).
GN Name=Kcnd2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hippocampus;
RA MEDLINE=92000693; PubMed=1840649; DOI=10.1016/0896-6273(91)90299-F;
RA Baldwin T.J., Tsaur M.-L., Lopez G.A., Jan Y.-N., Jan L.Y.;
RT "Characterization of a mammalian cDNA for an inactivating voltage-
RT sensitive K+ channel.";
RL Neuron 7:471-483(1991).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley; TISSUE=Heart;
RX MEDLINE=9115694; PubMed=1705709;
RA Roberds S.L., Tankun M.M.;
RT "Cloning and tissue-specific expression of five voltage-gated
RT potassium channel cDNAs expressed in rat heart.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1798-1802(1991).
RN [3]
RP INTERACTION WITH KCNIP1, KCNIP2 AND KCNIP3.
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
RA An W.-F., Bowlby M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
RA Hinson J.W., Matteson K.I., Strassie B.W., Trimmer J.S., Rhodes K.J.;
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RT "Modulation of A-type potassium channels by a family of calcium
RT sensors.";
RT Nature 403:553-556(2000).
RL [4]
RN INTERACTION WITH KCNIP1 AND FREGO.
RX MEDLINE=21532927; PubMed=11606724; DOI=10.1073/pnas.221168498;
RA Nakamura T.Y., Pountney D.J., Ozaita A., Nandi S., Ueda S., Rudy B.,
RA Coetzee W.A.;
RT "A role for frequenin, a Ca2+-binding protein, as a regulator of Kv4
RT K+-currents.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12808-12813(2001).
RN [5]
RP INTERACTION WITH KCNIP4.
RX MEDLINE=21964093; PubMed=11847232; DOI=10.1074/jbc.M200897200;
RA Morohashi Y., Hatano N., Ohya S., Takikawa R., Watabiki T.,
RA Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.;
RT "Molecular cloning and characterization of CALP/KChIP4, a novel EF-
RT hand protein interacting with presenilin 2 and voltage-gated potassium
RT channel subunit Kv4.";
RL J. Biol. Chem. 277:14965-14975(2002).
RN [6]
RP MOTOGENESIS OF 627-VAL--LEU-630, AND INTERACTION WITH DLG4.
RX MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;
RA Wong W., Newell E.W., Jungloff D.G.M., Jones O.T., Schlichter L.C.;
RT "Cell surface targeting and clustering interactions between
RT heterologously expressed PSD-95 and the Shal voltage-gated potassium
RT channel, Kv4.2.";
RL J. Biol. Chem. 277:20423-20430(2002).
RN [7]
RP INTERACTION WITH DPP6.
RX MEDLINE=22464931; PubMed=12575952; DOI=10.1016/S0896-6273(02)01185-6;
RA Nadal M.S., Ozaita A., Amariello Y., Vega-Saenz de Miera E., Ma Y.,
RA Mo W., Goldberg E.M., Mismuni Y., Ikebara Y., Neubert T.A., Rudy B.;
RT "The CD26-related dipeptidyl aminopeptidase-like protein DPPX is a
RT critical component of neuronal A-type K+ channels.";
RL Neuron 37:449-461(2003).
RN [8]
RP -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
RP inactivating A-type potassium channels. May contribute to I(to)
RP current in heart and I(Sa) current in neurons. Channel properties
RP are modulated by interactions with other alpha subunits and with
RP regulatory subunits.
RN CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
RN CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
RN CC KCNIP4. Interacts with FLNA and FLNC (By similarity). Interacts
RN CC with DPP6, DLG4 and FREGO.
RN CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Interaction with
RN CC DPP6, DLG4 or FREGO may increase cell surface expression.
RN CC -1- TISSUE SPECIFICITY: Highly expressed in heart and throughout the
RN CC brain, with similar levels in cortex and hypothalamus, and much
RN CC higher levels in hippocampus, dentate gyrus and the habenular
RN CC nucleus of the thalamus. Detected at similar levels in heart
RN CC atrium and ventricle. Detected in aorta, cardiac and smooth
RN CC muscle.
RN CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
RN CC characterized by a series of positively charged amino acids at
RN CC every third position.
RN CC -1- PTM: Phosphorylated on serine and threonine residues (By
RN CC similarity).
RN CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
RN CC subfamily.
RN CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
RN CC frameshift in position 477.
RN CC -----
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DR EMBL; S64320; AAB19939.1; -; ALT_FRAME.
DR EMBL; M59980; AAA40929.1; ALT_FRAME.

DR PIR; J00271; J00271.
DR PDB; 1S6C; X-ray; B=1-30.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR 3D-structure; Ion transport; Ionic channel; Multigene family;
KW Phosphorylation; Potassium; Potassium channel; Potassium transport;
KW Transmembrane; Transport; Voltage-gated channel.
KW DOMAIN 1 183 Cytoplasmic (Potential).
FT TRANSMEM 184 204 Segment S1 (Potential).
FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 630 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphothreonine (By similarity).
FT MOD_RES 552 552 Phosphoserine (By similarity).
FT MOD_RES 602 602 Phosphothreonine (By similarity).
FT MOD_RES 607 607 Phosphothreonine (By similarity).
FT MOD_RES 616 616 Phosphoserine (By similarity).
FT MOD_RES 627 630 Missing: Abolishes interaction with DLG4.
FT MUTAGEN 630 AA; 70548 MW; FDE57E8A5113BABF CRC64;
SQ SEQUENCE 630 AA; 70548 MW; FDE57E8A5113BABF CRC64;
Query Match 73.3%; Score 2499.5; DB 1; Length 630;
Best Local Similarity 73.6%; Pred. No. 2.4e-148;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;
QY 1 MAAGVAAWLPARRAAAGMMPVANCMPMLAPADKNR-QDELIVLVSGRRFQWRTTLE 59
DB 1 MAAGVAAWLPARRAAAGMMPVANGMPMPADPRQERKRTQDALIVLVSGSTRFQWDTLE 60
QY RYPDTLLGSTEKEFFENEDTKERFDRDPEVRCVNFYRTGTLHYPRYCISAYDDELA 119
DB RYPDTLLGSSSEDFHYHPETQYFFDRDDIFRHLNFPYRTGLHYPRHCISAYDEBLA 120
QY 60 RYPDTLLGSTEKEFFENEDTKERFDRDPEVRCVNFYRTGTLHYPRYCISAYDDELA 119
DB 61 RYPDTLLGSSSEDFHYHPETQYFFDRDDIFRHLNFPYRTGLHYPRHCISAYDEBLA 120
QY 120 FYGLIPEIIGCCYEEYKDRKRENAERLMDNDSENQES-MPSLSFRQTMRAFENPHT 178
DB 121 FFGLIPEIIGCCYEEYKDRRRENAERLQDDADTNTGESALPTMTAKORVWRAFENPHT 180
QY 179 STLALVYVYTGFFIAVSITNVETVPGCTVPGS-KELPGCBRYSAVFCLDTACVMIF 237
DB 181 STMALVYVYTGFFIAVSIVIANVETVPGSSPGHKELPGBERYAVAFCLDTACVMIF 240
QY 238 TVEYLLRLFAAPSRYSRYSVMSIIDVVAIMPYIYGLVMTNEDVSGAFVTLRYRVFRI 297
DB 241 TVEYLLRLFAAPSRYSRYSVMSIIDVVAIMPYIYGLVMTNEDVSGAFVTLRYRVFRI 300
QY 298 FKFSSHSQGLRILGYTLKSCASBLGFLSLTMAITIPATWIFYAEKSSASKTSIPAS 357
DB 301 FKFSSHSQGLRILGYTLKSCASBLGFLSLTMAITIPATWIFYAEKSSASKTSIPAA 360
QY 358 FMYITVMTTLGYGDMVPTKIAKIFGSIKSLGVLVIALPVVIVSNFSRIYHONORAD 417
DB 361 FMYITVMTTLGYGDMVPTKIAKIFGSIKSLGVLVIALPVVIVSNFSRIYHONORAD 420
QY 418 KRRACKARLARIRVAKTSSNAYLHSGKNGLNAELTGTPEEHNGKTSILIESQHH 477

Db 421 KRRQAQKRLARIRAKSGSANAYMQSKRNLSTNQLQ-SEDEPAFVSKSGSSFETQHH 479
Qy 478 HLHCLKTKTGLSYLVDPLLSVRTSTIKNHEFIDEQMFQNCMESSMONTSTRSPSL 537
480 HLHCLKTKT-----NHEFDEQVFEBSCEMVAATVNRPSHSPSL 520
Qy 538 SHPGLTTCSSRSRKKTTLHPLNSLPAATRLRSMQELSTHIOGSEQPSLTTSRSLNKA 597
521 SQGVSTSTCSSRRHKKSFRIPIANVSGSHRGVDELSTIQRCVERTPLSNGRSSLNKA 580
Qy 598 DDGLRPNCSTQITTAIISIPPPALPEGESRP-PPASGPNNTNIPITSNVKSVL 655
581 EECVKLNCQDPYVTTAIIISIPFPVTPEGDDRPESPEYSGG-----NIVRSAL 630
Db
RESULT 13
KCND2_HUMAN STANDARD; PRT; 630 AA.
AC Q9NZV8; O95012; O95021; Q9UBV7; Q9UN98; Q9UNH9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
potassium channel subunit Kv4.2).
GN Name=KCND2; Synonyms=KIAA1044;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K.-I., Hirosewa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
RN [3]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.
RX MEDLINE=20017432; PubMed=10551270;
RA Zhu X.-R., Wolf A., Schwarz M., Isbrandt D., Pongs O.;
RT "Characterization of human Kv4.2 mediating a rapidly-inactivating
transient voltage-sensitive K+ current.";
RL Recept. Channels 6:387-400(1999).
RN [4]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain cortex;
RX MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;
RA Isbrandt D., Leicher T., Waldschuetz R., Zhu X.-R., Luhmann U.,
Michel U., Sauter K., Pongs O.;
RT "Gene structures and expression profiles of three human KCND (Kv4)
potassium channels mediating A-type currents I(TO) and I(SA).";
RL Genomics 64:144-154(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22616434; PubMed=12690205; DOI=10.1126/science.1083423;
RA Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayashi K.,
Herbick J.-A., Carson A.R., Parker-Katirae L., Skaug J., Knaja R.,
Zhang J., Hudak A.K., Li M., Haddad M., Duggan G.E., Fernandez B.A.,
Kanematsu E., Gentile S., Christopoulos C.C., Choufani S.,
Kwanicka D., Zheng X.H., Lai Z., Nusser K.D., Zhang Q., Gu Z., Lu F.,
Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C.,
Weksberg R., Zackai E.H., Grebe T.A., Cox S.R., Kirkpatrick S.J.,

RA Rahman N., Friedman J.M., Heng H.H.Q., Pelicci P.G., Lo-Coco F.,
RA Belloni E., Shaffer L.G., Pober B., Morton C.C., Guesella J.F.,
RA Bruns G.A.P., Korf B.R., Quade B.J., Ligon A.H., Ferguson H.,
RA Higgins A.W., Leach N.T., Herrick S.R., Lemye E., Parra C.G.,
RA Kim H.-G., Summers A.M., Gripp K.W., Roberts W., Szatmari P.,
RA Winsor E.J.T., Grzeschik K.-H., Teebi A., Minassian B.A., Kere J.,
RA Armengol L., Pujana M.A., Estivill X., Wilson M.D., Koop B.F.,
RA Toes S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B.,
RA Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner H.,
RA Doehner K., Rommens J.M., Vincent J.B., Venter J.C., Li P.W.,
RA Mural R.J., Adams M.D., Tsui L.-C.;
RT "Human chromosome 7: DNA sequence and biology.";
RL Science 300:767-772(2003).
RN [6]
RP MUTAGENESIS OF 601-PRO--PRO-604, SUBCELLULAR LOCATION, AND INTERACTION
RP WITH FLNA AND FLNC.
RX MEDLINE=20556633; PubMed=11102480;
RA Petrecca K., Miller D.M., Shrier A.;
RT "Localization and enhanced current density of the Kv4.2 potassium
channel by interaction with the actin-binding protein filamin.";
RL J. Neurosci. 20:8736-8744(2000).
CC -I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
inactivating A-type potassium channels. May contribute to I(TO)
current in heart and I(Sa) current in neurons. Channel properties
are modulated by interactions with other alpha subunits and with
regulatory subunits.
CC -I- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
KCNIP4. Interacts with DPP6, Dlg4 and FREQ (By similarity).
CC Interacts with FLNA and FLNC.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Detected in
dendrites in cultured hippocampal neurons.
CC -I- TISSUE SPECIFICITY: Highly expressed throughout the brain.
CC Expression is very low or absent in other tissues.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
every third position.
CC -I- PTM: Phosphorylated on serine and threonine residues (By
similarity).
CC -I- SIMILARITY: Belongs to the potassium channel family. D (Shal)
subfamily.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF121104; AAD22053.1; -;
DR EMBL; AB028967; BAAB2996.2; ALT_INIT.
DR EMBL; AJ010969; CAB56841.1; -;
DR EMBL; AF166008; AAF65618.1; -;
DR EMBL; AF166007; AAF65618.1; JOINED.
DR EMBL; AC004888; AAC83405.1; -;
DR EMBL; AC004946; -; NOT ANNOTATED_CDS.
DR EMBL; AF142568; AAD52159.1; -;
DR HSSP; Q16968; 1A68.
DR Genew; HGNC:6238; KCND2.
DR H-InvDB; HIX0007027; -;
DR MIM; 605410; -;
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; CHANNEL.

DR PRINTS; PRO1517; KV42CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
KW PRINTS; PRO1497; SHALCHANNEL.
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 183 Cytoplasmic (Potential).
FT TRANSMEM 184 204 Segment S1 (Potential).
FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 430 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphothreonine (By similarity).
FT MOD_RES 552 552 Phosphoserine (By similarity).
FT MOD_RES 602 602 Phosphothreonine (By similarity).
FT MOD_RES 607 607 Phosphothreonine (By similarity).
FT MOD_RES 616 616 Phosphoserine (By similarity).
FT MUTAGEN 601 604 PRPP->ATPA: Abolishes interaction with PLNC.
FT CONFLICT 450 450 N -> S (in Ref. 1).
FT CONFLICT 464 464 Q -> P (in Ref. 1).
FT CONFLICT 550 550 Q -> R (in Ref. 1).
FT CONFLICT 553 553 I -> V (in Ref. 1).
SQ SEQUENCE 630 AA; 70536 MW; 0C11E62FFA220421 CRC64;
Query Match 73.2%; Score 2498.5; DB 1; Length 630;
Best Local Similarity 73.6%; Pred. No. 2.8e-148;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;
QY 1 MAAGYAAWLPFARAALGMPVANCMPPLADKNKR-QDELIVLVNSGRRFQWRRTTLE 59
Db 1 MAAGYAAWLPFARAALGMPVANCMPPLADKNKR-QDELIVLVNSGRRFQWRRTTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKKEYFFDRDPEVERCVLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTLLGSSERDFFYHPETQYFFDRDPDIFRHILNFRYRTGKLHYPRHICISAYDELA 120
QY 120 FYGLIPEIIGDCCYEYKYDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKYDRRRENAERLQDDADDTYAGESALPMTARQVRMRAFENPHT 180
QY 179 STLALVFYVYTGFFIAVSVITNVVETPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STMALVFYVYTGFFIAVSVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRRYRFRIRSVMSIIDVAIMPYIIGLWMTNEDVSGAFVTLRVERVRI 297
Db 241 TVEYLRLFAAPSRRYRFRIRSVMSIIDVAIMPYIIGLWMTNEDVSGAFVTLRVERVRI 300
QY 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMYFAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMYFAEKSSASKFTSIPAA 360
QY 358 FWYTIIVMTTLGYGDMVPEKTIAGKIFGSIISGLVLYIALPVPVIVSNFSRIYHONORAD 417
Db 361 FWYTIIVMTTLGYGDMVPEKTIAGKIFGSIISGLVLYIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRRACKARLARIRVAKTSSNAVILSKRNLNLEALELTGTPEEHHMGKTSILESQHH 477
Db 421 KRRACKARLARIRVAKTSSNAVILSKRNLNLEALELTGTPEEHHMGKTSILESQHH 479
QY 478 HLHCLKTKTGLSYLVDDPLSVRSTIKNHEFIDEQMEONCESSMNYNPTSTRSPLS 537
Db 480 HLHCLKTKT-----NHEFVDEQVFEESCEVATVNRPSHSPSLS 520
QY 538 SHGILTTCCSRRSKKTTHLPNSULPATRLRSMOELSTIHIQSEQPSLITSTRSSLNKA 597

Db 521 SQQGVSTCCSRRHKKTERIPNANVSGHSGSIQELSTIQICVERTPLSNRSSLNAM 580
QY 598 DGLRPNCKTISQITTAISIPTPALPEGESRP--PPASPGPNTNIPITSNVYKSVL 655
Db 581 EECVXKNCEQPYVTTAISIPTPVTTPEGDRPESPEYSG-----NIVRVLSAL 630
RESULT 14
ID Q8UW33 PRELIMINARY; PRT; 632 AA.
Q8UW33
AC Q8UW33;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Shal-like voltage-gated potassium channel.
GN Name=kva.2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakai Y., Sokolowski B.H.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075160; AAL56633.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF02214; K tetra; 1.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1517; KV42CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
DR PRINTS; PRO1497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 632 AA; 70982 MW; 147C92979F2297D9 CRC64;
Query Match 73.2%; Score 2497.5; DB 2; Length 632;
Best Local Similarity 74.0%; Pred. No. 3.3e-148;
Matches 489; Conservative 62; Mismatches 75; Indels 35; Gaps 7;
QY 1 MAAGYAAWLPFARAALGMPVANCMPPLADKNKR-QDELIVLVNSGRRFQWRRTTLE 59
Db 1 MAAGYAAWLPFARAALGMPVATGMPAPAPROEKRSQDSILVLANVSGIQFQWLDTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKKEYFFDRDPEVFRVCLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTLLGSSERDFFYHPETQYFFDRDPDIFRHILNFRYRTGKLHYPROECISAYDELA 120
QY 120 FYGLIPEIIGDCCYEYKYDRKRENAERLMDNDSENNQES-SMPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKYDRRRENAERLQDDADQHTAESLPSMTARQVRMRAFENPHT 180
QY 179 STLALVFYVYTGFFIAVSVITNVVETPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STLALVFYVYTGFFIAVSVIANVETVPCGVS PGRIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRRYRFRIRSVMSIIDVAIMPYIIGLWMTNEDVSGAFVTLRVERVRI 297
Db 241 TVEYLRLFAAPSRRYRFRIRSVMSIIDVAIMPYIIGLWMTNEDVSGAFVTLRVERVRI 300
QY 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMYFAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMYFAEKSSASKFTSIPAA 360
QY 358 FWYTIIVMTTLGYGDMVPEKTIAGKIFGSIISGLVLYIALPVPVIVSNFSRIYHONORAD 417

Db 361 FWYTIWMTLLGYGDMVPKTIAGKIFGISCISLGVLIAPVPIVSNFSRIYHONCRAD 420
Qy 418 KRRQKARLARIIVAKTSSNAYLHNRGNLELTGTPEE-HMGKTSLIESQH 476
Db 421 KRRQKARLARIIVAKTSSNAYLHNRGNLELTGTPEE-HMGKTSLIESQH 480
Qy 477 HHLHLEKRTGLSLVDDPLSVRTSTIKNHEPDEOMFEQNCMESSMONTSTRSPSL 536
Db 481 HHLHLEKRTGLSLVDDPLSVRTSTIKNHEPDEOMFEQNCMESSMONTSTRSPSL 521
Qy 537 SSHPGLTTCCSRSKKTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTSSSLNLK 596
Db 522 SSQGGVTGTCSSRRHKTYRILPNTALTGSRHGVQELSTIQIRCEVPTLSNRSLSNAK 581
Qy 597 ADDGLRPNCCKTSQITTAIISTPPTALPGESERP--PPASGPNINIPITSNVKYSV 654
Db 582 VEECVKNCBQPVYTAIISTPPTALPGESERP--PPASGPNINIPITSNVKYSV 631
Qy 655 L 655
Db 632 L 632

RESULT 15
KCD1_MOUSE STANDARD; PRT; 651 AA.
ID KCD1_MOUSE STANDARD; PRT; 651 AA.
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 1 (Voltage-gated
DE potassium channel subunit Kv4.1) (mshal).
GN Name=Kcnd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Brain;
RC MEDLINE=91239573; PubMed=2034678;
RX Pak M.D., Baker K., Covarrubias M., Butler A., Ratcliffe A.,
RA Salkoff L.,
RT "mshal, a subfamily of A-type K+ channel cloned from mammalian
RT brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4386-4390(1991).
RN [2]
RP SEQUENCE OF 145-647 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guslich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawaji J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [3]
RP INTERACTION WITH KCNIP1.
RX MEDLINE=21316019; PubMed=11423117; DOI=10.1016/S0014-5793(01)02560-1;
RA Nakamura T.Y., Nandi S., Pountney D.J., Artman M., Rudy B.,
RA Coetzee W.A.,
RT "Different effects of the Ca(2+)-binding protein, KCNIP1, on two Kv4
RT subfamily members, Kv4.1 and Kv4.2."
RL FEBS Lett. 499:205-209(2001).
CC -I- FUNCTION: pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in the heart and I(Sa) current in neurons. Channel
CC properties are modulated by subunit assembly.
CC -I- SUBUNIT: Homotrimer or heterotrimer with KCND2 and/or KCND3.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4 (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -I- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -----
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CC -----
DR EMBL: M64226; AAA39745.1; -.
DR EMBL: AK033805; BAC28480.1; -.
DR PIR: A39372; A39372.
DR HSSP: Q16968; 1A68.
DR MGD; MGI:96671; Kcnd1.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003131; K tetra.
DR InterPro; IPR004054; KV4channel.
DR InterPro; IPR003968; Kv channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal channel.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF02214; K tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01516; KV4CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KW Ion transport; Ionic channel; Multigene family; Potassium;
KW Potassium channel; Potassium transport; Transmembrane; Transport;
KW Voltage-gated channel.
FT DOMAIN 1 184 Cytoplasmic (Potential).
FT TRANSMEM 185 205 Segment S1 (Potential).
FT TRANSMEM 227 247 Segment S2 (Potential).
FT DOMAIN 248 261 Cytoplasmic (Potential).
FT TRANSMEM 262 282 Segment S3 (Potential).
FT TRANSMEM 292 312 Segment S4 (Potential).
FT DOMAIN 313 325 Cytoplasmic (Potential).
FT TRANSMEM 326 346 Segment S5 (Potential).
FT TRANSMEM 365 385 Segment S6 (pore-forming) (Potential).
FT TRANSMEM 387 407 Segment S6 (Potential).
FT DOMAIN 408 651 Cytoplasmic (Potential).
FT SITE 372 377 Selectivity filter (By similarity).
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 651 AA; 71697 MW; 801DBCC3C56C721F CRC64;

Query Match	62.2%;	Score 2122;	DB 1;	Length 651;
Best Local Similarity	63.8%;	Pred. No. 1.1e-124;		
Matches 434;	Conservative 76;	Mismatches 116;	Indels 54;	Gaps 14;

QY	I	MAGVAAAMLPFARAALAGMMVAVANCMPPLAPADKNKRODELIVLVNSGRPRQWRTTLER	60
Db	1	MAGVATWLPFARAAGVWLPPLAQOPLPAPAEVYKASRGDEVLVNVNSGRRETWKTLLDR	60
QY	61	YBDTLLGSTEKEFFENEDTKKEYFFDDRDEPVFRCVLNFYRTGKLHYPRYECISAYDELA	120
Db	61	YBDTLLGSSEKEFFDYDAESGEYFFDRPDMFRVULNFYRTGRLLHCPROECTIQAFDELA	120
QY	121	YGLPEITGDCCEYEYKDKRENAERLMDNDNSENQESMPSL---SFRQTMWRAPENP	176
Db	121	YGLVPELVGDCCEYEYRDKRENAERLADEDEAQAGEG-PALPAGSSLLQRLWRAFENP	179
QY	177	HTSTLALVFYVVTGFFIAVSVITNVETVPCCGTVP--GSKELPCGERYSVAFFCLTACV	234
Db	180	HTSTALVFYVVTGFFIAVSIVANVETI PCRGTPRWPSKEQSCGDRFPTAFECMDTACV	239
QY	235	MIFTEVYLRLFAAPSRYPRIFRSVMSIIDVVAIMPYYIGLWMTNNEVDVSGAFVTLRFRV	294
Db	240	LIFTGEYLRLFAAPSRCRFLRSVMSLIDVVAILPYYIGLVFKNDVDVSGAFVTLRFRV	299
QY	295	RIIFKFSRHSQGLRILGYTLKSCASELGLPLSLTMAIIFATWIFYAEKSSASKFTSI	354
Db	300	RIIFKFSRHSQGLRILGYTLKSCASELGLPLSLTMAIIFATWIFYAEKGTSKTFTSI	359
QY	355	PASFWMYITVTMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHQO	414
Db	360	PASFWMYITVTMTLGYGDMVPSTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHQO	419
QY	415	RADKRRAOQKARLARIRVAKTGSSNAVILHSKNGLNLNELLTGTPEEBHN-GKTTSLIE	473
Db	420	RADKRRAOQKVRLARIRLARSCTMNAFLQYKONG---GLSDSGGDGMCLCVRSRSAFE	475
QY	474	SOHHHLHLCLEKTTGLSYLVDDPLLSVTRSTTIKNHFIDEQMFEQNCMESSMONTYSTRS	533
Db	476	QOHHHLHLCLEKTT-----CHEFTDELTFSEALGAVSLGGRTS-RS	515
QY	534	PSLSSHP---GLTTTCCSR-SKTTTHLPNSULPATRLRSMQELSTIHIOGSEQPSLTT	588
Db	516	TSVSSQPMGPGSLFSSCCSKRVNRRAIRLANSTASVSR-GSMQELDT--LAGLRRSPAPQ	572
QY	589	SRSSLNKLKADDLGRLPNCKTSQITTAIISIPTEPALTPEGESRPPSPG-----PNTNI	642
Db	573	TRSSLNAKPHDSLINDCSDHDFVAAIISIPTEPANTPD-ESQPSPPSGGGSGGTPTNTTL	631
QY	643	-----PSITSNVKVSVL 655	
Db	632	RNSSLGTPCLLPETVYKISSL 651	

Search completed: April 6, 2005, 07:13:40
Job time : 617.889 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 00:35:45 ; Search time 482.789 Seconds
(without alignments)
509.498 Million cell updates/sec

Title: US-10-062-879-4
Perfect score: 3320
Sequence: 1 MAGVAAALPFAAAAIIGWM.....PGPNTNIPSITSNVKVSVL 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3320	100.0	636	5	ABB79585	Abb79585 Human Kv4
2	3311	99.7	636	2	AAW79589	Aaw79589 Human Kv
3	3300.5	99.4	655	5	ABB79584	Abb79584 Human Kv4
4	3291.5	99.1	655	2	AAW79590	Aaw79590 Human Kv
5	3291.5	99.1	655	8	ADF91398	Adf91398 Wild-type
6	3285	98.9	636	2	AAW79591	Aaw79591 Human Kv
7	3284.5	98.9	655	7	ADD48188	Add48188 Rat Prote
8	3283.5	98.9	655	8	ADSL6294	Adsl6294 Human vol
9	3279.5	98.8	655	4	AAB86321	Aab86321 Human Kv4
10	3055	92.0	611	7	ADE61252	Ad61252 Rat Prote
11	2518	75.8	630	7	ADM10929	Adm10929 Human O64
12	2518	75.8	630	7	ADM10928	Adm10928 Human O64
13	2518	75.8	630	7	ADM10930	Adm10930 Human O64
14	2518	75.8	630	7	ADM10927	Adm10927 Human O64
15	2518	75.8	630	8	ADJ11257	Adj11257 Human ova
16	2518	75.8	630	8	ADJ11260	Adj11260 Human ova
17	2518	75.8	630	8	ADJ11258	Adj11258 Human ova
18	2518	75.8	630	8	ADJ11259	Adj11259 Human ova
19	2518	75.8	630	8	ADM43520	Adm43520 Human ova
20	2518	75.8	630	8	ADM43519	Adm43519 Human ova
21	2518	75.8	630	8	ADM43521	Adm43521 Human ova
22	2518	75.8	630	8	ADM43518	Adm43518 Human ova
23	2516	75.8	630	2	AAI13523	Aay13523 Amino aci
24	2513	75.7	629	4	AAB86319	Aab86319 Human Kv4
25	2132.5	64.2	647	4	AAW25597	Aam25597 Human pro

26	2127.5	64.1	646	4	AAB86318	Aab86318 Human Kv4
27	2121.5	63.9	646	2	AAY34123	Aay34123 Human pot
28	1955	58.9	571	4	ABB71722	Abb71722 Drosophil
29	894	26.9	217	4	AAB86320	Aab86320 Human Kv4
30	869	26.2	214	2	AAY13524	Aay13524 Amino aci
31	844.5	25.4	255	7	ADM10926	Adm10926 Human O64
32	844.5	25.4	255	8	ADJ11256	Adj11256 Human ova
33	844.5	25.4	255	8	ADM43517	Adm43517 Human ova
34	774.5	23.3	806	7	ADJ79875	Adj79875 CTKA_huma
35	766	23.1	911	7	ADJ69676	Adj69676 Human hea
36	758	22.8	985	8	ADI30147	Adi30147 Drosophil
37	758	22.8	985	8	ADI30143	Adi30143 Drosophil
38	750	22.6	854	6	ABP58354	Abp58354 Human pot
39	750	22.6	854	7	ADJ79874	Adj79874 CTKA_huma
40	750	22.6	858	2	AAI32015	Aay32015 Human cat
41	750	22.6	858	5	AAO17058	Aao17058 Human KCN
42	750	22.6	858	8	ADI38328	Adi38328 Human cat
43	749	22.6	985	4	ABB57774	Abb57774 Drosophil
44	747	22.5	1019	4	ABB67198	Abb67198 Drosophil
45	746	22.5	149	8	ADJ25645	Adj25645 Voltage-g

ALIGNMENTS

RESULT 1
ABB79585
ID ABB79585 standard; protein; 636 AA.

AC ABB79585;
XX
XX
DT 01-OCT-2002 (first entry)
XX
XX
DE Human Kv4.3 potassium channel (short form).
XX
XX
KW Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KW neurotropic; neuroprotective; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
XX
FN US6395477-B1.
XX
XX
PD 28-MAY-2002.
XX
XX
PF 23-OCT-1998; 98US-00178109.
XX
XX
PR 23-OCT-1998; 98US-00178109.
XX
XX
(AMHP) AMERICAN HOME PROD CORP.
XX
XX
PI Cockett MI, Dilks DW, Ling HC, Sokol PT;
XX
XX
DR WPI; 2002-556093/59.
DR N-PSDB; ABN84401.
XX
XX
PT New isolated polynucleotide encoding human Kv4.3 potassium channel
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT diseases.
XX
XX
PS Claim 1; Col 23-26; 19pp; English.
XX
XX
CC The present sequence is the protein sequence of the short isoform of
CC novel human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been
CC identified: a full-length form (hKv4.3 long) (see ABB79584); and the
CC short form, which has a deletion of 19 amino acids in the carboxy domain
CC after the predicted sixth transmembrane domain (hKv4.3 short). Human
CC heart primarily expresses hKv4.3 long, whereas human brain contains both
CC forms. The invention provides Kv4.3 polypeptides, polynucleotides, and
CC methods for producing these polynucleotides. The Kv4.3 polypeptides and
CC polynucleotides are useful in the diagnosis, treatment and screening of
CC human diseases relating to an excess or deficiency of hKv4.3 activity,
CC including Alzheimer's disease and heart disease

XX Sequence 636 AA;
SQ

Query Match 100.0%; Score 3320; DB 5; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.6e-313;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAGVAAWLFPARAAAIIGMPVANCMPMLAPADKXKRQDELIVLVNSGRRFQRTWRTTLER 60
DB 1 MAAGVAAWLFPARAAAIIGMPVANCMPMLAPADKXKRQDELIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAEPNPTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAEPNPTST 180
QY 181 LALVFFYYVTGFFIAVSITNVVETVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTYE 240
DB 181 LALVFFYYVTGFFIAVSITNVVETVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTYE 240
QY 241 YLLRLFAAPSRRYRFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVPRVFRIFKE 300
DB 241 YLLRLFAAPSRRYRFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVPRVFRIFKE 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRR 420
QY 421 AOKKARLARIRVAKTSSNAYLHRSKNGLINEALELTGPBEEHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTSSNAYLHRSKNGLINEALELTGPBEEHMGKTTSLIESQHHL 480
QY 481 HCLEKTTHNEFIDEQMEQNCMESSMONYPSTRSPSLSSHPLTTTCCSRSKKTHLPN 540
DB 481 HCLEKTTHNEFIDEQMEQNCMESSMONYPSTRSPSLSSHPLTTTCCSRSKKTHLPN 540
QY 541 SNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSLNKADGRLPNCKTSQITTAIISIP 600
DB 541 SNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSLNKADGRLPNCKTSQITTAIISIP 600
QY 601 PPALTPGEGSRPPAPSPGPNNTIPSITSNVVKSVL 636
DB 601 PPALTPGEGSRPPAPSPGPNNTIPSITSNVVKSVL 636
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RESULT 2
AAW79589
ID AAW79589 standard; protein; 636 AA.

```
XX AC AAW79589;
XX DT 11-JAN-1999 (first entry)
XX DE Human Kv potassium channel hKv4.3 (shorter isoform).
XX KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
XX therapy; diagnosis.
XX OS Homo sapiens.
XX PN WO9842833-A2.
XX PD 01-OCT-1998.
XX PF 23-MAR-1998; 98WO-EP001901.
XX
```

PR 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.

XX (SMK) SMITHKLINE BEECHAM LAB PHARM.

XX Bril AMA, Calmels TPG, Fatvre JSP, Javre J, Rouanet S;

XX WPI; 1998-542277/46.

DR N-PSDB; AAV61571.

PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT polynucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.

XX Claim 2; Page 25; 47pp; English.

CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3
CC polynucleotide (see AAV61571), and has 99% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC Kv family related proteins. A longer isoform (see AAW79590) has been
CC identified, which has an additional 19 amino acids inserted between amino
CC acids 487 and 488. The invention relates to hKv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hKv4.3 polypeptides can be used to identify
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilising such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hKv4.3 expression or
CC activity

XX Sequence 636 AA;

Query Match 99.7%; Score 3311; DB 2; Length 636;
Best Local Similarity 99.7%; Pred. No. 1.2e-312;
Matches 634; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MAAGVAAWLFPARAAAIIGMPVANCMPMLAPADKXKRQDELIVLVNSGRRFQRTWRTTLER 60
DB 1 MAAGVAAWLFPARAAAIIGMPVANCMPMLAPADKXKRQDELIVLVNSGRRFQRTWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAEPNPTST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMWRAEPNPTST 180
QY 181 LALVFFYYVTGFFIAVSITNVVETVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTYE 240
DB 181 LALVFFYYVTGFFIAVSITNVVETVPCGTVPKSGKELPCGERYSVAFFCLDTACVMIFTYE 240
QY 241 YLLRLFAAPSRRYRFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVPRVFRIFKE 300
DB 241 YLLRLFAAPSRRYRFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVPRVFRIFKE 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRR 420
QY 421 AOKKARLARIRVAKTSSNAYLHRSKNGLINEALELTGPBEEHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTSSNAYLHRSKNGLINEALELTGPBEEHMGKTTSLIESQHHL 480
QY 481 HCLEKTTHNEFIDEQMEQNCMESSMONYPSTRSPSLSSHPLTTTCCSRSKKTHLPN 540
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Db 481 HCLEKTTNHEFIDEQMFEONCMESSMONTPTSTRSPSLSSHPGLTTTCCSRRSKKTTHLPN 540
Qy 541 SNLPATRLRSMQELSTIHIOGSEQPSLTTSRSSLNKADDDLPRNCKTSQITTAISIPT 600
Db 541 SNLPATRLRSMQELSTIHIOGSEQPSLTTSRSSLNKADDDLPRNCKTSQITTAISIPT 600
Qy 601 PPALTPGESRPPASPSPNTNIPISITSNVVKVSVL 636
Db 601 PPALTPGESRPPASPSPNTNIPISITSNVVKVSVL 636

RESULT 3

ABR79584
ID ABR79584 standard; protein; 655 AA.
XX
AC ABR79584;
XX
DT 01-OCT-2002 (first entry)
XX
DE Human Kv4.3 potassium channel (long form).
XX
KW Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KW nootropic; neuroprotective; cardiac; gene therapy.
XX
OS Homo sapiens.
XX
PN US6395477-B1.
XX
PD 28-MAY-2002.
XX
PF 23-OCT-1998; 98US-00178109.
XX
PR 23-OCT-1998; 98US-00178109.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Cockett MI, Dilks DW, Ling HC, Sokol PT;
XX
XX WPI; 2002-556093/59.
DR N-PSDB; ABN84400.
XX
XX
PT New isolated polynucleotide encoding human Kv4.3 potassium channel
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT diseases.
XX
XX
PS Claim 1; Col 16-20; 19pp; English.
XX
CC The present sequence is the protein sequence of the long isoform of novel
CC human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been
CC identified: the present full-length form (hKv4.3 long); and a second form
CC (see ABR79585), which has a deletion of 19 amino acids in the carboxy
CC domain after the predicted sixth transmembrane domain (hKv4.3 short).
CC Human heart primarily expresses hKv4.3 long, whereas human brain contains
CC both forms. The invention provides Kv4.3 polypeptides, polynucleotides,
CC and methods for producing these polynucleotides. The Kv4.3 polypeptides
CC and polynucleotides are useful in the diagnosis, treatment and screening
CC of human diseases relating to an excess or deficiency of hKv4.3 activity,
CC including Alzheimer's disease and heart disease
XX
SQ Sequence 655 AA;

Query Match 99.4%; Score 3300.5; DB 5; Length 655;
Best Local Similarity 97.1%; Pred. No. 1.3e-311;
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
Qy 1 MAAGVAAWLPFAAAAI GWMPVANCMPPLAPADKNKRODELIVNVSGRRFQTWRITLER 60
Db 1 MAAGVAAWLPFAAAAI GWMPVANCMPPLAPADKNKRODELIVNVSGRRFQTWRITLER 60
Qy YPDTILGSTEKEFFFNEDTKYFFPRDPEVFRVCVLFNYRTGKLHYPRYECISAYDELAFL 120
DR ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 YPDTILGSTEKEFFFNEDTKYFFPRDPEVFRVCVLFNYRTGKLHYPRYECISAYDELAFL 120
Qy 121 YGILPEIIGDCCEYBYKDKRENAERLMDNDSENNOESMPSISFROTWMRAFENPHST 180
Db 121 YGILPEIIGDCCEYBYKDKRENAERLMDNDSENNOESMPSISFROTWMRAFENPHST 180
Qy 181 LALVFYVVTGFFIAVSVITNVEIVPCGIVPGSKELPCGERYSVAFFCLDTACVMIFTV 240
Db 181 LALVFYVVTGFFIAVSVITNVEIVPCGIVPGSKELPCGERYSVAFFCLDTACVMIFTV 240
Qy 241 YLLRLFAAPSRYRFRISVWSIIDVVAIMPYIIGLVMTNNEVDVGAFTLVFRVFRIFKE 300
Db 241 YLLRLFAAPSRYRFRISVWSIIDVVAIMPYIIGLVMTNNEVDVGAFTLVFRVFRIFKE 300
Qy 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPASFMY 360
Db 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPASFMY 360
Qy 361 TIVMTTLGYGDMVPKTTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORADKRR 420
Db 361 TIVMTTLGYGDMVPKTTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORADKRR 420
Qy 421 AOKKARLARIRVAKTGSSNAYLHSGRNGLINEALLETGTPEEEMGKTTSLIESQHHL 480
Db 421 AOKKARLARIRVAKTGSSNAYLHSGRNGLINEALLETGTPEEEMGKTTSLIESQHHL 480
Qy 481 HCLEKTT-----NHEFIDEQMFEONCMESSMONTPTSTRSPSLSSHP 521
Db 481 HCLEKTTGLSYVDPLISVRTSTIKNHEFIDEQMFEONCMESSMONTPTSTRSPSLSSHP 540
Qy 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTTSRSSLNKADG 581
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIOGSEQPSLTTSRSSLNKADG 600
Qy 582 LRPNCSTQITTAIISIPTPALTPGESRPPASPSPNTNIPISITSNVVKVSVL 636
Db 601 LRPNCSTQITTAIISIPTPALTPGESRPPASPSPNTNIPISITSNVVKVSVL 655

RESULT 4

AAW79590
ID AAW79590 standard; protein; 655 AA.
XX
XX AAW79590;
AC
XX
DT 11-JAN-1999 (first entry)
XX
XX
DE Human Kv potassium channel hKv4.3 (longer isoform).
XX
KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 488..506
FT /note="extra residues of longer hKv4.3 isoform"
PN WO9842833-A2.
PD 01-OCT-1998.
XX
XX 23-MAR-1998; 98WO-EP001901.
XX
XX 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.
PI Bril AWA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
XX WPI; 1998-542277/46.
DR

DR N-PSDB; AAV61572.
XX New potassium channel polypeptides, hkv4.3 - and hkv4.3-encoding
PT polynucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
XX Claim 2; Page 26-27; 47pp; English.
XX
CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hkv4.3. The sequence was deduced from an isolated hkv4.3
CC polynucleotide (see AAV61572), and has 97% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC Kv family related proteins. A shorter isoform (see AAV79589) has been
CC identified, which lacks amino acid residues 488-506 of the longer
CC isoform. The invention relates to hkv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hkv4.3 polypeptides can be used to identify
CC agonists and antagonists of hkv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilizing such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hkv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hkv4.3 expression or
CC activity
XX
XX Sequence 655 AA;
SQ
Query Match 99.1%; Score 3291.5; DB 2; Length 655;
Best Local Similarity 96.8%; Pred. No. 1e-310;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFARAAAIIGMPVANCMPPLAPADKNKRQDELIIVLVNSGRRFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIIGMPVANCMPPLAPADKNKRQDELIIVLVNSGRRFQWRTTLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEXYFFDRDPEVFRVNLNFRYRGLHYPRYECISAYDDEIAF 120
DB 61 YPDTLLGSTEKEFFFNEDTKEXYFFDRDPEVFRVNLNFRYRGLHYPRYECISAYDDEIAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFROCTWRAENPH1ST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSLSFROCTWRAENPH1ST 180
QY 181 LALVFFYYVTGFFIAVSITNNVETVPCGTVPGSKELPCGERYSVAFPLDTACWIFVE 240
DB 181 LALVFFYYVTGFFIAVSITNNVETVPCGTVPGSKELPCGERYSVAFPLDTACWIFVE 240
QY 241 YLRLPAPSRNRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRIKRF 300
DB 241 YLRLPAPSRNRYRFRISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRIKRF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIVTMTLLGYGDMVPKTIAGKIFGSGISLGLVIALPVPIVSNFSRIYHQNORADKRR 420
DB 361 TIVTMTLLGYGDMVPKTIAGKIFGSGISLGLVIALPVPIVSNFSRIYHQNORADKRR 420
QY 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALBELTGTPEEHMGKTSLSIESQHHL 480
DB 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALBELTGTPEEHMGKTSLSIESQHHL 480
QY 481 HCLEKTY-----NHEFIDEQMEQNCMESSMONTSTRSPSLSSHP 521
DB 481 HCLEKTYGLSYLVDDPLLSVRISTIKNHEFIDEQMEQNCMESSMONTSTRSPSLSSHP 540
QY 522 GLTTTCCSRKSKKTHLPNSNLPAFRLRSMOELSTHIOGSEQPSLTSSRLNLKADGD 581
DB 541 GLTTTCCSRKSKKTHLPNSNLPAFRLRSMOELSTHIOGSEQPSLTSSRLNLKADGD 600
QY 582 LRPNCKTSQITTAIISIPFPALTPEGESRPPASPGPNTNIPISITSNVVKVSVL 636
DB 582 LRPNCKTSQITTAIISIPFPALTPEGESRPPASPGPNTNIPISITSNVVKVSVL 636

DB 601 LRPNCKTSQITTAIISIPFPALTPEGESRPPASPGPNTNIPISITSNVVKVSVL 655
RESULT 5
ID ADF91398 standard; protein; 655 AA.
XX ADF91398;
AC ADF91398;
XX
DT 26-FEB-2004 (first entry)
XX
DE Wild-type hkv4.3 #SEQ ID 5.
XX
KW Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective;
KW tranquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;
KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;
KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;
KW tachycardia; congestive heart failure; epilepsy; stroke;
KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;
KW Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO2003097682-A1.
XX
PD 27-NOV-2003.
XX
PF 14-MAY-2003; 2003WO-IB002453.
XX
PR 15-MAY-2002; 2002GB-00011123.
PR 15-MAY-2002; 2002US-0378076P.
PR 15-MAY-2002; 2002US-0378131P.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Kalecta TJ, Dewulf NE, Plaetnick GKM;
XX WPI; 2004-061981/06.
DR N-PSDB; ADF91397.
XX
PT New nematode worm expressing a heterologous nucleotide sequence encoding
PT a functional voltage-gated potassium channel of the Kv4 family, useful
PT for determining compounds that interact with the voltage-gated potassium
PT channel.
XX
PS Example 1; SEQ ID NO 5; 82pp; English.
XX
CC The invention relates to a nematode worm that expresses a heterologous
CC nucleotide sequence encoding a functional voltage-gated potassium channel
CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,
CC part or fragment. The nematode worm is useful in determining whether a
CC compound interacts with the voltage-gated potassium channel of the Kv4
CC family or whether a compound is an agonist, antagonist, opener and/or
CC blocker of the voltage-gated potassium channel expressed by the nematode
CC worm. The methods are used for identifying and developing compounds that
CC interact with voltage-gated potassium channels of the Kv4 family. The
CC compounds may be used in the development and/or preparation of
CC compositions for pharmaceutical, agrochemical and/or veterinary use.
CC These may be used in preparing compositions for preventing or treating
CC diseases or conditions such as arrhythmia, tachycardia, congestive heart
CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,
CC Alzheimer's disease or Parkinson's disease. The current sequence
CC represents wild-type hkv4.3.
XX
XX
SQ Sequence 655 AA;
Query Match 99.1%; Score 3291.5; DB 8; Length 655;
Best Local Similarity 96.8%; Pred. No. 1e-310;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFARAAAIIGMPVANCMPPLAPADKNKRQDELIIVLVNSGRRFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAIIGMPVANCMPPLAPADKNKRQDELIIVLVNSGRRFQWRTTLER 60

QY YPDTLLGSTEKEFFFNEDTKYFEPDRDPEVFRVCVLFNFYRTGKLHYPRYECISAYDELAIF 120
DB 61 YPDTLLGSTEKEFFFNEDTKYFEPDRDPEVFRVCVLFNFYRTGKLHYPRYECISAYDELAIF 120
QY 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHTST 180
QY 181 LALVFYVVTGFFIAVSVTINVTETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE 240
DB 181 LALVFYVVTGFFIAVSVTINVTETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE 240
QY 241 YLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVFRIFKF 300
DB 241 YLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVFRIFKF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
DB 361 TIVMTTLLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
QY 421 AOKKARLARIRIVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRIVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHHMGKTTSLIESQHHL 480
QY 481 HCLEKTT-----NHEFIDEQMFQONCMESMOMNYPSTRSPSLSSH 521
DB 481 HCLEKTTGLSYIVDDPLISVTRSTIKNHEFIDEQMFQONCMESMOMNYPSTRSPSLSSH 540
QY 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTTSRSSLNKADDG 581
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTTSRSSLNKADDG 600
QY 582 LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGBNTNIPISITSNVKVSYL 636
DB 601 LRPNCKTSQITTAIISIPTPALTPEGESRPPASPGBNTNIPISIASNVKVSAL 655
RESULT 6
ID AAW79591 standard; protein; 636 AA.
XX AAW79591;
AC AAW79591;
XX 11-JAN-1999 (first entry)
DT 11-JAN-1999 (first entry)
XX Human Kv potassium channel hKv4.3.
DE Human Kv potassium channel hKv4.3.
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
KM therapy; diagnosis.
XX Homo sapiens.
OS Homo sapiens.
XX WO9842833-A2.
PN WO9842833-A2.
XX 01-OCT-1998.
PD 01-OCT-1998.
XX 23-MAR-1998; 98WO-EP001901.
PF 23-MAR-1998; 98WO-EP001901.
XX 27-MAR-1997; 97GB-00006377.
PR 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX (SMIK) SMITHKLINE BEECHAM LAB PHARM.
PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.
XX Bril AMA, Calmels TFG, Faivre JSP, Javre J, Rouanet S;
PI Bril AMA, Calmels TFG, Faivre JSP, Javre J, Rouanet S;
XX WPI; 1998-542277/46.
DR WPI; 1998-542277/46.
DR N-PSDB; AAV61573.

XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX Claim 19; Page 28; 47pp; English.
XX This is the amino acid sequence for an isoform of human Kv potassium
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3
CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all
CC Kv family related proteins. hKv4.3 isoforms (see AAW79589 and AAW79590)
CC are also claimed. The invention relates to hKv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hKv4.3 polypeptides can be used to identify
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilizing such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hKv4.3 expression or
CC activity
XX Sequence 636 AA;
SQ

Query Match 98.9%; Score 3285; DB 2; Length 636;
Best Local Similarity 99.1%; Pred. No. 4.1e-310;
Matches 630; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFAAAALGMPVANCMPPLAPADKNKQDELIVLVNSGRRFQTMRTLLER 60
DB 1 MAAGVAAWLPFAAAALGMPVANCMPPLAPADKNKQDELIVLVNSGRRFQTMRTLLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKYFEPDRDPEVFRVCVLFNFYRTGKLHYPRYECISAYDELAIF 120
DB 61 YPDTLLGSTEKEFFFNEDTKYFEPDRDPEVFRVCVLFNFYRTGKLHYPRYECISAYDELAIF 120
QY 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAFENPHTST 180
QY 181 LALVFYVVTGFFIAVSVTINVTETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE 240
DB 181 LALVFYVVTGFFIAVSVTINVTETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE 240
QY 241 YLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVFRIFKF 300
DB 241 YLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVFRIFKF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
DB 361 TIVMTTLLGYGDMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIYHONORADKRR 420
QY 421 AOKKARLARIRIVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHHMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRIVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHHMGKTTSLIESQHHL 480
QY 481 HCLEKTTNHEFIDEQMFQONCMESMOMNYPSTRSPSLSSHPLTTTCCSRRSKKTTHLPN 540
DB 481 HCLEKTTNHEFIDEQMFQONCMESMOMNYPSTRSPSLSSHPLTTTCCSRRSKKTTHLPN 540
QY 541 SNLPATRLRSMQELSTIHIGSEQPSLTTSRSSLNLKADDGARPNCCKTSQITTAIISIP 600
DB 541 SNLPATRLRSMQELSTIHIGSEQPSLTTSRSSLNLKADDGARPNCCKTSQITTAIISIP 600
QY 601 PPALTPEGESRPPASPGBNTNIPISITSNVKVSYL 636
DB 601 PPALTPEGESRPPASPGBNTNIPISIASNVKVSAL 636

RESULT 7
ADD48188
ID ADD48188 standard; protein; 655 AA.
XX
XX ADD48188;
AC
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
DT
XX
DE Rat Protein AAB53321, SEQ ID NO 13886.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS Unidentified.
XX
XX MO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002MO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Belfort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; AAB53321.
XX
PT New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 655 AA;
SQ

Query Match 98.9%; Score 3284.5; DB 7; Length 655;
Best Local Similarity 96.6%; Pred. No. 4.8e-310;

Matches 633; Conservative 1; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFADAAAIAGMPVANCMPPLADKDKRQDELIVLVNSGRFRQTWRTLLER 60
DB 1 MAAGVAAWLPFADAAAIAGMPVANCMPPLADKDKRQDELIVLVNSGRFRQTWRTLLER 60
QY YPDTLLGSTEKEPFENEDTKEXYFFPDRDPEVFRCVLNFYRTGKLYHPRYECISAYODELAF 120
DB YPDTLLGSTEKEPFENEDTKEXYFFPDRDPEVFRCVLNFYRTGKLYHPRYECISAYODELAF 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLFRQTMWRAFENPHST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLFRQTMWRAFENPHST 180
QY 181 LALVFYVYTGFFLAHSVITNVETVPCGTVPESKELPCGERYSVAFFCLDTACVMITFVE 240
DB 181 LALVFYVYTGFFLAHSVITNVETVPCGTVPESKELPCGERYSVAFFCLDTACVMITFVE 240
QY 241 YLLRLFAAPSRYPFRIRSVMSIIDVVAIMPYIYGLVMTNEDVSGAFVTLRVRVFRIFKF 300
DB 241 YLLRLFAAPSRYPFRIRSVMSIIDVVAIMPYIYGLVMTNEDVSGAFVTLRVRVFRIFKF 300
QY 301 SRHSQGLRILGYTLKSCASLGFLFSLTMAIIIPATWFAEAKGSSASKTSIPASFMY 360
DB 301 SRHSQGLRILGYTLKSCASLGFLFSLTMAIIIPATWFAEAKGSSASKTSIPASFMY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYQONRADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYQONRADKRR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNLEALGTPEEHNKGTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKRNGLNLEALGTPEEHNKGTSLIESQHHL 480
QY 481 HCLEKTT-----NHEFIDQMEQCMESSMNYPTSRPSLSHP 521
DB 481 HCLEKTTGLSYLVDDPLSVRSTIKNHEFIDQMEQCMESSMNYPTSRPSLSHS 540
QY 522 GLTTCCSRRSKTTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSLSLKKADG 581
DB 541 GLTTCCSRRSKTTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSLSLKKADG 600
QY 582 LRPNCKTSQITTAIISIPTPALTPGESRPPASPPTNPISITSNVAVSVL 636
DB 601 LRPNCKTSQITTAIISIPTPALTPGESRPPASPPTNPISITSNVAVSVL 655
RESULT 8
ADS16294
ID ADS16294 standard; protein; 655 AA.
XX
XX AC ADS16294;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Human voltage-dependent potassium channel (Hsapkv4.3) protein.
XX
XX DE Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; human.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Region 180..206
FT /note= "Hydrophobic region (S1)"
FT Region 225..248
FT /note= "Hydrophobic region (S2)"
FT Region 254..281
FT /note= "Hydrophobic region (S3)"
FT Region 286..305
FT /note= "Hydrophobic region (S4)"
FT Region 315..343

FT /note= "Hydrophobic region (S5) "
FT Region 355..365
FT /note= "Pore region (P) "
FT Region 374..400
FT /note= "Hydrophobic region (S6) "
XX US2004175761-A1.
PN
XX
XX
PD 09-SEP-2004.
XX
XX 01-MAR-2003; 2003US-00377139.
PF
XX
XX 01-MAR-2003; 2003US-00377139.
PR
XX
XX (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX
XX Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
PI
XX
XX WPI; 2004-642122/62.
DR
XX GENBANK; AF120491.
XX
XX
XX Screening drug candidates that target voltage dependent ion channel
XX protein, involves contacting screening protein with chemical compound,
XX PT which is drug candidate and determining whether chemical compound binds
XX PT to screening protein.
XX
XX
XX Disclosure; SEQ ID NO 6; 61pp; English.
XX
XX
XX The invention relates to the composition of matter suitable for use in
XX identifying chemical compounds that bind to voltage-dependent ion channel
XX protein. The composition comprises a screening protein that consists of
XX an ion channel voltage sensor domain of the ion channel protein
XX immobilised on a solid support. The invention is useful for identifying
XX chemical compounds (drug candidate) that bind to voltage-dependent ion
XX channel proteins. The drug candidate of the invention is utilised for
XX treating a condition mediated by aberrant electrical activity that
XX initiates uptake or release of neurotransmitters and contraction of
XX muscles. The drug candidate of the invention is also utilised for
XX treating epilepsy and arrhythmia. The present sequence is a voltage-
XX dependent potassium (Kv) channel protein.
XX
XX
XX Sequence 655 AA;
SQ
Query Match 98.8%; Score 3283.5; DB 8; Length 655;
Best Local Similarity 96.8%; Pred. No. 6.1e-310;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFARAALGMPVANCMPPLAPADKXKODELIYLVNSGRRFQTWRTTLER 60
DB 1 MAAGVAAWLPFARAALGMPVANCMPPLAPADKXKODELIYLVNSGRRFQTWRTTLER 60
QY 61 YPDTLLGSTEKFEFFNEDTKEYFPDRDPEVRCVLNFEYRTGKLYPRYECISAYDEELAF 120
DB 61 YPDTLLGSTEKFEFFNEDTKEYFPDRDPEVRCVLNFEYRTGKLYPRYECISAYDEELAF 120
QY 121 YGILPEIIGDCCEYEYKDRKRENAERLMDNDSENNOESMPSLSFRQIMRAFENDHTST 180
DB 121 YGILPEIIGDCCEYEYKDRKRENAERLMDNDSENNOESMPSLSFRQIMRAFENDHTST 180
QY 181 LALVEYVVTGFEIYAVSVITNVEATPCGTGVSKEPLCGEYSAVAFCLDTACVMIFTE 240
DB 181 LALVEYVVTGFEIYAVSVITNVEATPCGTGVSKEPLCGEYSAVAFCLDTACVMIFTE 240
QY 241 YLLRLEFAAPSRFRFIRSVMSIIDVAIMPIYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
DB 241 YLLRLEFAAPSRFRFIRSVMSIIDVAIMPIYIGLVMTNNEDEVSGAFVTLRVRFRIFKE 300
QY 301 SRHSOGLRIILGYTLKSCASELGFLLSLTMAIIFATVMFYAEKSSASAKFTSIPASFWY 360
DB 301 SRHSOGLRIILGYTLKSCASELGFLLSLTMAIIFATVMFYAEKSSASAKFTSIPASFWY 360

QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNRADKR 420
DB 361 TIVMTTLGYGDMVLTAKIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNRADKR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHSGKNGLNLEALGTGPEEEMGKTSLLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHSGKNGLNLEALGTGPEEEMGKTSLLIESQHHL 480
QY 481 HCLEKTT-----NHEFIDEQMFQNCMESSMONTPTSPSPSSSH 521
DB 481 HCLEKTTGLSYLVDPLLSVRTSTIKNHEFIDEQMFQNCMESSMONTPTSPSPSSSH 540
QY 522 GLTTCCSRSSKKTTHLPNSNLPATRLRSQELSTHIQGSQPSLTSSSLNLKADDG 581
DB 541 GLTTCCSRSSKKTTHLPNSNLPATRLRSQELSTHIQGSQPSLTSSSLNLKADDG 600
QY 582 LRPNCKTSQITTAIISIPPPALPTEGESRPPASPGPNTNIPSTSNVYKSVL 636
DB 601 LRPNCKTSQITTAIISIPPPALPTEGESRPPASPGPNTNIPSTSNVYKSVL 655
RESULT 9
AAB86321
ID AAB86321 standard; protein; 655 AA.
XX
XX AAB86321;
XX AC
XX
XX 13-SEP-2001 (first entry)
XX
XX
XX Human Kv4.3 protein.
XX
XX
XX Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;
XX neurodegenerative disease; ischemia; stroke; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;
XX learning capacity; protein kinase activator; anti-arrhythmic.
XX
XX Homo sapiens.
XX
XX DE19963612-A1.
XX
XX 12-JUL-2001.
XX
XX
XX 29-DEC-1999; 99DE-01063612.
XX
XX 29-DEC-1999; 99DE-01063612.
XX
XX 29-DEC-1999; 99DE-01063612.
XX
XX (GENI-) FORSCHUNGSELSCHAFT GENION MBH.
XX
XX WPI; 2001-426637/46.
XX
XX
XX New potassium channel subunit proteins, useful for identifying and
XX testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological
XX agents.
XX
XX Claim 4; Page 32-33; 50pp; German.
XX
XX
XX This invention describes a novel potassium channel protein (I) that is
XX either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium
XX channels containing (I) are used to identify and test: (i) compounds for
XX treatment of neurodegenerative diseases (autism, epilepsy, ischemia,
XX stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac
XX arrhythmia, or those that improve learning capacity and memory; and (ii)
XX activators of protein kinases. Host cells that express (I) can identify
XX agents that do not interact significantly with channels and control I to
XX (a quickly activated transient current), so lack the side effects of
XX known anti-arrhythmic agents. They also eliminate, or reduce, the need
XX for testing on organ cultures
XX
XX
XX Sequence 655 AA;
SQ
Query Match 98.8%; Score 3279.5; DB 4; Length 655;
Best Local Similarity 96.6%; Pred. No. 1.5e-309;

Matches	633;	Conservative	0;	Mismatches	3;	Indels	19;	Gaps	1
QY		1	MAAGVAAWLPFARAAAI	IGMPPVANCMPMLAPADKXKRODEL	VLNVSGRRFQTRTTLLR	60			
Db		1	MAAGVAAWLPFARAAAI	IGMPPVANCMPMLAPADKXKRODEL	VLNVSGRRFQTRTTLLR	60			
QY		61	YPDTLLGSTEKEFEFF	NEDTKKEYFPDRDPEVRCVLNPFYRTGKLHYPRYCISAYDDELAF	120				
Db		61	YPDTLLGSTEKEFEFF	NEDTKKEYFPDRDPEVRCVLNPFYRTGKLHYPRYCISAYDDELAF	120				
QY		121	YGILPEIIGDCCYEYK	KORKRENAERLMDNDSENNOESMPSISFRQTMRAFENPHST	180				
Db		121	YGILPEIIGDCCYEYK	KORKRENAERLMDNDSENNOESMPSISFRQTMRAFENPHST	180				
QY		181	LALVFYVVTGFFIAVS	VITNVVETPCGTVPGSKELPCGERISVAFCLDTCVMIPTVE	240				
Db		181	LALVFYVVTGFFIAVS	VITNVVETPCGTVPGSKELPCGERISVAFCLDTCVMIPTGE	240				
QY		241	YLRLFAAPSRVRFIR	SVNSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVERIFKF	300				
Db		241	YLRLFAAPSRVRFIR	SVNSIIDVVAIMPYIIGLVMTNNEDEVSGAFVTLRVFRVERIFKF	300				
QY		301	SRHSQGRILGYTLK	SCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY	360				
Db		301	SRHSQGRILGYTLK	SCASELGFLLFSLTMAIIIFATVMFYAEKSSASKFTSIPASFWY	360				
QY		361	TIVTMTLLGYGDMV	PKTIAGKIFGSI	CSLGLVLIALPVPVIVSNFSRIYHQNQRADKR	420			
Db		361	TIVTMTLLGYGDMV	LKTIAGKIFGSI	CSLGLVLIALPVPVIVSNFSRIYHQNQRADKR	420			
QY		421	AOKKARLARIRVAK	TGSSNAVYLSKRNGLNEAL	ELTGTPEEBHMGKTSLSIESQHHL	480			
Db		421	AOKKARLARIRVAK	TGSSNAVYLSKRNGLNEAL	ELTGTPEEBHMGKTSLSIESQHHL	480			
QY		481	HCLEKTT-----	NHEFIDEQMEQN	CMESSMONYPSTRSPSLSSHP	521			
Db		481	HCLEKTTGLSYLVD	PLSVRTSTIKNHEFIDEQMEQN	CMESSMONYPSTRSPSLSSHP	540			
QY		522	GLTTCCSRRSKKTH	LPSNLPATRLRSMQELSTIH	QGSQPSLTTGRSSLN	KADDG 581			
Db		541	GLTTCCSRRSKKTH	LPSNLPATRLRSMQELSTIH	QGSQPSLTTGRSSLN	KADDG 600			
QY		582	LRPNCKTSQITTA	IIISIPRPALTPEGESRPPAS	PGPNTNIPISITSNVKVSYL	636			
Db		601	LRPNCKTSQITTA	IIISIPRPALTPEGESRPPAS	PGPNTNIPISITSNVKVSAL	655			
RESULT 10									
ADE61252									
ID			ADE61252	standard; protein; 611 AA.					
XX			ADE61252;						
AC			29-JAN-2004	(first entry)					
XX									
DE			Rat Protein AAA80459, SEQ ID NO 7170.						
XX									
KW			Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;						
XX			chronic constriction injury; CCI; spared nerve injury; SNr; Chung.						
OS			Rattus norvegicus.						
XX									
PN			WO2003016475-A2.						
XX									
PD			27-FEB-2003.						
XX									
PF			14-AUG-2002; 2002WO-US025765.						
XX									
PR			14-AUG-2001; 2001US-0312147P.						
XX									
PR			01-NOV-2001; 2001US-0346382P.						
XX									
XX			26-NOV-2001; 2001US-0333347P.						
PA			(GEHO) GEN HOSPITAL CORP.						

PA	(FARB) BAYER AG.
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M;
XX	
DR	WPI; 2003-268312/26.
XX	GENSEBANK; AAA80459.
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PS	Claim 1, Page; 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	which is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. gene
CC	therapy). The sequence presented is a rat protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 611 AA;
	Query Match 92.0%; Score 3055; DB 7; Length 611;
	Best Local Similarity 99.3%; Pred. No. 9.6e-288;
	Matches 584; Conservative 2; Mismatches 2; Indels 0; Gaps 0
OY	1 MAAGVAAWLPPAPAAAAIGMMPVANCPMLPADKNKODELIVLVNSGRRFQTWTTLER 60
DB	1 MAAGVAAMLPPARAAAIGMMPVANCPMLPADKNKODELIVLVNSGRRFQTWTTLER 60
OY	61 YPDTLLSGTEKEFFFNEDTKKEYFPDPDPEVRVCVLNFRYRTGKHYPREYCISAYDEELAF 120
DB	61 YPDTLLSGTEKEFFFNEDTKKEYFPDPDPEVRVCVLNFRYRTGKHYPREYCISAYDEELAF 120
OY	121 YGILLPEITIGDCCYEYKDKRRENARELTMDNDSENNOESMSPSLSFROTMRAFENHTST 180
DB	121 YGIHPEIIGDCCYEYKDKRRENARELTMDNDSENNOESMSPSLSFROTMRAFAENHTST 180
OY	181 LALVFYYVTGFFLAVSVITNVVEITVPDGTGVSGSKELPCGERYSVAFFCLDTACVMIFTV 240
DB	181 LALVFYYVTGFFLAVSVITNVVEITVPDGTGVSGSKELPCGERYSVAFFCLDTACVMIFTV 240
OY	241 YILRLFAAPSRIRYRIRSVMSIIDVAIMPYIIGLVMTNNEDVSAGAFVTLRVFRVRIKF 300
DB	241 YILRLFAAPSRIRYRIRSVMSIIDVAIMPYIIGLVMTNNEDVSAGAFVTLRVFRVRIKF 300
OY	301 SRHSQGAILIGYTLKSCASBELGLFLSLTMAIIIFATVMFYAEKGSSASKFTSIPASF 360
DB	301 SRHSQGAILIGYTLKSCASBELGLFLSLTMAIIIFATVMFYAEKGSSASKFTSIPASF 360
OY	361 TIVTMTTILGYGDWPCKTIAGKIFGSICSLSGVLVIALFVPVIVSNFSRIYHONRADKR 4200
DB	361 TIVTMTTILGYGDWPCKTIAGKIFGSICSLSGVLVIALFVPVIVSNFSRIYHONRADKR 4200

OY 421 AOKKARLARIRVAKTSSNAVYLSKNGNLNLEALLETGTPEEHNGKTTSLIESQHHL 480
|||
Db 421 AOKKARLARIRVAKTSSNAVYLSKNGNLNLEALLETGTPEEHNGKTTSLIESQHHL 480
OY 481 HCLEKTTNHEFIDEQMEFONCMESMOMYPTSTRSPSLSGHPGLTTCCSRSKTTHLPN 540
|||
Db 481 HCLEKTTNHEFIDEQMEFONCMESMOMYPTSTRSPSLSGHPGLTTCCSRSKTTHLPN 540
OY 541 SNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNLKADGRLPNCKT 588
|||
Db 541 SNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNLKADGRLPNCKT 588

RESULT 11

ADM10929
ID ADM10929 standard; protein; 630 AA.
XX
AC ADM10929;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue protein #4.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cyostatic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX

PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX

PA (CORI-) CORIXA CORP.

XX
PI Fanger GR, Fling SP;
XX

DR WPI; 2003-901037/82.
XX
DR N-PSDB; ADM10923.
XX

PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX

PS Example 12; SEQ ID NO 260; 221pp; English.
XX

CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cyostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX

XX
SQ Sequence 630 AA;

Query Match 75.8%; Score 2518; DB 7; Length 630;

Best Local Similarity 75.8%; Pred. No. 2e-235;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

OY 1 MAAGVAAWLPFAAALAIIGMMPVANCMPPLADKNR-QDELIVLVNSGRFPQTRTLE 59
|||
Db 1 MAAGVAAWLPFAAALAIIGMMPVANCMPPLADKNR-QDELIVLVNSGRFPQTRTLE 60
OY 60 RYPTLLGSTEKEFEFNEPTKEFFPDPEVRCVLNFRYTKLHYPRYECISAYDELA 119
|||
Db 61 RYPTLLGSSERDFEYHPEYQYFFPDPDIFRHLINFRYTKLHYPRHECISAYDELA 120
OY 120 FYGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
|||
Db 121 FFGILPEIIGDCCYEYKDKRRENAERLQDDADTDITAGESALPTMTARQYWRAFENPHT 180
OY 179 STLALVFFYVVGFFIAVSITNVVETVPCGTVPGS-KELPCGERYSVAFCLDTACWIF 237
|||
Db 181 STMALVFFYVVGFFIAVSITANVETVPCGSSPGHKEKPCGERYAVAFCLDTACWIF 240
OY 238 TVEYLLRLFAAPSRFRFIRSVMSIIDVAIMPYYIGVMTNNEVSGAFYTLRVFRYERI 297
|||
Db 241 TVEYLLRLFAAPSRFRFIRSVMSIIDVAILPYIIGVMTNNEVSGAFYTLRVFRYERI 300
OY 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMPYAEKGSASKFTSIPAS 357
|||
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMPYAEKGSASKFTSIPAS 360
OY 358 FWYTIYMTTLLGYDMVPKTIAGKIFGSLGSLGVLYALPVPYIVSNFRIRYHONRAD 417
|||
Db 361 FWYTIYMTTLLGYDMVPKTIAGKIFGSLGSLGVLYALPVPYIVSNFRIRYHONRAD 420
OY 418 KRAOKKARLARIRVAKTSSNAVYLSKNGNLNLEALLETGTPEEHNGKTTSLIESQH 477
|||
Db 421 KRAOKKARLARIRVAKTSSNAVYLSKNGNLNLEALLETGTPEEHNGKTTSLIESQH 479
OY 478 HLHLCLEKTTNHEFIDEQMEFONCMESMOMYPTSTRSPSLSGHPGLTTCCSRSKTTH 537
|||
Db 480 HLHLCLEKTTNHEFIDEQMEFONCMESMOMYPTSTRSPSLSGHPGLTTCCSRSKTTH 539
OY 538 LPNSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNLKADGRLPNCKTQITTAIIS 597
|||
Db 540 LPNSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNLKADGRLPNCKTQITTAIIS 599
OY 598 IPTPPALTPEGESRP--PPASPGPNTNIPSLITSNVKYSVL 636
|||
Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSLITSNVKYSVL 630

RESULT 12

ADM10928
ID ADM10928 standard; protein; 630 AA.
XX

AC ADM10928;
XX

DT 20-MAY-2004 (first entry)
XX

DE Human O647SgenomicContig3 homologue protein #3.
XX

KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cyostatic; gene therapy; human; ds.
XX

OS Homo sapiens.
XX

PN US2003206918-A1.
XX

PD 06-NOV-2003.
XX

PF 05-FEB-2003; 2003US-00361811.
XX

PR 10-SEP-1999; 99US-00394374.
XX

PR 01-MAY-2000; 2000US-00561778.
XX
PR 15-AUG-2000; 2000US-00640173.
XX
PR 07-SEP-2000; 2000US-00656668.
XX

PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2003-901037/82.
DR N-PSDB; ADM10922.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 259; 221bp; English.
XX
XX This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 630 AA;
XX
Query Match 75.8%; Score 2518; DB 7; Length 630;
Best Local Similarity 75.8%; Pred. No. 2e-235;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
XX
QY 1 MAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
1 MAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
DB 1 MAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 60
60 RYPTDILGSTEKEFFENEDTKYFEDRDEVERCVLNFYRTGKLHYRYECISAYDDELA 119
61 RYPTDILGSESRDFEYHPEQYFDRDPIFRHILNFYRTGKLHYRYECISAYDDELA 120
XX
QY 120 FYGILPEIIGDCCYEEYKDRKNAERLMDNDSENNOES-MPSLSPQTMWEAFENPHT 178
121 FFGILPEIIGDCCYEEYKDRKNAERLMDNDSENNOES-MPSLSPQTMWEAFENPHT 180
DB 121 FFGILPEIIGDCCYEEYKDRKNAERLMDNDSENNOES-MPSLSPQTMWEAFENPHT 180
179 STVALVFYVYTGFFIAVSITNVETVPGTVPGS-KELPCGERYSVAFECIDTACVMIF 237
181 STVALVFYVYTGFFIAVSITNVETVPGTVPGS-KELPCGERYSVAFECIDTACVMIF 240
DB 181 STVALVFYVYTGFFIAVSITNVETVPGTVPGS-KELPCGERYSVAFECIDTACVMIF 240
XX
QY 238 TVEYLRLFAAPSRYSRVSIIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVFR 297
241 TVEYLRLFAAPSRYSRVSIIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVFR 300
DB 241 TVEYLRLFAAPSRYSRVSIIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVFR 300
XX
QY 298 FKFSRHSQGRILGYLTKSCABELGFLFSLTMAIIFATWFFYAEKSSASAKFTSIPAS 357
301 FKFSRHSQGRILGYLTKSCABELGFLFSLTMAIIFATWFFYAEKSSASAKFTSIPAS 360
DB 301 FKFSRHSQGRILGYLTKSCABELGFLFSLTMAIIFATWFFYAEKSSASAKFTSIPAS 360
XX
QY 358 FWYTIVTMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVIVSFRSRIYHONORAD 417
361 FWYTIVTMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVIVSFRSRIYHONORAD 420
DB 361 FWYTIVTMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVIVSFRSRIYHONORAD 420
XX
QY 418 KRRBAQKARLARIRVAKTSSNAYLHRSKRNGLNLEALLETGTPEEHNGKTSIIIESQHH 477
421 KRRBAQKARLARIRVAKTSSNAYLHRSKRNGLNLEALLETGTPEEHNGKTSIIIESQHH 479
DB 421 KRRBAQKARLARIRVAKTSSNAYLHRSKRNGLNLEALLETGTPEEHNGKTSIIIESQHH 479
XX
QY 478 HLHLCLEKTNHFEIDQMEQNCMESSMONTPTSPSLSHPGTLTCCSRSKKTTT 537
480 HLHLCLEKTNHFEIDQMEQNCMESSMONTPTSPSLSHPGTLTCCSRSKKTTT 539
DB 480 HLHLCLEKTNHFEIDQMEQNCMESSMONTPTSPSLSHPGTLTCCSRSKKTTT 539

QY 538 LPNSNLPATRLRSNQELSTHIIQGSBQPSLTTSRSSLNKADGHRPNCKTSQITTAIIS 597
540 IPVANVSGSHQGSIQELSTHIIQGSBQPSLTTSRSSLNKADGHRPNCKTSQITTAIIS 599
DB 540 IPVANVSGSHQGSIQELSTHIIQGSBQPSLTTSRSSLNKADGHRPNCKTSQITTAIIS 599
XX
QY 598 IPTPALTPGESRP--PRASPGPNTNIPSTSNVXSVL 636
600 IPTPALTPGESRP--PRASPGPNTNIPSTSNVXSVL 630
DB 600 IPTPALTPGESRP--PRASPGPNTNIPSTSNVXSVL 630
XX
RESULT 13
ADM10930
ID ADM10930 standard; protein; 630 AA.
XX
AC ADM10930;
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE Human O648SgenomicContig_ORF protein.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytostatic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2003-901037/82.
DR N-PSDB; ADM10931.
XX
XX New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
XX Example 12; SEQ ID NO 261; 221bp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 630 AA;
XX
Query Match 75.8%; Score 2518; DB 7; Length 630;
Best Local Similarity 75.8%; Pred. No. 2e-235;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
XX
QY 1 MAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59
1 MAGVAAWLPFARAALIGMPVANCMPPLAPADKNKR-ODELIVLVNSGRRFQWRTTLE 59

Db 1 MAAGVAAWLPFARAALIGMWPVAGSMPAPRQERKRTQDALIVLVNSGTRFQTWDTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKKEYFPDRDPEVERCVLNFYRTGKLIHYPRYECISAYDELA 119
Db 61 RYPTLLGSSSERDFYHPETQOYFPDRDPDIFRHILNFRYTGKLIHYPRHECISAYDELA 120
QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDRRRENAERLQDDADDTAGESALPTMTARQVRWRAFENPHT 180
QY 179 STLALVEYYVTGFFIAVSITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STMALVEYYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRYRFRIRSVMSIIDVVAIMPYYIGLVMTNNEVDVSGAFVTLRVFRVRI 297
Db 241 TVEYLRLFAAPSRYRFRVRSVMSIIDVVAILPYIIGLVMTNNEVDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAA 360
QY 358 FWYITVTMTTLGYGDMVPKTIAGKIFGSGISLGLVIALPVPIVIVNSFRIRYHONORAD 417
Db 361 FWYITVTMTTLGYGDMVPKTIAGKIFGSGISLGLVIALPVPIVIVNSFRIRYHONORAD 420
QY 418 KRRQKKARLARIRVAKTGSSNAVYLSKRNGLNEALELTGPREEHMGKTTSLIESQHN 477
Db 421 KRRQKKARLARIRAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHN 479
QY 478 HLHCLKETTNEHFIDEQMFQONCMESSMONYPSTRSPSLSSHGLTTCCSRRSKKTTH 537
Db 480 HLHCLKETTNEHFVDEQVFEESCMEVATVNRPSHSPSLSSQOGVSTCCSRRHKKTER 539
QY 538 LPNSNLPATRLRSMQELSTIHIOGSEOPSLTTSRSLNLKADGLRPNCCKTSQITTAIIS 597
Db 540 IPNAVSGSHQSIGELSTIQIRCVERTPLSNSRSSSLNAKMECEVKLNCEQPYVTTAIIS 599
QY 598 IPTPALTPEGESRP--PPASPGPNTNIPSTITSNVKVSVL 636
Db 600 IPTPALTPEGESRPESPEYSGS-----NIVRSAL 630

RESULT 14
ADM10927
ID ADM10927 standard; protein; 630 AA.
XX
AC ADM10927;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue protein #2.
XX
KM ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cytosstatic; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX

PA (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
XX
XX WPI; 2003-901037/82.
DR N-PSDB; ADM10921.
XX
XX New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
XX Example 12; SEQ ID NO 258; 221pp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 630 AA;
Query Match 75.8%; Score 2518; DB 7; Length 630;
Best Local Similarity 75.8%; Pred. No. 2e-235;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
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Db 1 MAAGVAAWLPFARAALIGMWPVAGSMPAPRQERKRTQDALIVLVNSGTRFQTWDTLE 60
QY 60 RYPTLLGSTEKEFFFNEDTKKEYFPDRDPEVERCVLNFYRTGKLIHYPRYECISAYDELA 119
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QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDRRRENAERLQDDADDTAGESALPTMTARQVRWRAFENPHT 180
QY 179 STLALVEYYVTGFFIAVSITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STMALVEYYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRYRFRIRSVMSIIDVVAIMPYYIGLVMTNNEVDVSGAFVTLRVFRVRI 297
Db 241 TVEYLRLFAAPSRYRFRVRSVMSIIDVVAILPYIIGLVMTNNEVDVSGAFVTLRVFRVRI 300
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QY 418 KRRQKKARLARIRVAKTGSSNAVYLSKRNGLNEALELTGPREEHMGKTTSLIESQHN 477
Db 421 KRRQKKARLARIRAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHN 479
QY 478 HLHCLKETTNEHFIDEQMFQONCMESSMONYPSTRSPSLSSHGLTTCCSRRSKKTTH 537
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QY 538 LPNSNLPATRLRSMQELSTIHIOGSEOPSLTTSRSLNLKADGLRPNCCKTSQITTAIIS 597
Db 540 IPNAVSGSHQSIGELSTIQIRCVERTPLSNSRSSSLNAKMECEVKLNCEQPYVTTAIIS 599
QY 598 IPTPALTPEGESRP--PPASPGPNTNIPSTITSNVKVSVL 636

Db 600 IPTPPVTPEGDDBRPSPEYSGG-----NIVRSAL 630

RESULT 15
ADJ11257
ID ADJ11257 standard; protein; 630 AA.

XX AC ADJ11257;

DT 15-APR-2004 (first entry)

DE Human ovarian tumour antigen polypeptide SegID 258.

KM human; ovarian cancer; immunogenic; antibody; antigen presenting cell;
KW APC; immune system cell; T cell; tumourigenic; cytostatic.

OS Homo sapiens.

PN US2003232056-A1.

PD 18-DEC-2003.

PF 14-FEB-2003; 2003US-00369186.

PR 10-SEP-1999; 99US-00394374.

PR 01-MAY-2000; 2000US-00561778.

PR 15-AUG-2000; 2000US-00640173.

PR 07-SEP-2000; 2000US-00656668.

PR 14-NOV-2000; 2000US-00713550.

PR 03-APR-2001; 2001US-00825294.

PR 02-OCT-2001; 2001US-00970966.

PR 02-AUG-2002; 2002US-00212677.

PR 05-FEB-2003; 2003US-00361811.

XX PA (CORI-) CORIXA CORP.

XX PI Fanger GR, Fling SP;

XX DR WPI; 2004-178717/17.

XX DR N-PSDB; ADJ11251.

XX PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor

XX PT polypeptide, useful as probes of primers for detecting presence of cancer

XX PT in a patient.

XX PS Example 12; SEQ ID NO 258; 222pp; English.

XX CC This invention relates to novel isolated polynucleotides and methods for

XX CC the therapy and diagnosis of cancer, particularly ovarian cancer.

XX CC Specifically, it refers to these polynucleotides and the encoded

XX CC polypeptides thereof, as well as immunogenic peptides, antibodies,

XX CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)

XX CC that are targeted to those cells expressing the proteins of interest. The

XX CC present invention describes methods that are useful for stimulating and/

XX CC or expanding T cells specific for a tumourigenic protein (i.e. T cell

XX CC therapy). Furthermore, compositions can be used for the diagnosis,

XX CC treatment and/or prevention of ovarian cancer by stimulating an immune

XX CC response in a patient. Accordingly, these compositions exhibit cytostatic

XX CC activity. This polypeptide is a human ovarian tumour antigen protein

XX CC sequence given in an exemplification of the invention.

XX SQ Sequence 630 AA;

Query Match 75.8%; Score 2518; DB 8; Length 630;

Best Local Similarity 75.8%; Pred. No. 2e-235;

Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

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Db 1 MAAGVAAWLPFAAAAIIGMPVASCMPMPAPRQRRKRTQDALIVANVSGTRFQTRTTLE 60

QY 60 RYPTLLGSTEKEFFENEDTKKEYFPDRDPEVFRCVINFYRTGKLHYPRYECISAYDDELA 119

Db 61 RYPTDLGSSSERDFEYHPETQOQYFFRDPDIFRHILNFRTGKLHYPRHECISAYDEELA 120

QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178

Db 121 FEGLIPEIIGDCCYEYKDRKRENAERLQDDADTDGASALPTWTARQVRFAFENPHT 180

QY 179 STLALVFYVTGFFIAVSVTNNVETVPCGTVPGS-KELPCGERISVAFPCIDTACWIF 237

Db 181 STMALVFYVTGFFIAVSVTNNVETVPCGTVPGS-KELPCGERISVAFPCIDTACWIF 240

QY 238 TVEYLRLFAAPSRFRFIRSVMSIIDVVAIMPYYIGLVMTNNEDEYSGAFVTLRVFRVERI 297

Db 241 TVEYLRLFAAPSRFRFIRSVMSIIDVVAIMPYYIGLVMTNNEDEYSGAFVTLRVFRVERI 300

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Job time : 483.789 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:58:11 ; Search time 104.44 Seconds
(without alignments)
454.585 Million cell updates/sec

Title: US-10-062-879-4
Perfect score: 3320
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545.seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	636	US-09-178-109-4	Sequence 4, Appl1
2	3311	99.7	636	US-09-142-791A-2	Sequence 2, Appl1
3	3300.5	99.4	655	US-09-178-109-2	Sequence 2, Appl1
4	3291.5	99.1	655	US-09-142-791A-4	Sequence 4, Appl1
5	3285	98.9	636	US-09-142-791A-6	Sequence 6, Appl1
6	2518	75.8	630	US-09-949-016-6828	Sequence 6828, Ap
7	2121.5	63.9	646	US-09-336-643A-10	Sequence 10, Appl
8	865.5	26.1	260	US-09-949-016-8327	Sequence 8327, Ap
9	774.5	23.3	806	US-09-833-466-13	Sequence 13, Appl
10	750	22.6	854	US-09-833-466-12	Sequence 12, Appl
11	750	22.6	858	US-09-275-252A-6	Sequence 6, Appl1
12	726.5	21.9	539	US-08-464-340A-13	Sequence 13, Appl
13	723	21.8	616	US-09-275-252A-4	Sequence 4, Appl1
14	719	21.7	552	US-09-949-016-8164	Sequence 8164, Ap
15	718	21.6	523	US-09-949-016-6195	Sequence 6195, Ap
16	712.5	21.5	528	US-08-527-152-2	Sequence 2, Appl1
17	710.5	21.4	495	US-09-275-252A-5	Sequence 5, Appl1
18	704	21.2	446	US-10-162-012-8	Sequence 8, Appl1
19	704	21.2	601	US-09-336-643A-4	Sequence 4, Appl1
20	703	21.2	532	US-10-162-012-13	Sequence 13, Appl
21	696	21.0	757	US-09-949-016-7121	Sequence 7121, Ap
22	695	20.9	532	US-08-288-405A-10	Sequence 10, Appl
23	689	20.8	556	US-09-275-252A-8	Sequence 8, Appl1
24	678	20.4	159	US-08-606-143-45	Sequence 45, Appl1
25	675	20.3	529	US-09-949-016-6196	Sequence 6196, Ap
26	675	20.3	538	US-09-949-016-8017	Sequence 8017, Ap
27	635.5	19.1	162	US-08-606-143-44	Sequence 44, Appl

28	632	19.0	490	3	US-09-336-643A-6	Sequence 6, Appl1
29	632	19.0	491	4	US-09-181-339-12	Sequence 12, Appl
30	632	19.0	507	4	US-09-949-016-9860	Sequence 9860, Ap
31	629	18.9	494	4	US-09-949-016-7475	Sequence 7475, Ap
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33	622	18.7	494	1	US-08-464-340A-4	Sequence 4, Appl1
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36	598	18.0	513	4	US-09-949-016-10288	Sequence 10288, A
37	597	18.0	477	3	US-09-336-643A-18	Sequence 18, Appl
38	584	17.6	513	1	US-08-464-340A-2	Sequence 2, Appl1
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40	569	17.1	506	4	US-09-719-919A-1	Sequence 1, Appl1
41	564	17.0	519	4	US-09-719-919A-17	Sequence 17, Appl
42	557.5	16.8	545	4	US-09-833-466-3	Sequence 3, Appl1
43	529	15.9	497	4	US-09-181-339-3	Sequence 3, Appl1
44	410	12.3	423	4	US-09-181-339-9	Sequence 9, Appl1
45	370.5	11.2	256	4	US-09-181-339-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1									
US-09-178-109-4									
; Sequence 4, Application US/09178109									
; Patent No. 6395477									
; GENERAL INFORMATION:									
; APPLICANT: Cockett, Mark I.									
; APPLICANT: Dllks, Daniel W.									
; APPLICANT: Sokol, Patricia T.									
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and									
; FILE REFERENCE: Polypeptides and Uses Therefor									
; CURRENT APPLICATION NUMBER: US/09/178, 109									
; CURRENT FILING DATE: 1998-10-23									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: Patentn Ver. 2.0									
; SEQ ID NO 4									
; LENGTH: 636									
; TYPE: PRT									
; ORGANISM: human									
US-09-178-109-4									
Query Match									
Best Local Similarity 100.0%; Score 3320; DB 3; Length 636;									
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	YPDTLIGSTEKEFFFNEDTKEYFFDRDPEVRCVILNFRYTGKLIHYPRYECISAYDELA	120						
DB	61	YPDTLIGSTEKEFFFNEDTKEYFFDRDPEVRCVILNFRYTGKLIHYPRYECISAYDELA	120						
QY	121	YGIILPEIIGDCCEYKRRKRENAERLMDNDSENNQESMPSISFRQTMRAFAENDHTST	180						
DB	121	YGIILPEIIGDCCEYKRRKRENAERLMDNDSENNQESMPSISFRQTMRAFAENDHTST	180						
QY	181	LALVFYVVTGFPIAVSVITNVETVPCGTVGSKELPCGERYSVAFFCLDTACVMIFTV	240						
DB	181	LALVFYVVTGFPIAVSVITNVETVPCGTVGSKELPCGERYSVAFFCLDTACVMIFTV	240						
QY	241	YLLRLFAAPSRRFRFRSWSIIDVAIMPYITGLVMTNNEVDGAFVTLRVRFRIFKF	300						
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Db	361	TIVTMTILGYGDMVPKTIAGKIFGSI	CSLSGVLI	ALPVPVI	YSNFSRI	IYHQNQ	RD	KRR	420
QY	421	AQKKARLARIRVAKTGSSNAYLH	SKRNGLN	ALNELTGP	PEEHNGK	TTSLIESQ	HLL		480
Db	421	AQKKARLARIRVAKTGSSNAYLH	SKRNGLN	ALNELTGP	PEEHNGK	TTSLIESQ	HLL		480
QY	481	HCLEKTNHFEIDQMF	EQNCMESSM	QNYPTSR	PSLSHPGL	TTTTCCS	RRSK	KT	THLPN
Db	481	HCLEKTNHFEIDQMF	EQNCMESSM	QNYPTSR	PSLSHPGL	TTTTCCS	RRSK	KT	THLPN
QY	541	SNLPATRLRSMQEL	STIHIOGSEQ	PSLTTSRS	SLNLKAD	DGLRPNCK	T	SOIT	TALISPT
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RESULT 2

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US-09-142-791A-2
; Sequence 2, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Fai
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-2

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Best Local Similarity	99.7%	Pred. No. 8.4e-309;		
Matches 634; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

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Dd	241	YLRLFAAPSRIRYRIFRSVMSIIDVVAIMPYICGLVMTNNEDVSGAFVTLRVFRVRIKFK	300
Qy	301	SRHSQGRILIGTLLKSCASELGFLLPSLTMAIIIPATVMFYAEKGSASKFTSIDASFMY	360
Dd	301	SRHSQGRILIGTLLKSCASELGFLLPSLTMAIIIPATVMFYAEKGSASKFTSIDASFMY	360
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Dd	361	TIVTMTLLGYGDMVPKTTIAGKIFGSIICSLSGVLVIALPVPIVIVSNFSRIYHONRADKRR	420
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Dd	421	AOKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEHEMGKTTSLIESQHHL	480
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Dd	481	HCLEKTNHFEIDQMFQNCMESMÖNYPSSTRSPSLSHPGITTTCCSRRSKKTTHLPN	540
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RESULT 3

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US-09-178-109-2
; Sequence 2, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: human
US-09-178-109-2

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Query Match	99.4%	Score 3300.5;	DB 3;	Length 655;
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Db 481 HCLEKTTNHEFIDEQMEQONCMESMOMYPTSTRSPSLSHPGLTTCSSRSKKTTHLPN 540
QY 541 SNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSSLNLKADDLRPNCCKTSQITTAIISPT 600
Db 541 SNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSSLNLKADDLRPNCCKTSQITTAIISPT 600
QY 601 PPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636
Db 601 PPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636

RESULT 6
US-09-949-016-6828
; Sequence 6828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 6828
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6828
```

```
Query Match 75.8%; Score 2518; DB 4; Length 630;
Best Local Similarity 75.8%; Pred. No. 1.2e-232;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
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QY 1 MAAGVAAWLPFAAIAAGMPVANCPMPLAPADKNKR-ODELIVLVNSGRFOTWRTTLE 59
Db 1 MAAGVAAWLPFAAIAAGMPVANCPMPLAPADKNKR-ODELIVLVNSGRFOTWRTTLE 59
QY 60 RYPTLLGSTKEKFFENEDTKKEYFFDRDPEVFRVAVNFYRTGKLHYPYECISAYDDELA 119
Db 60 RYPTLLGSTKEKFFENEDTKKEYFFDRDPEVFRVAVNFYRTGKLHYPYECISAYDDELA 119
QY 61 RYPTLLGSSERDFFHYHETQYFFDRDPDIFRHILNFRYRTGKLHYPYECISAYDDELA 120
Db 61 RYPTLLGSSERDFFHYHETQYFFDRDPDIFRHILNFRYRTGKLHYPYECISAYDDELA 120
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QY 120 FYGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSPROTMMRAFENPHT 178
Db 120 FYGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSPROTMMRAFENPHT 178
QY 179 STIALVFYVYVTFPIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 179 STIALVFYVYVTFPIAVSVITNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
QY 238 TVEYLLRLFAAPSRYYRFRIRSVMSIIDVVAIMPYYIGLWMTNNEVSGAFVTLRVFRVRI 297
Db 238 TVEYLLRLFAAPSRYYRFRIRSVMSIIDVVAIMPYYIGLWMTNNEVSGAFVTLRVFRVRI 297
QY 241 TVEYLLRLFAAPSRYYRFRIRSVMSIIDVVAIMPYYIGLWMTNNEVSGAFVTLRVFRVRI 300
Db 241 TVEYLLRLFAAPSRYYRFRIRSVMSIIDVVAIMPYYIGLWMTNNEVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPAS 357
Db 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPAS 357
QY 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPAS 360
Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIPAS 360
QY 358 FWYTTIVMTTTLGYGDMVPKTIAGKIFGSGISLGVLYIALPVPVIVSNFSRIYHONORAD 417
Db 358 FWYTTIVMTTTLGYGDMVPKTIAGKIFGSGISLGVLYIALPVPVIVSNFSRIYHONORAD 417
QY 361 FWYTTIVMTTTLGYGDMVPKTIAGKIFGSGISLGVLYIALPVPVIVSNFSRIYHONORAD 420
Db 361 FWYTTIVMTTTLGYGDMVPKTIAGKIFGSGISLGVLYIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRAOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 477
Db 418 KRAOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 477
QY 421 KRAOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 479
Db 421 KRAOKKARLARIRVAKTGSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 479
QY 478 HLIHCLEKTTNHEFIDEQMEQONCMESMOMYPTSTRSPSLSHPGLTTCSSRSKKTTH 537
Db 478 HLIHCLEKTTNHEFIDEQMEQONCMESMOMYPTSTRSPSLSHPGLTTCSSRSKKTTH 537
QY 480 HLIHCLEKTTNHEFIDEQMEQONCMESMOMYPTSTRSPSLSHPGLTTCSSRSKKTTH 539
Db 480 HLIHCLEKTTNHEFIDEQMEQONCMESMOMYPTSTRSPSLSHPGLTTCSSRSKKTTH 539
QY 538 LENSNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSSLNLKADDLRPNCCKTSQITTAIIS 597
Db 538 LENSNLPATRLRSQMOELSTIHIQSEOPSLTTSRSSSLNLKADDLRPNCCKTSQITTAIIS 597
QY 540 IPNAVSGSHQSGIQLSTIQRVETRTPLSNRSRLNKAKECVKLNCEQYVTTAIS 599
Db 540 IPNAVSGSHQSGIQLSTIQRVETRTPLSNRSRLNKAKECVKLNCEQYVTTAIS 599
QY 598 IPTPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636
Db 598 IPTPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636
QY 600 IPTPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636
Db 600 IPTPALTPEGESRPPSPGPNNTNIPSTSNVVKVSVL 636
```

```
RESULT 7
US-09-336-643A-10
; Sequence 10, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 10
; LENGTH: 646
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(646)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-10
```

```
Query Match 63.9%; Score 2121.5; DB 3; Length 646;
Best Local Similarity 65.1%; Pred. No. 1.5e-194;
Matches 428; Conservative 78; Mismatches 116; Indels 35; Gaps 13;
```



```
Qy 1 MAAGVAAWLPAPAAAIGMNPVANCMPPLADKNKRODELIYLVNSGRRQTWRTTLER 60
Db 1 MAAGLATWLPAPAAAAGVWLPAPQGLPAPAGVKASRGDXVLVNVNSGRRETWKNLDR 60
Qy 61 YPDTLLGSTEKEEFENEDTKEEYFFDDOBEVFCVLNFYRTGKLMHPRYECISAYDEELAF 120
Db 61 YPDTLLGSSSEKEEFFYDADSGEYFPDRDPMFRHVLNFYRTGRLHCPROECTQAFDEELAF 120
Qy 121 YGILPEIIGDCCEYEYKDKRRENAERLMDNDSENNOESMPSL----SFRQTMWRAFENP 176
Db 121 YGILPELVGDCCLEBYRDKKENAERLAEDEAEQAAGDG-PALPAGSSILRQLMRAFENP 179
Qy 177 HTSTLALVFYVYTGFFIAVSIVITNVETVPC--GTVPGSKELPGGERYSVAFCLDTACV 234
Db 180 HTSTALVFYVYTGFFIAVSIVIANVETIPCRGSARBSRREQPCGERFPOAFPCMDTACV 239
Qy 235 MIFTEYLLRLFAAPSRVRFIRSVMISIDVVAIMPYYIGLVMTNNEVDVSGAFVTLAEVRV 294
Db 240 LIFTEGYLLRLFAAPSRRCFLRSVMSLIDVVAILPYIIGLVLPKNDVDVSGAFVTLAEVRV 299
Qy 295 FRIEFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKRTSI 354
Db 300 FRIEFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGTNKTMTSI 359
Qy 355 PASFWYTVITVMTTLGYGDMVNPKTIAKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNQ 414
Db 360 PAFWYTVITVMTTLGYGDMVNPSTIAKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNQ 419
Qy 415 RADKRAAQKARLARIRVAKTGSSNAYLHSKKNGLNLEALGTPEEHEM-GKTTSLIE 473
Db 420 RADKRAAQKARLARIRLAKSGITNAFLQYKONG---GLEDSGSGEEQALCVRRNSAFE 475
Qy 474 SQHHHLHCLLEKTTNHEPDEQMPONCMESMONTSTRSPSLSSHP---GLTTTCCS 529
Db 476 QQHHHLHCLLEKTTNHEPDELTSE-ALGAVSPGRTSRSTSVSSQPVPGSLSSCCP 534
Qy 530 RRSK-KTTHLPNSNLPATRLRSMOELSTIHIOGSEQPSLTSSRLNKADGLRPNCXT 588
Db 535 RRAKRRAIRLANSTASVSR-GSMQELDM--LAGLRSHAPOSSSLNAKPHDSLDCNCS 591
Qy 589 SQITTAIISIPPPALPEGESRPPPPASPG-----PNTNIPISITSNVKVS 634
Db 592 RDPVAALISIPPPANTPD-ESQ--PSSPGGGGAGSTLRNSLIGTPCLEPETYKIS 645
```

RESULT 8
US-09-949-016-8327
Sequence 8327, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8327
LENGTH: 260
TYPE: PRT
ORGANISM: Human
US-09-949-016-8327

Query Match 26.1%; Score 865.5; DB 4; Length 260;
Best Local Similarity 64.2%; Pred. No. 1.4e-74;

Matches 174; Conservative 35; Mismatches 49; Indels 13; Gaps 3;
Qy 368 LGYDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRAQKARL 427
Db 1 LRGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADKRAQKARL 60
Qy 428 ARIRVAKTGSSNAYLHSKKNGLNLEALGTPEEHEMKTTSILSQQHHLHCLLEKTT 487
Db 61 ARIRAAKSGSANAAYMOSKKNGLNSNQLQ--SSEDEQAFVSKSGSFETQHHHLHCLLEKTT 119
Qy 488 NHEFDQMPONCMESMONTSTRSPSLSSHPGLTTTCCSRSKTTHLPNSNLPATR 547
Db 120 NHEFDQMPONCMESMONTSTRSPSLSSHPGLTTTCCSRSKTTHLPNSNLPATR 547
Qy 548 LRSMOELSTIHIOGSEQPSLTSSRLNKADGLRPNCXTSQITTAIISIPPPALTPPE 607
Db 180 QGSIQELSTIQRCVERTPPLSNRSSSLNAKMECEVKLNCEQPVYTTAISIPPPVTTPE 239
Qy 608 GESRP--PPASPGPNTNIPISITSNVKVSVL 636
Db 240 GDDRPESPEYSGG-----NIVRVSL 260

RESULT 9
US-09-833-466-13
Sequence 13, Application US/09833466
Patent No. 6727353
GENERAL INFORMATION:
APPLICANT: Jégla, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-gated Potassium Channel From
FILE REFERENCE: 018512-005910US
CURRENT APPLICATION NUMBER: US/09/833,466
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 806
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human voltage-gated potassium channel Kv2.2
US-09-833-466-13

Query Match 23.3%; Score 774.5; DB 4; Length 806;
Best Local Similarity 27.7%; Pred. No. 4.7e-65;
Matches 220; Conservative 116; Mismatches 243; Indels 215; Gaps 26;

Qy 27 MPLAPAD--KNKRODELIYLVNSGRRFQT--WRTTLERYPDTLLG-----STEKEFF---- 74
Db 20 LPPEYVDIIRSKTCSRRAVKINVGGLNHEVLMR-TLDRLPTRLGKLRDONTHESSLEVC 78
Qy 75 -FNEDTKEYFPDRDPEVFRVAVNFYRTGKLMHPRYECISAYDEELAFYGLPEIIGDCCY 133
Db 79 DYNLANENEYFDRHFGAFTSILNFYRTGKLMHEMICALSFGQELDYNGIDEIYESCCQ 138
Qy 134 EEEYKDRK-----RENAERLMDNDSENNOESMPSLSFRQTMWRAFENPHTSTLALVFY 186
Db 139 ARYHQKKEQNMNELRREAETMRDGESEFPNTCCPDK--RKQLMDLLEKPNSSVAKILA 196
Qy 187 YVTGFFIAVSIVITNVETVP-----CGTVPGSKELPGGERYSVAFCLDTACVMIFTV 239
Db 197 IVSILFIVLSTIALSLNTLPLOETDEFGQLNDNROLA-----HVEAVCIAMFTM 246
Qy 240 EYLRLFAAPSRVRFIRSVMISIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVF 292
Db 247 EYLRLFAAPSRVRFIRSVMISIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVF 292
Qy 293 RVFRIEFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFT 352

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Db 307 RILRLKLARHSTGLQSLGFTLRRSYNELGLILFLAMGIMIFSSIVFPAEKEDATKFT 366
Qy 353 SLPASFVTVITMTLGYDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHQ 412
Db 367 SLPASFVWATITMTVGYDIPKTLGKIVGGLCCIAGVLIALPIPIVNNFSEFYKE 426
Qy 413 NORADK---RRAOKKAR-----LARIKRVAKTSS-----NAY 441
Db 427 QKROEKAIKRREALERAKRNGSIVSMNLKDAFARSMELIDVAVEKAGESANTKDSADNH 486
Qy 442 LH-----SKRNGLINEALELTGTPREEHMGKTSL-----IESQHHLH-- 481
Db 487 LSPSRMKARKALSETSSNKSRENKYQEVSOQDSHQNLNTPSSSPQHLSAQKLEMLYNE 546
Qy 482 -----CLEKTTNHFIDE--QMFQONCMESSM---QNYFSTRSPSLSSHPL 523
Db 547 IFTKQPHSHNPDCQEKPERPSAYEBEIEMBEVCPQEQGLAQAQTEVIVDMKSTSSISF 606
Qy 524 TTTCSSRRSKTTHLPNSNLPAATRLRSMOELSTHIOGSEQ-----PSLTTSR----- 571
Db 607 TS---CATDFTETERSP--LPPPSASHLQMKFPTDLPGTEEHQARAGPPFLTLSREKGA 661
Qy 572 -----SSL-----NLKA 578
Db 662 ARDGTLEVAPVDITVNLDSAGSQGLHSPLOSDNATDSPKSSLKGSNPLKSRSLKXNFE 721
Qy 579 DDGLRPNCKTS-----QITTAIISITPPAL-----TPGESRP----- 612
Db 722 NRGSAPOPTPSTARPPLVTTADFSITPTQHIISTILLETPSQGDRPCWALRQRLVRLP 781
Qy 613 ---PPASGENTNI 623
Db 782 KGCPPGPPSRNCSL 795
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RESULT 10
US-09-833-466-12
; Sequence 12, Application US/09833466
; Patent No. 6727353
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.1
US-09-833-466-12
```

```
Query Match 22.6%; Score 750; DB 4; Length 854;
Best Local Similarity 29.2%; Pred. No. 1.2e-62;
Matches 189; Conservative 114; Mismatches 220; Indels 124; Gaps 18;

Qy 27 MPLAPAD--KNKRODELIVLVNSGRFRQT-WRTTLERYPDTLG-----STEKEFF----- 74
Db 12 LPEPEMEIVRSKACSRVRVNLVGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLEVC 70
Qy 75 -FNEDTKEYFPDRDPEVFRVCLNLFYRTGKLHYPRYECISAYDELAFAFGILPEIIGDCCY 133
Db 71 DYSLDNNEVFFDRHGAFTSLNLFYRTGRLHMMEMCALSFQGLDYWGIDELIYLESQQ 130
Qy 134 EBYDKRRENAERLMDNSENNOE-----SMPSLFRQTMWRAFENPHSTTLALVFYV 188
Db 134 EBYDKRRENAERLMDNSENNOE-----SMPSLFRQTMWRAFENPHSTTLALVFYV 188
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Db 131 ARYHQKEQMNBEUKREAEATLREBEGEEFDNTCAEKRRKMLWDLLEKPNSSVAAKILAI 190
Qy 189 TGFPIAVSVITNVETVPCGTVPKSGELPCGERYSVA-----FPCLDTACMIFTVEYLL 243
Db 191 SIMFIYSTIALSNTLP-----ELQSLDEFGQSTDNQGLAHVEAVCLAMFTMEYLL 242
Qy 244 RLFAAPRRYRFRIRSVMSIIDVVAIMPYIIGLVMTNN-----EDVSGAFVTLRVFVR 296
Db 243 RFLSSPKWKFFKGPLNADLALIPYVYVTFPLETSNKSVLQFQVNRVVOIFRIMRILR 302
Qy 297 IFKFSRSQGLRILGYTLKSCASELGLFLFSLTMAIIFATVMFYAEKGSASKFTSIPA 356
Db 303 ILKLARHSTGLQSLGFTLRRSYNELGLILFLAMGIMIFSSIVFPAEKEDBDTKFKSIPA 362
Qy 357 SFWYTVITMTLGYDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHQORA 416
Db 363 SFWMATITMTVGYDIPKTLGKIVGGLCCIAGVLIALPIPIVNNFSEFYKEQKRO 422
Qy 417 DKRAOKKARLARIRVAKTGSSNAVYLSKRNGLL-----NEALELTGTPREEH 464
Db 423 EKAIRKREA-LER-----AKRNGSIVSMNLKDAFARSIEMMDIVKNGEN 467
Qy 465 MGKTSLSIESQHHLHLCLEKTTNHFIDEQMFQONCMESSMONTPTSTRPSLSHGLT 524
Db 468 MGKKDKV---QDNHLSPNKKMKTKRL--SETSSSKSFETKEQGSPEK----- 510
Qy 525 TTTCSSRRSKTTHLPNSNLPAATRLRSMOELSTHIOGSEQPSLTSTRSLNLKADDCRLP 584
Db 511 ---ARSSSPQHL-----NVQLEDMYNMMAKTOSQPIILNTKESAQSKPEEL-- 556
Qy 585 NCKTSQITTAIISITPPALTPGESRPPAPSGPNTNIPSITSNV 631
Db 557 -----EMESIPSPVAP-----LPRTREGVI 576
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RESULT 11
US-09-275-252A-6
; Sequence 6, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-6
```

```
Query Match 22.6%; Score 750; DB 4; Length 858;
Best Local Similarity 29.2%; Pred. No. 1.2e-62;
Matches 189; Conservative 114; Mismatches 220; Indels 124; Gaps 18;

Qy 27 MPLAPAD--KNKRODELIVLVNSGRFRQT-WRTTLERYPDTLG-----STEKEFF----- 74
Db 16 LPEPEMEIVRSKACSRVRVNLVGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLEVC 74
Qy 75 -FNEDTKEYFPDRDPEVFRVCLNLFYRTGKLHYPRYECISAYDELAFAFGILPEIIGDCCY 133
Db 75 DYSLDNNEVFFDRHGAFTSLNLFYRTGRLHMMEMCALSFQGLDYWGIDELIYLESQQ 134
```



```
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-275-252A-4

Query Match      21.8%; Score 723; DB 4; Length 616;
Best Local Similarity 32.3%; Pred. No. 2.7e-60;
Matches 170; Conservative 105; Mismatches 156; Indels 96; Gaps 13;

QY 40 ELIVLNSGRFQRTWRTTLERYPDLLGSTEKEF-FENEDTKEYFPDRDPEVRCVINY 98
DB 97 ERYVINVSGLRFETQLRTLNQPDLLGDPARLRRLRYFDPLRNEYFEDRSRPSDAILYY 156
QY 99 RT-GKLHYRYECISAYDDELAIFYGILPEIIGDCCYEYKDRKRENAERLMDNSENNO 157
DB 157 QSGRLRRVNVPLDVFESEIKFEY-----LGDQAINKRE-----DEGFIKEE 201
QY 158 ESMSLSFRQTMWRAPENPHSTLALVFYVVGFFIYVSVITNVETVP----- 206
DB 202 RPLPDNEKQKRWMLFEYEPESQARVAIISVFVILLSTIVIFCLETLRPFKHYKVNTT 261
QY 207 -CGTVPGSKELPCGERYSVAFCCLDTACVMIFTVEYLLRLPAAPSRYRFRISVMSIIDV 265
DB 262 TNGTKIEDEVP--DITDPFLIETLCIIFTELTFRFLACPKNKINFCRDVNNVIDII 318
QY 266 AIMPYYIGLV-----MTNNEVDSGAFV-TLVRFRVRIIFKESGH 303
DB 319 AIIIFYTILATVAEEDTLNLPKAPVSPQDKSSNQAMSLAILRVIRLVRVRIIFKLSRH 378
QY 304 SOGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPASFWYITV 363
DB 379 SKGLQILGRLLKASMRLEGLLIFLFGVLLFSSAVYFAAGSENSPFKSIDPAFWMAVY 438
QY 364 TMTTLGYGMVPKTIAGKIFGSLCSGLVIALPVPVIVSNFSRIYHONORADKRRQK 423
DB 439 TMTTVGYGDMTPVGFWGKIVGSLCVIAGVLTIALPVPVIVSNFNYFTHREADREEMQSN 498
QY 424 KARLARIRVAKTGSSNAYL-----HSKRNGL-----LNEALELTGPREEHMGKT 468
DB 499 FNVH-----TSCSYLPGALGOHLKSSLSSESSDIMDLDDGIDATTPGLDHTGR- 548
QY 469 TSLIESQHHLHLHLEKTTNHEFIDEQMEFQNCMESSMONYPSTRSP 515
DB 549 -----HMVPFLR-----TQSFKEQQLQLQLQOQSQSP 578

RESULT 14
US-09-949-016-8164
; Sequence 8164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 8164
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8164

Query Match      21.7%; Score 719; DB 4; Length 552;
Best Local Similarity 31.2%; Pred. No. 5.5e-60;
Matches 176; Conservative 105; Mismatches 172; Indels 112; Gaps 16;
```

```
QY 18 GMPVANC-----PMP--LAPADKNKRODELIVLNSGRRFQRTWRTTLERYPDLL 66
DB 48 GAPPOGGCGGCGCDRYEPLPPLSPAGEQDCCGERVIVINSGLRFETQLKQFETLL 107
QY 67 STEKEF-FENEDTKEYFPDRDPEVRCVINYRT-GKLHYRYECISAYDDELAIFYGIL 124
DB 108 GDPKRRMRYFDPLRNEYFEDRNPSPDAILYYQSGGRIRRPVNVPIIDISEIRFYQ-- 165
QY 125 PEIIGDCCYEYKDRKRENAERLMDNSENNOESMPSLSFRQTMWRAPENPHSTLALV 184
DB 166 ---LGEEAMEKFRE-----DEGFLREERPLPRRDFOQWMLFEPYESSGPARG 212
QY 185 FYVVTGFFIYVSVITNVETVPCGTVPGSKELPC-----GER-----YSV 224
DB 213 IAVSVILVILISIVIFCLETLR--EPRDEKDYPASTQDSFEAAGNSTSGSAGASSPSD 270
QY 225 AFCLDTACVMIFTVEYLLRLPAAPSRYRFRISVMSIIDVVAIMPYYIGLV-----T 277
DB 271 PEFVETICTIIFWSEFLVRFACPSKATFSRNIMNLDIVAITPYFITLGTLEAERQGN 330
QY 278 NNEVDGSAFV-TLVRFRVRIIFKESRHSGRLILGYTLKSCASELGFLLFSLTMAIIFA 336
DB 331 GQAMSLAILRVIRLVRVRIIFKLSRHSGRLILGYTLKASMRLEGLLIFLFGVILFS 390
QY 337 TWMFYAEKSSASKFTSIPASFWYITVMTTLGYGMVPKTIAGKIFGSLCSGLVIA 396
DB 391 SAVFYAEADDPISGFSSIPDAFWMAVMTTVGYGDMHPVTIGKIVGSLCAIAGVLTIA 450
QY 397 LPVPVIVSNFSRIYHONORADKRRQKARLARIRVAKTGSSNAYLHRSKRNGLNEALEL 456
DB 451 LPVPVIVSNFNYFHRETEBEQ-----SQYMH-----VGSQHL 485
QY 457 TGPEEHEHMGKTSLIESQHHLHLHLEKTTNHEFIDEQMEFQNCMESSMONYPSTRSP 516
DB 486 SSSAEELRKARSNTLSKSEWVIE--EGGMNHSAPQPPK----- 525
QY 517 LSHPLGTTTCCSRRSKTTHL PNS 541
DB 526 ----TGNSTATCT-----TNNPNPS 541

RESULT 15
US-09-949-016-6195
; Sequence 6195, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 6195
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6195

Query Match      21.6%; Score 718; DB 4; Length 523;
Best Local Similarity 31.2%; Pred. No. 6.3e-60;
Matches 176; Conservative 105; Mismatches 172; Indels 112; Gaps 16;
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Db 19 GAPPGCGCGGCDRIEPLPSLPAPAGEQDCGERVINISGVRETOQLKTLQFPETLL 78

QY 67 GSTEKEF-FFNEPTKEFFEDRDPEYERCVLNEVRT-GKLHYPRYECISAYDELAIFYIL 124

Db 79 GDPKRRMRYYFDPLRNEYFFDRNRPSPDALIYYQSGGRIRRPVNVPIIDIPSEIRFYQ-- 136

QY 125 PEIGDCCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMWRAFENPHSTLALV 184

Db 137 ---LGEAMEKERE-----DEGFLREEREPPLPRDFQROVWLLFEYPSSGPARG 183

QY 185 FYYVTGFPIAVSVITNVETVPCGTVPGSKELPC-----GER-----YSV 224

Db 184 IAVSVLVILISIVIFCLETLF--EPRDEKDYPASTQDSFEAGNSTSGSRAGASSFSD 241

QY 225 AFFCLDTACVMIFTVVEYLRLFAAPSRYPFIRSVMSIIDVVAIMPYYIGLWM-----T 277

Db 242 PFFVVEVTLCTIWFSEFELVRFACPSKATFSRNIMNLIIDVAILPYFITLGTELABRQGN 301

QY 278 NNEDVSGAFV-TLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGLFSLTMAIIFI 336

Db 302 GQQAMSLAILRIVIRLVFRIRFKLSRHSKGLQILGQTLKASMRLEGLLIFFLFIGVILFS 361

QY 337 TVMFVAEKSSASKFTSIPASFMTITVTMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIA 396

Db 362 SAVYFAEADDPFSGFSSIPDAFWMAVVTMTVGYGDMHPVTIGKIVGSLCAIAGVLTIA 421

QY 397 LPVPVIVSNFRIYHONORADKRAQKKARLARIRVAKTGSSNAVYLSKRNGLNEALEL 456

Db 422 LPVPVIVSNFNYFYHRETEGEQ-----SQYMH-----VGSQOHL 456

QY 457 TGTPEEEMGKTTSLIESQHHLHLCLEKTNNHEFIDEQMFEOCMESSMONYPSTRSPS 516

Db 457 SSSAEERKARSNSTLSKSEYVIE--EGMNHSAFPQTPFK----- 496

QY 517 LSSHPIGLTTCCSRRSKKTTHLPNS 541

Db 497 ---TGNSTATCT-----TNNNPNS 512

Search completed: April 6, 2005, 07:21:30
Job time : 106.44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 07:13:52 ; Search time 442.392 Seconds
(without alignments)
477.292 Million cell updates/sec

Title: US-10-062-879-4
Perfect score: 3320
Sequence: 1 MAAGVAAWLPFARAAAGWM.....PGPNTNIPSITSNVKSVL 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	636	US-10-062-879-4	Sequence 4, Appli
2	3300.5	99.4	655	US-10-062-879-2	Sequence 2, Appli
3	3283.5	98.9	655	US-10-377-139-6	Sequence 6, Appli
4	2518	75.8	630	US-10-212-677-258	Sequence 258, App
5	2518	75.8	630	US-10-212-677-259	Sequence 259, App
6	2518	75.8	630	US-10-212-677-260	Sequence 260, App
7	2518	75.8	630	US-10-212-677-261	Sequence 261, App
8	2518	75.8	630	US-10-361-811-258	Sequence 258, App
9	2518	75.8	630	US-10-361-811-259	Sequence 259, App
10	2518	75.8	630	US-10-361-811-260	Sequence 260, App
11	2518	75.8	630	US-10-361-811-261	Sequence 261, App
12	2518	75.8	630	US-10-369-186-258	Sequence 258, App
13	2518	75.8	630	US-10-369-186-259	Sequence 259, App

14	2518	75.8	630	US-10-369-186-260	Sequence 260, App
15	2518	75.8	630	US-10-369-186-261	Sequence 261, App
16	2132.5	64.2	647	US-10-296-115-1112	Sequence 1112, Ap
17	2121.5	63.9	646	US-10-121-746-10	Sequence 10, Appli
18	844.5	25.4	255	US-10-212-677-257	Sequence 257, App
19	844.5	25.4	255	US-10-361-811-257	Sequence 257, App
20	844.5	25.4	255	US-10-369-186-257	Sequence 257, App
21	774.5	23.3	806	US-09-833-466-13	Sequence 13, Appli
22	774.5	23.3	806	US-10-199-869-6	Sequence 6, Appli
23	774.5	23.3	806	US-10-815-297-13	Sequence 13, Appli
24	766	23.1	911	US-10-408-765A-1482	Sequence 1482, Ap
25	758	22.8	985	US-10-154-086-20	Sequence 20, Appli
26	750	22.6	854	US-09-833-466-12	Sequence 12, Appli
27	750	22.6	854	US-10-199-869-5	Sequence 5, Appli
28	750	22.6	854	US-10-815-297-12	Sequence 12, Appli
29	736.5	22.2	857	US-10-377-139-5	Sequence 5, Appli
30	735	22.1	656	US-10-377-139-4	Sequence 4, Appli
31	726.5	21.9	539	US-10-325-891-13	Sequence 13, Appli
32	721.5	21.7	456	US-09-993-811-2	Sequence 2, Appli
33	721.5	21.7	456	US-09-974-712-2	Sequence 2, Appli
34	721.5	21.7	456	US-09-989-920-175	Sequence 175, App
35	721.5	21.7	456	US-10-254-010-4	Sequence 4, Appli
36	721.5	21.7	539	US-09-804-014A-27	Sequence 27, Appli
37	721	21.7	559	US-09-804-014A-8	Sequence 8, Appli
38	719	21.7	523	US-10-408-765A-2015	Sequence 2015, Ap
39	719	21.7	523	US-10-772-636-10	Sequence 10, Appli
40	718.5	21.6	525	US-10-400-435A-2	Sequence 2, Appli
41	718.5	21.6	585	US-10-322-281-766	Sequence 766, App
42	717.5	21.6	499	US-10-322-281-93	Sequence 93, Appli
43	717	21.6	524	US-10-322-281-93	Sequence 93, Appli
44	715.5	21.6	499	US-10-322-281-763	Sequence 763, App
45	715	21.5	16	US-10-322-281-763	Sequence 763, App

ALIGNMENTS

RESULT 1
US-10-062-879-4
; Sequence 4, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hui-ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062, 879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
; US-10-062-879-4

Query Match 100.0%; Score 3320; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.4e-278;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGVAAWLPFARAAAGWMPVANCMPPLAPADKXKQDELIVLVNSGRRFQWTTTLR 60
DB 1 MAAGVAAWLPFARAAAGWMPVANCMPPLAPADKXKQDELIVLVNSGRRFQWTTTLR 60
QY YPDTLLGSTEKEFFFNEDTKYFFDRDPEVFCVINFYRTGKLHYPRYECISAYDELAF 120
DB YPDTLLGSTEKEFFFNEDTKYFFDRDPEVFCVINFYRTGKLHYPRYECISAYDELAF 120


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Db 121 YGILPEIIGDCCEYKORRENAERLMDNDSENQESMPSLSFRQTMRAFENPHST 180
Qy 181 LALVFYVYVTFGFFIAVSVITNVVEVPCGTVPGSG-KELPCGERYSVAFFCLDTACVMIF 240
Db 181 LALVFYVYVTFGFFIAVSVITNVVEVPCGTVPGSG-KELPCGERYSVAFFCLDTACVMIF 240
Qy 241 YLRLFAAPSRRYRFRSVMSSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
Db 241 YLRLFAAPSRRYRFRSVMSSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
Qy 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKTSIPASFWY 360
Db 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKTSIPASFWY 360
Qy 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHONORADKR 420
Db 361 TIVMTTLGYGDMVPKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHONORADKR 420
Qy 421 AOKKARLARIRVAKTSSNAAYLHRSKRNGLNEALELTGTPEEHEMGKTSLSIESQHHL 480
Db 421 AOKKARLARIRVAKTSSNAAYLHRSKRNGLNEALELTGTPEEHEMGKTSLSIESQHHL 480
Qy 481 HCLEKT-----NHEFIDQMEONCMESMOMNYPSTRSPSLSSHP 521
Db 481 HCLEKTGLSYLVDPDPLSVRTSTIKNHEFIDQMEONCMESMOMNYPSTRSPSLSSHP 540
Qy 522 GLTTCCSRSSKKTTHLPNSNLPAFRLRSMOELSTIHIQSEQPSLTSSSLNLKADG 581
Db 541 GLTTCCSRSSKKTTHLPNSNLPAFRLRSMOELSTIHIQSEQPSLTSSSLNLKADG 600
Qy 582 LRPNCSTQITTAIISIPPPALTPEGESRPPSPSGPNTNIPSTSNVYKSVL 636
Db 601 LRPNCSTQITTAIISIPPPALTPEGESRPPSPSGPNTNIPSTSNVYKSVL 655

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RESULT 4

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US-10-212-677-258
; Sequence 258, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-258

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Query Match 75.8%; Score 2518; DB 14; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
Qy 1 MAAGVAAWLPFAAAAGMMPVANCMPPLADKNKR-QDELIYLVNSGRRFQWTTLTLE 59
Db 1 MAAGVAAWLPFAAAAGMMPVANCMPPLADKNKR-QDELIYLVNSGRRFQWTTLTLE 60
Qy 60 RYPTLLGSTEKEFFFNEDTKEFFDRDPEVRCVUNFYRTGKLYHPRYECISAYDELA 119
Db 61 RYPTLLGSSSEDFFYHETQYFFDRDPDIFRHILNFYRTGKLYHPRYECISAYDELA 120
Qy 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENQES-MPSLSFRQTMRAFENPH 178
Db 121 FFGLPEIIGDCCEYKORRENAERLMDNDSENQES-MPSLSFRQTMRAFENPH 180

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Qy 179 STLALVFYVYVTFGFFIAVSVITNVVEVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
Db 181 STLALVFYVYVTFGFFIAVSVITNVVEVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF 240
Qy 238 TVEYLRLFAAPSRRYRFRSVMSSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 297
Db 241 TVEYLRLFAAPSRRYRFRSVMSSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFRIFKE 300
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKTSIPAS 357
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKTSIPAS 360
Qy 358 FWTYITMTTLGYGDMVPKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHONORAD 417
Db 361 FWTYITMTTLGYGDMVPKTIAGKIFGSLGSLGVLYIALPVPIVSNFSRIYHONORAD 420
Qy 418 KRAOKKARLARIRVAKTSSNAAYLHRSKRNGLNEALELTGTPEEHEMGKTSLSIESQH 477
Db 421 KRAOKKARLARIRVAKTSSNAAYLHRSKRNGLNEALELTGTPEEHEMGKTSLSIESQH 479
Qy 478 HILHCLEKTTHNEFIDQMEONCMESMOMNYPSTRSPSLSSHPGLTTCCSRSSKKTTH 537
Db 480 HILHCLEKTTHNEFIDQMEONCMESMOMNYPSTRSPSLSSHPGLTTCCSRSSKKTTH 539
Qy 538 LPSNLPATRLRSMOELSTIHIQSEQPSLTSSSLNLKADGRLPNCSTQITTAIIS 597
Db 540 LPSNLPATRLRSMOELSTIHIQSEQPSLTSSSLNLKADGRLPNCSTQITTAIIS 599
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Db 600 IPTPALTPEGESRPPSPSGPNTNIPSTSNVYKSVL 630

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RESULT 5

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US-10-212-677-259
; Sequence 259, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-259

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Query Match 75.8%; Score 2518; DB 14; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
Qy 1 MAAGVAAWLPFAAAAGMMPVANCMPPLADKNKR-QDELIYLVNSGRRFQWTTLTLE 59
Db 1 MAAGVAAWLPFAAAAGMMPVANCMPPLADKNKR-QDELIYLVNSGRRFQWTTLTLE 60
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Db 61 RYPTLLGSSSEDFFYHETQYFFDRDPDIFRHILNFYRTGKLYHPRYECISAYDELA 120
Qy 120 FYGLPEIIGDCCEYKORRENAERLMDNDSENQES-MPSLSFRQTMRAFENPH 178
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Qy	179	STLALVPPYVTGFFIAVSVTNNVETVPCGVPGS-KELPCGERSVAFFCLDTACVMIF	237
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Qy	238	TVEYLRLFAAPSRVRFIRSVMISIDVVAIMPYIIGLVMTNNEBDSGAFYTLRVFEVERI	297
Db	241	TVEYLRLAAPSRVRFVRSVMSIIDVVAIIIPYIIGLVMTNNEBDSGAFYTLRVFEVERI	300
Qy	298	EKFSRHSOGLRIIGVTLKSCASLGLFLSLTMAIIIPATVMFYAEKSSASAKFTSIPAS	357
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Qy	358	FWYTIIVMTTLGYGDMVPKTIAGKIFGSCISLSGLVLTALPVPIVSNFSRIYHQORAD	417
Db	361	FWYTIIVMTTLGYGDMVPKTIAGKIFGSCISLSGLVLTALPVPIVSNFSRIYHQORAD	420
Qy	418	KRAQKARLARIRIVAKTSSNAYLHSCRNGLIENALBLTGTPEEHMGKTSLSLSQH	477
Db	421	KRAQKARLARIRAKSGSANAYMOSKRNGLISNOLQ-SSEDOAFVSKSGSSFETQH	479
Qy	478	HLHLCLEKTTNHEFIDEOMEQNCMESSMONTYSTRSPSLSSHPLTTCCSRSKKTH	537
Db	480	HLHLCLEKTTNHEFIDEQVEEESCMBAVTNRPSSHSPSLSSQGVSTTCCSRHKKTFR	539
Qy	538	LPNSNLPATRLRSMOELSTIHIGSEQEOPSLTTRSSLINLKADDLGRPNCKTSQITTAIIS	597
Db	540	IPNANVSGSHSQIGELSTIGIRCVERTPLSNRSSLNAKMEECVGLNCEQPYVTTAIIS	599
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RESULT 6
US-10-212-677-260
; Sequence 260, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-260

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Query Match	75.8%;	Score 2518;	DB 14;	Length 630;
Best Local Similarity	75.8%;	Pred. No. 4.7e-209;		
Matches 486;	Conservative 69;	Mismatches 70;	Indels 16;	Gaps 6;
QY	1	MAAGVAAML.PFARAAAIGWMPVANCMPPLAPADKNKR-QDEILIVLNSGRRFQTRTILE	59	
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QY	60	RYPDTLIGSTEKEFFENEDTKEYFFEDRDPEVFRCLVNFYRTGKLHYRVECSAYDDELA	119	
Db	61	RYPDTLIGSSSERDFYHPEYQYFFEDRDPDIFRHLINFYRTGKLHYRHECISAYDESLA	120	
QY	120	FYGLLPEIIGDCCYEEYKDKRKRENAERLMDNDSENNQES-NPSLSFQTMBAFENPHT	178	
Db	121	PFGLIPEIIGDCCYEEYKDKRRRENAERLQDDADTDTAGESALPTMTARQVRBAFENPHT	180	
QY	179	STLALVYYVVTGFPIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF	237	

Db	181	STMAVEYYVTGFEIAVSVIANVETVPCGSSPGHITKELPCGERYAAVAFCLDTACWIF	240
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Db	241	TVEYLLRLAAPSRYRFRSVMSIIDVALLPYIGLVMTNNEDEVSGAFVTLRVRVFR	300
Qy	298	EKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFVYAEKSSASKEFSIPAS	357
Db	301	EKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFVYAEKSSASKEFSIPAA	360
Qy	358	FWYTYVTMTTGLGYDMVPKTIAGKIFGSISSLSGVIALPVPVIVSNFSRIYHONORAD	417
Db	361	FWYTYVTMTTGLGYDMVPKTIAGKIFGSISSLSGVIALPVPVIVSNFSRIYHONORAD	420
Qy	418	KRAOKKARLARIRVAKTGSSNAYLHSKRNGLNEALELGTPEEHNMGKTTSLIESOH	477
Db	421	KRAOKKARLARIRVAKTGSSNAYLHSKRNGLNEALELGTPEEHNMGKTTSLIESOH	479
Qy	478	HLHLCKEKTTHNEFIDQMEONCESSMONYPSTRSPSLSHPGLTTCSSRSRCKTTH	537
Db	480	HLHLCKEKTTHNEFVDEQVFEESCMEVATYNRPSSHSPLSSQOGVTSTCCSRHKTFR	539
Qy	538	LPNSNLPATRLSMQELSTHIIHQSEQPSLTSSRSNLKADGLRPNCQTSQITTAIS	597
Db	540	IPNANVSGSHQGSIOELSTIQRCEVTRPLSNRSRSSLNAKMEBCVKLNCEQPYVTTAIS	599
Qy	598	IPTPALTPEGESRP--PPASPGPNTNIPSTSNVVKVSVL	636
Db	600	IPTPVTTPBGGDRPESPEYSGG-----NIVRSVAL	630

```

RESULT 7
US-10-212-677-261
; Sequence 261, Application US//10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-261

```

[illegible]


```
Db 181 STMALVFYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLRLFAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 297
Db 241 TVEYLRLAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 300
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIYMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIRVAKTGSSNAYLHSKRNLNLEALGTPEBEHMGKTSLSIESQHH 477
Db 421 KRAQKARLARIRVAKTGSSNAYLHSKRNLNLEALGTPEBEHMGKTSLSIESQHH 479
Qy 478 HLHCKEKTTHNEFIDEQMFQONCESSMONYPSTRSPSLSHGGLTTCCSRRSKKTTH 537
Db 480 HLHCKEKTTHNEFIDEQMFQONCESSMONYPSTRSPSLSHGGLTTCCSRRSKKTTH 539
Qy 538 LPNSNLPATRLRSMQELSTIHQSSQPSLTSSSLNLKADGLRPNCCKTSQITTAIIS 597
Db 540 IPNAVSGSHQSIQELSTIQIRCYERTPLSNSRSLNAKMECVKLCNCEQPYVTTAIIS 599
Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKVSVL 636
Db 600 IPTPPVTTPEGDDRPESEYSGG-----NIVRVSAAL 630
```

```
RESULT 8
US-10-361-811-258
; Sequence 258, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-258
```

```
Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAWLPFARAAGMMPVANCMPPLAPADKNKR-QDELIIVLVSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAAGMMPVASCMPAPRQERKKTQDALIVLVSGTRFQWQDTLE 60
Qy 60 RYPTDLIGSTEKEFFENEDTKYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLIGSSSERDFYHPEYTOQYFDRDPDIFRHILNFRYRTGKLHYPRHBCISAYDELA 120
Qy 120 FYGLPEIIGDCYEEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMWRAPENPHT 178
Db 121 FFGLIPEIIGDCYEEYKDRRENAERLQDDADTDPTAGESALPTMTARQVWRAFENPHT 180
Qy 179 STALVFYVTGFFIAVSIVTNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLRLFAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 297
```

```
Db 241 TVEYLRLAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 300
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLFSLTMAIIFATVMFYAEKSSASKFTSIPAA 360
Qy 358 FWYTIYMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQAD 417
Db 361 FWYTIYMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQAD 420
Qy 418 KRAQKARLARIRVAKTGSSNAYLHSKRNLNLEALGTPEBEHMGKTSLSIESQHH 477
Db 421 KRAQKARLARIRVAKTGSSNAYLHSKRNLNLEALGTPEBEHMGKTSLSIESQHH 479
Qy 478 HLHCKEKTTHNEFIDEQMFQONCESSMONYPSTRSPSLSHGGLTTCCSRRSKKTTH 537
Db 480 HLHCKEKTTHNEFIDEQMFQONCESSMONYPSTRSPSLSHGGLTTCCSRRSKKTTH 539
Qy 538 LPNSNLPATRLRSMQELSTIHQSSQPSLTSSSLNLKADGLRPNCCKTSQITTAIIS 597
Db 540 IPNAVSGSHQSIQELSTIQIRCYERTPLSNSRSLNAKMECVKLCNCEQPYVTTAIIS 599
Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKVSVL 636
Db 600 IPTPPVTTPEGDDRPESEYSGG-----NIVRVSAAL 630
```

```
RESULT 9
US-10-361-811-259
; Sequence 259, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-259
```

```
Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAWLPFARAAGMMPVANCMPPLAPADKNKR-QDELIIVLVSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAAGMMPVASCMPAPRQERKKTQDALIVLVSGTRFQWQDTLE 60
Qy 60 RYPTDLIGSTEKEFFENEDTKYFFDRDPEVRCVNLNFRYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLIGSSSERDFYHPEYTOQYFDRDPDIFRHILNFRYRTGKLHYPRHBCISAYDELA 120
Qy 120 FYGLPEIIGDCYEEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMWRAPENPHT 178
Db 121 FFGLIPEIIGDCYEEYKDRRENAERLQDDADTDPTAGESALPTMTARQVWRAFENPHT 180
Qy 179 STALVFYVTGFFIAVSIVTNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYVTGFFIAVSIVANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
Qy 238 TVEYLRLFAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 297
Db 241 TVEYLRLAAPSRYRFRVRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 300
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLFSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
```

Db 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASAKFTSIPAA 360
QY 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 417
Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 420
QY 418 KRAQOKARLARIRVAKTSSNAYLHSKRNGLINEALELTGTPEEHMGKTTSLIESQHH 477
Db 421 KRAQOKARLARIRAKSGSANAYMQSKRNGLSNQLQ-SSDEQAFVSKSGSSFETQHH 479
QY 478 HLHCEKTNHNEFIDEQMEQONCESSMONTPTSTRSPSLSSHPLGTTTCCSRRSKTTTH 537
Db 480 HLHCEKTNHNEFIDEQVFEESCMEVATVNRPSHSPSLSSQOGVTSTCCSRHKKTFR 539
QY 538 LENSNLPAITRLRSMQELSTIHIOGSEQPSLTSTRSSSLNLKADDLRPNCKTSQITTAIS 597
Db 540 IPNAVSGSHQSGIQLSTIQIRCVERTPLSNRSLSLNAKMEBCVKLNCEQPYVTTAIS 599
QY 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 636
Db 600 IPTPPVTTPEGDDRPESPESYSG-----NIVRSAL 630

RESULT 10

US-10-361-811-260
; Sequence 260, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-260

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNKR-ODELIIVLVNSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAALIGMMPVASCMPAPRQERKRTQDALIVLVNSGTRFQWQDTLE 60
QY 60 RYPTDLGSTEKEFFENEDTKEYFPDRDPEVRCVLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLGSSSRDFFYHPEYQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMWRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDRRRENAERLQDDADDTAGESALPTMTARQVRRAFENPHT 180
QY 179 STIALVFYYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRI 297
Db 241 TVEYLLRLFAAPSRFRFRVSMSIIDVVAILPYIIGLVMTNEDVSGAFVTLRVERVRI 300
QY 298 FKFSRHSQGLRIILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASAKFTSIPAS 357
Db 301 FKFSRHSQGLRIILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASAKFTSIPAA 360
QY 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 417

Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 420
QY 418 KRAQOKARLARIRVAKTSSNAYLHSKRNGLINEALELTGTPEEHMGKTTSLIESQHH 477
Db 421 KRAQOKARLARIRAKSGSANAYMQSKRNGLSNQLQ-SSDEQAFVSKSGSSFETQHH 479
QY 478 HLHCEKTNHNEFIDEQMEQONCESSMONTPTSTRSPSLSSHPLGTTTCCSRRSKTTTH 537
Db 480 HLHCEKTNHNEFIDEQVFEESCMEVATVNRPSHSPSLSSQOGVTSTCCSRHKKTFR 539
QY 538 LENSNLPAITRLRSMQELSTIHIOGSEQPSLTSTRSSSLNLKADDLRPNCKTSQITTAIS 597
Db 540 IPNAVSGSHQSGIQLSTIQIRCVERTPLSNRSLSLNAKMEBCVKLNCEQPYVTTAIS 599
QY 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 636
Db 600 IPTPPVTTPEGDDRPESPESYSG-----NIVRSAL 630

RESULT 11

US-10-361-811-261
; Sequence 261, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-261

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNKR-ODELIIVLVNSGRRFQWRTTLE 59
Db 1 MAAGVAAWLPFARAALIGMMPVASCMPAPRQERKRTQDALIVLVNSGTRFQWQDTLE 60
QY 60 RYPTDLGSTEKEFFENEDTKEYFPDRDPEVRCVLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLGSSSRDFFYHPEYQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMWRAFENPHT 178
Db 121 FFGILPEIIGDCCYEYKDRRRENAERLQDDADDTAGESALPTMTARQVRRAFENPHT 180
QY 179 STIALVFYYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
Db 181 STMALVFYYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLLRLFAAPSRFRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRI 297
Db 241 TVEYLLRLFAAPSRFRFRVSMSIIDVVAILPYIIGLVMTNEDVSGAFVTLRVERVRI 300
QY 298 FKFSRHSQGLRIILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASAKFTSIPAS 357
Db 301 FKFSRHSQGLRIILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASAKFTSIPAA 360
QY 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 417
Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONQAD 420
QY 418 KRAQOKARLARIRVAKTSSNAYLHSKRNGLINEALELTGTPEEHMGKTTSLIESQHH 477

```

Db      421 KRAQKARLARIRIAAKSGSANAYMOSKRNGILSNQLO-SSSEDEQA FVSKSGSSSFETQH 479
Oy      478 HLHCLERTTNHEFI DEOMFEQN CMESSMONTPTSRGSLSHFGLTTTCCSRRSKXTH 537
          ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      480 HLHCLERTTNHEFVDEQVEBSCMEVATVNRPSSHBSLSQQGVTSCTCSRHKTKFR 539
          ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Oy      538 LPSNLPATRLRSMQELSTHIQSGEQPLTTRRSSLNLKADGDGRPNCKXSQTITAIIS 597
          ::::: |::::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      540 IPNAVSGSHQSGSIQELSTIQRCVERTPLNSRRSSLNAKMEECVKLNCEQPYYVTIAIIS 599
          ::::: |::::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Oy      598 IPTPALTPGESRP--PPASPGPNTNIPITSNVKVSVL 636
          ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      600 ITPPVTVTEGGDRDPESPESYSG-----NIVRSAL 630
          ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
US-10-369-186-258
; Sequence 258, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-258
```

Query Match	75.8%	Score 2518	DB 15	Length 630			
Best Local Similarity	-75.8%	Pred. No. 4.7e-209					
Matches	486	Conservative	69	Mismatches 70			
			Indels	16			
			Gaps	6			
QY	1	MAAGVAAWLPFARA	AAIGMMPVANCMP	PLAPADKNKR-QDELI	VLNVNSGR	PQTWRTTLE	59
DB	1	MAAGVAAWLPFARA	AAAGMMPVASGMP	APRQERKRTQD	LLIVLVNSG	TRFQTDLTLE	60
QY	60	RYPDTLTGSTEKE	FFNFEDTKEYE	FFDRDPEVERCV	NEFYRTGKL	HYPRYECS	119
DB	61	RYPDTLTGSSSE	RDEFFYHBPETQ	QYFEFDRDPD	IFRHILNFY	RKTGLHYPRHEC	120
QY	120	FYGLPEIIGDCC	YEEYKDRKRENA	ERLMDNDSEN	NOES-MPSL	SFRQTMWEA	178
DB	121	FFGLPEIIGDCC	YEEYKDRRRENA	ERLQDDADT	PAGESALPT	MTARQVRWA	180
QY	179	STLALVFYVYV	GFIAVSVITNV	ETVPCGT	VPGS-KEL	PCGERYS	237
DB	181	STMALVFYVYV	TGFIAVSVIAN	VEVTPCG	SSPGHikel	PCGERYANA	240
QY	238	TVEYLRLFA	APSRRYRFRIS	VSMSIIDV	VAIMPYYIG	LVMTNNE	297
DB	241	TVEYLRLFA	APSRRYRFRIS	VSMSIIDV	VAIMPYYIG	LVMTNNE	300
QY	298	PKFSRHSQ	GLRILGYTLKS	CASEGLFL	PSLTMAII	IIFATW	357
DB	301	EKFSRHSQ	GLRILGYTLKS	CASEGLFL	PSLTMAII	IIFATW	360
QY	358	FWYTIIVMT	TGVDMPKTI	AGKIFG	SICSLG	VLVIALP	417
DB	361	FWYTIIVMT	TGVDMPKTI	AGKIFG	SICSLG	VLVIALP	420
QY	418	KRRAQKAR	LARIRVAKT	GSSNAV	ILHKS	KNGLNEAL	477
DB	421	KRRAQKAR	LARIRVAKT	GSSNAV	ILHKS	KNGLNEAL	479
QY	478	HLHCEKT	NHFEI	DEQMEF	QONCE	SSMONYP	537

```
Db      480 HLHCLERTNHEFVDEQVFEEESCMEVATNRPSHSPLSSQQGVTSITCCSRHKKTER   539
Oy      538 LPNSNLPAIRLSMOELSTIIHQSGEQPSLTTRSSLNLKADDELRPNCCKTQITTAIIS   597
       :|::: |::|||::: |: ||||| ::: |:::|||
Db      540 IPNAVSGSHGSIQELSTIQIRCVERTPLSNSRSSLNAKMEECVKLNCEDPYVTIAIIS   599

Oy      598 IPTPALTPGESRP--PPASGPNTNIPISTSVMKVSVL    636
       ||||| |||:: || | | | | | | | | | | | | | |
Db      600 IPTPVTTPEGDDRPESPESYSG-----NIVRSAL    630


RESULT 13
US-10-369-186-259
; Sequence 259, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRNET FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-369-186-259
```

Query Match	75.8%	Score 2518	DB 15	Length 630
Best Local Similarity	-75.8%	Pred. No. 4.7e-209		
Matches 486	Conservative 69	Mismatches 70	Indels 16	Gaps 6
QY	1	MAGVAAWLPPARAATGMPVANCMPPLAPADKNKR-QDEILVIANVSGRRFGQWRTTLE	59	
DB	1	MAGVAAWLPPARAATGMPVASCMPAPRGRKRTQDALIVIANVSGTRFGTWQDTLE	60	
QY	60	RYPDTLLGSTEKEFFEFNEDTKEXYFEDRDEVEFRVCYLNFPYRTGLHYPREYECISAYDELA	119	
DB	61	RYPDTLLGSSERDFEYHPEYQYFFDRDDEDI FRHILNFYRTGLHYPRHECISAYDEELA	120	
QY	120	FYGLIPEIIGDCYEEYKDKRENAERLMDNDSENNOES-MPSLSFRQTMWPAFENPHT	178	
DB	121	FFGLIPEIIGDCYEEYKDRRENAERLDDADDTTAGESALPTMTARQVRWPAFENPHT	180	
QY	179	STLALVYYVYGFPIANSVITNVETVPGCTVPGS-KELPGGERYSVAFPCLDTACVMIF	237	
DB	181	STMALVYYVYGFPIANSVIANVETVPGSSPGHKELPGERYANAFPCLDTACVMIF	240	
QY	238	TVEYLRLFAAPSRRYFRSRVMSIIDVVAIMPYYIGLVMTNNEDEVGSAFVTLRVERVFR	297	
DB	241	TVEYLRLFAAPSRRYFRSVMSIIDVVAIIPYYIGLVMTNNEDEVGSAFVTLRVERVFR	300	
QY	298	EKFSRHSQGLRILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASAKFTSIPAS	357	
DB	301	EKFSRHSQGLRILGYTLKSCASELGFLFSLTMAIIIFATVMFYAEKGSSASAKFTSIPAA	360	
QY	358	FWYTLVTMTTLGYGDMVPKTIAGKIFGSCSLSGVLVIALPVPVIVSNFSRIYHQNORAD	417	
DB	361	FWYTLVTMTTLGYGDMVPKTIAGKIFGSCSLSGVLVIALPVPVIVSNFSRIYHQNORAD	420	
QY	418	KRPAOKKARLARIRVAKTGSSNAYLHKSXKNGLINEALLETGTPPEEHHMGKTTSLIESQHH	477	
DB	421	KRPAOKKARLARIRAAKSGSANAYMQSKRNGLLSNQLO-SSEDEQAFVSKSGSFETQHH	479	
QY	478	HLHCLKLTNNHEFIDQMEFONCMESSMONYPSTRSPSLSSHPLGTLTTCCSRRSKKTTH	537	
DB	480	HLHCLKLTNNHEFVDEQVFEESCMEVATVNRPSHSPSLSSQGGVSTCCSRRHAKKTR	539	
QY	538	LPSNU.PATRLRSMOELSTIHQSGSEQPSLTTSRSLNKLKADDLGRPNCKTISQITTAIS	597	

Db 540 IPNAVSGSHQSIQELSTIQRCVERTPLNSRSSLNAKMECVLNCCEQPYVTTAIS 599
QY 598 IPTPPALTPEGESRP--PPASGPNTNIPSTISNVKVSVL 636
Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRSAL 630

RESULT 14
US-10-369-186-260
; Sequence 260, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-260

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPMLPADKNKR-ODELIVLVNSGRPRQTWRTTLE 59
Db 1 MAAGVAAWLPFARAALIGMMPVASCMPMPAPRQGRKRTQDALIVLVNSGTRFQTWQDTLE 60
QY 60 RYPTDLGSTEKEFFENEDTKKEYFFDRDPEVFRCLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLGSSERDFFYHPETQCYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
QY 120 FYGLPEIIGDCCYEEYKDRKKNENARLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEEYKDRRENAERLODDADDTAGESALPTMTARQVRWRAFENPHT 180
QY 179 STLALVFYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACWIF 237
Db 181 STMALVFYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACWIF 240
QY 238 TVEYLLRLFAAPSRYPFRSVWSIIDVAIMPYYIGLVMTNNEVDVSGAFVTLRVFRVRI 297
Db 241 TVEYLLRLAAPSRYPFRSVWSIIDVAILPYIIGLVMTNNEVDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLRILGYTLKSCASBLGFLFSLTMAIIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASBLGFLFSLTMAIIIFATVMFYAEKSSASKFTSIPAA 360
QY 358 FWYTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 417
Db 361 FWYTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRAQOKKARLARIRVAKTGSSNAYLHSKRNGLNLEALGTPTPEEHMGKTSLSIESQHH 477
Db 421 KRAQOKKARLARIRAKSGSANAYMOSKRNGLSNQLQ-SSEDEQA FVSKSSSFFETQHH 479
QY 478 HLHGLEKTNHFEIDQMFQONCMESMONTPTSPSPSSHPGLTTTCCSRRSKKTTH 537
Db 480 HLHGLEKTNHFEVDQVFEESCMEVATVNRPSHSPSSSQQGVSTCCSRRHKKTFR 539
QY 538 LPNSNLPATRLRSQMOELSTIHQSGEQPSLTSRSLSLNKADGLRPNCCKTSQITTAIS 597
Db 540 IPNAVSGSHQSIQELSTIQRCVERTPLNSRSSLNAKMECVLNCCEQPYVTTAIS 599
QY 598 IPTPPALTPEGESRP--PPASGPNTNIPSTISNVKVSVL 636
Db 598 IPTPPALTPEGESRP--PPASGPNTNIPSTISNVKVSVL 636

Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRSAL 630

RESULT 15
US-10-369-186-261
; Sequence 261, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-261

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAAGVAAWLPFARAALIGMMPVANCMPMLPADKNKR-ODELIVLVNSGRPRQTWRTTLE 59
Db 1 MAAGVAAWLPFARAALIGMMPVASCMPMPAPRQGRKRTQDALIVLVNSGTRFQTWQDTLE 60
QY 60 RYPTDLGSTEKEFFENEDTKKEYFFDRDPEVFRCLNFYRTGKLHYPRYECISAYDELA 119
Db 61 RYPTDLGSSERDFFYHPETQCYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDELA 120
QY 120 FYGLPEIIGDCCYEEYKDRKKNENARLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
Db 121 FFGILPEIIGDCCYEEYKDRRENAERLODDADDTAGESALPTMTARQVRWRAFENPHT 180
QY 179 STLALVFYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACWIF 237
Db 181 STMALVFYVTGFFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACWIF 240
QY 238 TVEYLLRLFAAPSRYPFRSVWSIIDVAIMPYYIGLVMTNNEVDVSGAFVTLRVFRVRI 297
Db 241 TVEYLLRLAAPSRYPFRSVWSIIDVAILPYIIGLVMTNNEVDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLRILGYTLKSCASBLGFLFSLTMAIIIFATVMFYAEKSSASKFTSIPAS 357
Db 301 FKFSRHSQGLRILGYTLKSCASBLGFLFSLTMAIIIFATVMFYAEKSSASKFTSIPAA 360
QY 358 FWYTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 417
Db 361 FWYTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRAQOKKARLARIRVAKTGSSNAYLHSKRNGLNLEALGTPTPEEHMGKTSLSIESQHH 477
Db 421 KRAQOKKARLARIRAKSGSANAYMOSKRNGLSNQLQ-SSEDEQA FVSKSSSFFETQHH 479
QY 478 HLHGLEKTNHFEIDQMFQONCMESMONTPTSPSPSSHPGLTTTCCSRRSKKTTH 537
Db 480 HLHGLEKTNHFEVDQVFEESCMEVATVNRPSHSPSSSQQGVSTCCSRRHKKTFR 539
QY 538 LPNSNLPATRLRSQMOELSTIHQSGEQPSLTSRSLSLNKADGLRPNCCKTSQITTAIS 597
Db 540 IPNAVSGSHQSIQELSTIQRCVERTPLNSRSSLNAKMECVLNCCEQPYVTTAIS 599
QY 598 IPTPPALTPEGESRP--PPASGPNTNIPSTISNVKVSVL 636
Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRSAL 630

Search completed: April 6, 2005, 08:34:00

Thu Apr 7 08:08:07 2005

us-10-062-879-4.apr5.rapb

Page 9

Job time : 443.392 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:45:50 ; Search time 114.785 Seconds
(without alignments)
533.115 Million cell updates/sec

Title: US-10-062-879-4
Perfect score: 3320
Sequence: 1 MAAGVAAWLPFARAAAIAGWM.....PGPNTNIPSITSNVKXSVL 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2519	75.9	630	2	JU0271	voltage-sensitive
2	2141.5	64.5	651	2	A39372	potassium channel
3	1915.5	57.7	490	2	A5312	potassium channel
4	1103	33.2	236	2	I57681	potassium channel
5	770	23.2	802	2	JH0595	potassium channel
6	750	22.6	858	2	S31761	potassium channel
7	736.5	22.2	643	2	S00480	potassium channel
8	736.5	22.2	853	1	CHRTD1	potassium channel
9	736	22.2	602	2	JH0166	potassium voltage-
10	736	22.2	656	2	JH0193	potassium channel
11	735.5	22.2	924	2	S12746	potassium channel
12	726.5	21.9	857	2	I56529	potassium channel
13	719	21.7	598	2	I56669	potassium channel
14	719	21.7	602	2	A49507	potassium channel
15	718.5	21.6	525	2	A43531	potassium channel
16	718	21.6	523	2	A38101	potassium channel
17	717.5	21.6	585	2	A39395	delayed rectifier
18	717	21.6	499	2	I77466	potassium channel
19	716.5	21.6	924	2	B41359	potassium channel
20	715	21.5	499	2	I84204	potassium channel
21	715	21.5	499	2	A33814	potassium channel
22	715	21.5	769	2	I56546	shaw type potassiu
23	712.5	21.5	528	2	I84205	potassium channel
24	712	21.4	489	2	I51532	potassium channel
25	711.5	21.4	495	2	A40090	potassium channel
26	711.5	21.4	495	2	B39113	potassium channel
27	710.5	21.4	495	2	I57680	potassium channel
28	707.5	21.3	511	2	A46020	potassium channel
29	707	21.3	460	2	T27759	hypothetical prote

30	706.5	21.3	511	2	S07095	potassium channel
31	705	21.2	476	2	S21144	potassium channel
32	705	21.2	597	2	SS1212	BAK5 protein - bov
33	701.5	21.1	498	2	A41359	potassium channel
34	700	21.1	679	2	A42073	potassium channel
35	699.5	21.1	489	2	JC4787	shaw protein - Cal
36	699	21.1	499	2	JH0313	potassium channel
37	699	21.1	499	2	A48672	delayed rectifier
38	697.5	21.0	625	2	S13919	potassium channel
39	697	21.0	581	2	S17150	potassium channel
40	696	21.0	613	2	A39402	potassium channel
41	694.5	20.9	660	2	S24125	potassium channel
42	692.5	20.9	624	2	S22703	voltage-gated pota
43	692.5	20.9	653	2	A39922	potassium channel
44	692.5	20.9	654	2	S11049	potassium channel
45	691	20.8	558	2	T23991	hypothetical prote

ALIGNMENTS

RESULT 1

JU0271 voltage-sensitive potassium channel protein [validated] - rat
N:Alternate names: rat sha/1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JU0271; A39113
R:Baldwin, T.J.; Tsaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.
Neuron 7, 471-483, 1991
A:Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K+ c
A:Reference number: JU0271; MUID:92000693; PMID:1840649
A:Accession: JU0271.
A:Molecule type: mRNA
A:Residues: 1-630 <BAL>
A:Cross-references: UNIPROT:Q63881; GB:S64320; NID:G236196; PIDN:AAB19939.1; PID:G236197
A:Experimental source: hippocampus
R:Roberts, S.L.; Tankun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
A:Reference number: A39113; MUID:91156694; PMID:1705709
A:Accession: A39113
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>
A:Cross-references: GB:M59980; NID:G203467; PIDN:AAA40929.1; PID:G203468
C:Function:
A:Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [valida
C:Superfamily: potassium channel protein dxr1
C:Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel
F:38/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #sta
F:54,280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status
F:70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
F:101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F:113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase
F:592/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 75.9%; Score 2519; DB 2; Length 630;
Best Local Similarity 75.8%; Pred. No. 6.6e-186;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

OY	1	MAAGVAAWLPFARAAAIAGWMPVANCMPPLAPADKNR-QDELIVLVNSGRRFQWRRTTLE	59
DB	1	MAAGVAAWLPFARAAAIAGWMPVSGMPAPRQERKTQDALIVLVNSGTRFQWQDTLE	60
OY	60	RYPDITLIGSTKEFFFNEDTKETFFDRDPEVFRCVLNFYRTGKLHYPRYCISAVDELA	119
DB	61	RYPDITLIGSSSEDFYHETQGYFDRDPDIFRHILNFYRTGKLHYPRHCISAVDELA	120
OY	120	FYGLPEITIGDCCEYEYKDKRENAERLMDNDSENQES-MPSLSPROTMRAPEENPHT	178
DB	121	FFGLPEITIGDCCEYEYKDRRENAERLQDDADTDNTGESALPTMTARQVRARAPENPHT	180

```
Qy 179 STLALVFYVYTGFFIAVSVITNVEVETPCGTVPGS-KELPCGERYVAFFCLDTACWIF 237
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 STMALVFYVYTGFFIAVSVIANVETVPCGSSPGHIIKELPCGERYAVAFCLDTACWIF 240
Qy 238 TVEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRI 297
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TVEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERVRI 300
Qy 298 FKFSRHSOGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 357
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 FKFSRHSOGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 360
Qy 358 FWYTIIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPVIYSNFSRIYHQNQAD 417
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 FWYTIIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPVIYSNFSRIYHQNQAD 420
Qy 418 KRRARQKARLARIRVAKTGSSNAYLHSCRNGLNLEALDELGTPEEEMGKTSLLIESQHH 477
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 KRRARQKARLARIRVAKTGSSNAYLHSCRNGLNLEALDELGTPEEEMGKTSLLIESQHH 479
Qy 478 HLHLCLEKTNHEFIDEQMFECNCESSMONTPTSPSLSSHPGLTTTCCSRKSKTTH 537
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 HLHLCLEKTNHEFIDEQMFECNCESSMONTPTSPSLSSHPGLTTTCCSRKSKTTH 539
Qy 538 LPSNLPATRLRSMQELSTIHQSGEQPSLTTSRSSLNKADGLRNCKTSGITTAIS 597
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 540 LPSNLPATRLRSMQELSTIHQSGEQPSLTTSRSSLNKADGLRNCKTSGITTAIS 599
Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 636
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 630
```

RESULT 2

```
A39372
potassium channel protein Shal1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C/Accession: A39372
R/Pak, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salikoff, L.
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A/Title: shal1, a subfamily of A-type K(+) channel cloned from mammalian brain.
A/Reference number: A39372; MUID:91239573; PMID:2034678
A/Accession: A39372
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-651 <PAK>
A/Cross-references: UNIPROT:Q03719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813
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```
Query Match 64.5%; Score 2141.5; DB 2; Length 651;
Best Local Similarity 65.7%; Pred. No. 8.2e-157;
Matches 434; Conservative 76; Mismatches 116; Indels 35; Gaps 13;
```

```
Qy 1 MAGVAAMLFPARAALIGMMPVANCMPMLAPADKNKRQDELIVLVNSGRRFQTRTTLER 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MAGVAATWLPFARAALVGMPLAQQLPPAPEVKASRGDEVLVVNSGRRFETWKNITLDR 60
Qy 61 YPDTLLGSTEKEFFENEDTKYFFDRDPEVFRVCVLANFYRTGKLHYPRYECISAYDEELAF 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YPDTLLGSSSEKFEFFYDAESGEFFDRDPEMFRHVLNFRYRTGRLHCPQECIOAFDEELAF 120
Qy 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSL----SFRQTMWRAFENP 176
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 YGILPELVGDCCLLEERYDRKRENAERLAEDEAEQAGEG--PALPAGSSLRQRLWRAFENP 179
Qy 177 HTSTLALVFYVYTGFFIAVSVITNVEVETPCGTVP--GSKELPCGERYSVAFFCLDTACV 234
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HTSTALVFYVYTGFFIAVSVIANVETIPCRGTPRMWPSKQSCGDRPFTAFRCMDTACV 239
Qy 235 MIFTEYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERV 294
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 LIFTEGYLLRLFAAPSRIRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVERV 299
```

```
Qy 295 FRIFKFSRHSOGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASAKFTSIPAS 354
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 FRIFKFSRHSOGRLILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSTKINFTSI 359
Qy 355 PASFWYTIIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPVIYSNFSRIYHQNQ 414
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 PASFWYTIIVMTTLGYGDMVPSTIAGKIFGSIICSLSGVLVIALPVPVIYSNFSRIYHQNQ 419
Qy 415 RADKRRARQKARLARIRVAKTGSSNAYLHSCRNGLNLEALDELGTPEEEMH-GKTTSLIE 473
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 RADKRRARQKARLARIRVAKTGSSNAYLHSCRNGLNLEALDELGTPEEEMH-GKTTSLIE 475
Qy 474 SGHHHLHLCLEKTNHEFIDEQMFECNCESSMONTPTSPSLSSHP-----GLTTTCCS 529
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 476 QGHHHLHLCLEKTNHEFIDEQMFECNCESSMONTPTSPSLSSHP-----GLTTTCCS 534
Qy 530 RR-SKKTTHLPSNLPATRLRSMQELSTIHQSGEQPSLTTSRSSLNKADGLRNCKT 588
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 535 RRVNRRARIRLANSTVASVR-GSMQELDT--LAGLRSPAPQTRSSLNKADGLRNCKT 591
Qy 589 SQITTAISIPTPALTPEGESRPPASPG-----PNTNI-----PSITSNVVKSV 635
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 592 RQFVAALISIPTPALTPED--EQSSPSGGSGGCTPTNTTLRNSSLGTPCLLPETVAISS 650
Qy 636 L 636
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 651 L 651
```

RESULT 3

```
A35312
potassium channel protein Shal2 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C/Accession: A35312; S12747
R/Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salikoff, L.
Science 248, 599-603, 1990
A/Title: K+ current diversity is produced by an extended gene family conserved in Drosophila.
A/Reference number: A35312; MUID:90239553; PMID:2333511
A/Accession: S12747
```

```
A/Molecule type: mRNA
A/Residues: 1-490 <WEI>
A/Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-490 <WEI>
A/Cross-references: EMBL:M32660; NID:g158456; PID:g158457
A/Genetics:
A/Gene: shal2
A/Cross-references: FlyBase:FBgn0005564
C/Superfamily: potassium channel protein drk1
C/Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein
```

```
Query Match 57.7%; Score 1915.5; DB 2; Length 490;
Best Local Similarity 73.6%; Pred. No. 1.4e-139;
Matches 360; Conservative 61; Mismatches 63; Indels 5; Gaps 4;
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```
Qy 3 AGVAAMLFPARAALIGMMPVANCMPMLAPADKNKRQ--DELIIVLVNSGRRFQTRTTLER 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ASVAAMLFPARAALIGMMPVATATHPLPPMPKORRKTDEKLLIVNSGRRFETWKNITLDR 61
Qy 61 YPDTLLGSTEKEFFENEDTKYFFDRDPEVFRVCVLANFYRTGKLHYPRYECISAYDEELAF 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 YPDTLLGSGNEREFYDEDECKEYFFDRDPEIFRHLINLYRTGKLHYPKHECLTSYDEELAF 121
Qy 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOESMPSL--SFRQTMWRAFENPHTS 179
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 FGIMPDVIGDCCYEDYDRKRENAERLMDNDKJSENGDQNLQQLTNMRQKMWRAFENPHTS 181
```

Qy	180	TLALVFYVVTGFFIAVSVINNVETVPCGTVBG-SKELPCGGERISVAFCLDICTACVMIFT	238
Db	182	TSALVFYVVTGFFIAVSVMANVETVPCGHRGRAGITLPCGERIKIVFCLDICTACVMIFT	241
Qy	239	VEYLLRLFEAAPSRYSRIFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRYRIF	298
Db	242	AEYLLRLFEAAPDRCKEFSRVMSIIDVVAIMPYYIGLITDNDVSGAFVTLRVFRYRIF	301
Qy	299	KFSRHSOGLRIILGYTLKSCASELGFLLSLTMAIIIPATVMFVAEKSSASKFTSIPASF	358
Db	302	KFSRHSOGLRIILGYTLKSCASELGFVFLSLMAIIIPATVMFVAEKVNNGTNFTSIPAAF	361
Qy	359	WYTIIVMTTLGYGDMVPKTIAGKIFGSIISGLVLIATLPVPVIVSNFSRIYHONORADK	418
Db	362	WYTIIVMTTLGYGDMVPETIAGKIVGVCISLGLVLIATLPVPVIVSNFSRIYHONORADK	421
Qy	419	RRÄQKARLARIRVAKTGGSSNAYLHRSKRNGLNEALBELTGPBEEHMGKTSLSIQHHH	478
Db	422	RKAQQRKARLARIRIAKASSGAFAVSKKAAEARWAAQESGIELDNN-RDEDIFELQHHH	480
Qy	479	LLHCLEKTT 487	
Db	481	LIRCLEKTT 489	

RESULT 4

157681
potassium channel protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000
C:Accession: 157681
R:Rudy, B.; Kentros, C.; Vega-Saenz de Miera, E.C.
Mol. Cell. Neurosci. 2, 89-102, 1991
A:Title: Families of potassium channel genes in mammals: Toward an understanding of the
A:Reference number: 157681
A:Accession: 157681
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: GB:M74898; NID:g205040; PIDN:AAA41468.1; PID:g205041
C:Superfamily: potassium channel protein drk1

Query Match 33.2%; Score 1103; DB 2; Length 236;
Best Local Similarity 93.2%; Pred. No. 1.9e-77;
Matches 219; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

OY 170 WRAFENHTSTLALVFYYVTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCL 229
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
DB 1 WRAFENHTSTLALVFYYVTGFFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFFCL 60
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
OY 230 DTACVMIFTVESYLRLFAAPSRYRPIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTL 289
| | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
DB 61 DTACVMIFTVESYLRLFQHPAGYRPIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTL 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 290 RVFRVFRIFKFSRHSQGLRLGLYTLKSCASELGFLLPSLTMAIIIFATWIFYAEKSSAS 349
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 RVFRVFRIFKFSRHSQGLRLGLYTLKSCASELGFLLPSLTMAIIIFATWIFYAEKSSAS 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 350 KFTSIPASFMYITVTMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVVS 404
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 KFTSIPASFMYITVTMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVVS 235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5

JH0595
potassium channel protein cdrk - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 20-Aug-1999
C:Accession: JH0595
R:Hiwang, P.M.; Glatz, C.E.; Brecht, D.S.; Yellen, G.; Snyder, S.H.
Neuron 8, 473-481, 1992
A:Title: A novel K+ channel with unique localizations in mammalian brain: molecular cloning
A:Reference number: JH0595; MUID:92198655; PMID:1550672

A:Accession: UH0595
A:Molecule type: mRNA
A:Residues: 1-802 <HMA>
A:Cross-references: GB:M77482; NID:G203395; P1DN:AAA40905.1; PID:G203396
A:Experimental source: circuvallate papillae
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; phosphoprotein; transmembrane protein
F:191-212/Domain: transmembrane #status predicted <TM1>
F:233-554/Domain: transmembrane #status predicted <TM2>
F:265-286/Domain: transmembrane #status predicted <TM3>
F:299-320/Domain: transmembrane #status predicted <TM4>
F:335-356/Domain: transmembrane #status predicted <TM5>
F:397-418/Domain: transmembrane #status predicted <TM6>
F:187,287,419,446/Binding site: carboxylate (Asn) #covalent #status predicted
F:448,500/Binding site: phosphate (Ser) #covalent #status predicted

Query Match	23.2%;	Score 770;	DB 2;	Length 802;
Best Local Similarity	29.9%;	Pred. No. 4,6e-51;		
Matches 212;	Conservative 116;	Mismatches 256;	Indels 126;	Gaps 24;
Qy	27 MPLAPAD--KNKRQDELIVLNVSGRRFQT-WRTTLERYPDTLG-----STEKEFP----	74		
Db	20 LPPEEVDIIRSKTCSRKRVKINVGNHLEVMWR-TLDRLPRTRLGKLRDNCNTHESLLEVC	78		
Qy	75 -FNEDTKEYFPDRDPEVFRCVLNFYRTGKLHYPREYCISAYDELAFGILPEITGDCCY	133		
Db	79 DYNLENEYFFDRHFGCAFTSLINFYRTGKLHMEEMCALSPGQELDYWGIDEIYLESCCQ	138		
Qy	134 EEEYDKR-----RENAERLMDNDNSENNOESMPSLSRQTMWRAFENHTSTLALVFY	186		
Db	139 ARYHQKEQNMNELRREAETWRDGEGBFDNTCCPEK--RKKLMDLLEKNSSVAKILA	196		
Qy	187 YVTGFPFIASVITTNVETVPCGTVPGSKELPCGERY-----SVAFFCLDTACWMIPTVEY	241		
Db	197 IVSLIFIVLSTIALSLNTLP-----ELQENDEFQGPSDNKRKLAVEAVCIAMFTMEY	248		
Qy	242 LLRLFAAPSKRYRFRISVMSITDVVALMPYITGLVMTN-----EDVSGAFVTLRAVFRV	294		
Db	249 LLRLFLSSPNMKKFFKGPLNVLDLALIPYVITFLTESNKSVLQFQNVRRVVQIPRIMRI	308		
Qy	295 FRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWMEFYAEKSSASAKFTSI	354		
Db	309 LRILKLARHSTGLQSLGFTLRRSYNELGLLILFLAMGIMIFSSLVFFAEKDEDATKFTSI	368		
Qy	355 PASFWYITVMTTLGYGDMVPEKTIAGKIFGSIICSLSGVLVIALPVPVIVSNFSRIYHQNQ	414		
Db	369 PASFWMATITMTTGVGDIYPKTLGKIWGLCCIAGVLVIALPIPIVNNFSEFYKEQK	428		
Qy	415 RADK---RRAQKAR-----LARIRVAKTGSS-----NAYLH	443		
Db	429 ROEKAIKRRALERAKRNGSTIVSMNLKDAFARSMELIDVAVEKAGESANIKOSVDNHL	488		
Qy	444 SKRNGLLNEAL-----ELGTPEEHMGKTTSLIESQHHLHLCLF-----	484		
Db	489 PSRWKARKALSETSNKSYENKYEVSQKDSHEQLNNTSS--SSQHLASAQKLEMLYNE	546		
Qy	485 --KTTNHE-----FIDE-QMFEONCMESSM--ONYPSSTRSPSLSHPG	523		
Db	547 ITKTQTHSHNPDCQEQPERPSAYEEIEEMEYVCPQEQOLAVAQTEVIVDMKSTSIDSF	606		
Qy	524 TTTCSSRSRKKTHLPNSNLPATRLASMOELSTIHIOGSEQPSLTSRSNLNKKADGGLR	583		
Db	607 TS--CATDFETERSP--LPPSASHLQMKPPTDLPQMDHGHQVRAPRFLTLSRDKG--	659		
Qy	584 PNCKTSQITTAIISIPTP-PALTPEGESRPPASPGPNTNIPSTSNVVK	632		
Db	660 PAARBAALDYAPIDITVNLNLAGASHGDLQPSASDSFKSLKG--SNPLK	707		

RESULT 6
S31761
potassium channel protein DRK1 - human
C;Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31761
R:Albrecht, B.; Lorra, C.; Stocker, K.; Pongs, O.
submitted to the EMBL Data Library, September 1992
A:Description: Cloning, expression and chromosomal localization of the delayed rectifier
A:Reference number: S31761
A:Accession: S31761
A:Molecule type: DNA
A:Residues: 1-858 <ALB>
A:Cross-references: UNIPROT:Q14721; EMBL:X68302; NID:g30892; PIDN:CAA48374.1; PID:g30893
C:Genetics:
A:Gene: GDB:KCNB1, KV2.1, DRK1
A:Cross-references: GDB:128081; OMIM:600397
A:Map position: 20q13.2-20q13.2
C:Superfamily: potassium channel protein drk1

Query Match	22.6%;	Score 750;	DB 2;	Length 858;
Best Local Similarity	29.2%;	Pred. No. 1.7e-49;		
Matches 189;	Conservative 114;	Mismatches 220;	Indels 124;	Gaps 18

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QY 27 MFLPAD--KMKRODELIVANVSGRRFQT-WRTTLERPDITLG-----STEKEFF----- 74
Db 16 LPPEPMEIVRSKACSRVRINVGLAHEVLMR-TLDRLPRTRLGKLRDCNTHDSLLEVCD 74
QY 75 -FNEDTKEXEYFDDRDEVEFRCVILNFYRGTKLHYPRYECISAYDELAIFYGLPELIGDCCY 133
Db 75 DYSLDDNNEYFFDRHPGAFSTILNFYRGTLHMMEMWCALSFSQGLDYGWIDYEIESCCQ 134
QY 134 EYKDKRGENAERLMDNDSENNOE-----SNPSTLSFRQTMWRAFNPHSTLALVIFYV 188
Db 135 ARYHOKKEQMEBELKREAEFTLREBEHEEPDNTCCAERKKLMDLLEKPNSSVAAKILAITI 194
QY 189 TGFFIAVSVITNVETVPCCGTVPGSXELPCGERYSVA----FFCLDIACVMIFIVEYLL 243
Db 195 SIMEFIVSTIALSINTLP-----ELQSLDEFGQSIDNPQLAHVEAVCIAMFTMEYLL 246
QY 244 RLEFAPSRYRFRIRMSIIDVVAIMPYIIGLVMTNN-----EDVSGAEVTLRVRVER 296
Db 247 RLLSSPKMKKFFKGPILNAIDLAILPYVTITFLTESNKSVLQFPQNVRAVQIFRIMRILR 306
QY 297 IFKFSRHSQGLRIGYTLKSCASBLGFLFSLTMAIIPATVMFVAEKSSASAKFTSIPA 356
Db 307 ILKLARHSTGLQSLGFTLRSYNELGILLFLAMGIMIFSSLVEFAEKEDBDTKFSIPA 366
QY 357 SEWYITVMTTLGYGDMVPKTIAGKIFGSICSLGVLVIALPVPVIVSNSRIVHONORA 416
Db 367 SFWWATITMTTVGYGDIYPKTLGKIVGGLCCIAGVLVIALPIIVNNSEFYKEQKRO 426
QY 417 DKRRAQKARLARIRVAKTSSNAYLHRSKRNGL-----NEALELTGTPEEBH 464
Db 427 EKAIKRREA-LER-----AKRNGSIVSNMMDKDAFARSIEMMDIVENKNGEN 471
QY 465 MCKTTSLESQHHLHLHCKEKTNNHEFIDEQMFQONCMESSMOWNPSTRBPSLSHPGLT 524
Db 472 MGKDKDV---QDNHLSPNKMKWTKRTL--SETSSSKSPETKEQSSPEK----- 514
QY 525 TTCCSRASKKTTHLPNSNLBPATRLRSMOELSTIHIOGSEQPSLTTSRSSINLKADDELAR 584
Db 515 ----ARSSSSPQHL-----NVQOLEDMYNMMAKTQOPIILNTKESAQSKPKREL-- 560
QY 585 NCKTSQITTAIISIPTPALTPEGESRPPPAAPGPNINIPITSNNV 631
Db 561 -----EMESIPSPVAP-----LPRTREGVI 580

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RESULT 7
S00480
potassium channel protein A (clone Sh-beta) - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
C/Accession: S00480, S01111
R/Pong, O.; Keckemethy, N.; Mueller, R.; Krah-jentgens, I.; Baumann, A.; Kiltz, H.H.,
EMBO J. 7, 1087-1096, 1988

A,Title: Shaker encodes a family of putative potassium channel proteins in the nervous system
A,Reference number: S00479; MUID:88296413; PMID:2456921
A,Accession: S00480
A,Molecule type: DNA
A,Residues: 1-643 <PON>
A,Cross-references: EMBL:X07132; NID:g8602; PBDN:CAA30144.1; PID:g8603
A,Note: the clone is designated as Sh-beta
R,Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1988
A,Title: Multiple potassium-channel components are produced by alternative splicing at the Shaker locus
A,Reference number: S00508; MUID:88122563; PMID:2448635
A,Accession: S01111
A,Molecule type: mRNA
A,Residues: 1-643 <SCH>
A,Note: the clone is designated as ShD1
R,Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 332, 740, 1988
A,Reference number: S01113
A,Contents: annotation; erratum
C,Genetics:
A,Gene: Shaker
A,Cross-references: FlyBase:FBgn0003380
C,Superfamily: potassium channel protein drk1
C,Keywords: alternative splicing; transmembrane protein

Query Match	22.2%;	Score 736.5;	DB 2;	Length 643;
Best Local Similarity	31.7%;	Pred. No. 1.3e-48;		
Matches 181;	Conservative 106;	Mismatches 171;	Indels 113;	Gaps 14;

[illegible]

RESULT 8
CHRTD1
potassium channel protein drkl - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S05448; A44838
R:Frech, G.C.; Vandongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A:Title: A novel potassium channel with delayed rectifier properties isolated from rat b
A:Reference number: S05448; MUID:89365157; PMID:2770868
A:Accession: S05448
A:Molecule type: mRNA
A:Residues: 1-853 <PRE>
A:Cross-references: UNIPROT:P15387; EMBL:X16476; NID:g57785; PIDN:CAA34497.1; PID:g57786
A>Note: it is uncertain whether Met-1 or Met-17 is the initiator
R:Frech, G.C.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A:Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from diff
A:Reference number: A44838; MUID:92156897; PMID:1740690
A:Accession: A44838
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MPAG', 1-571 <DRE>
A:Cross-references: GB:M81783; NID:g205038
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:81768)
C:Genetics:
A:Gene: drkl
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane
F:1-182/Domain: intracellular #status predicted <INT1>
F:183-204/Domain: transmembrane #status predicted <TM1>
F:225-245/Domain: transmembrane #status predicted <TM2>
F:256-276/Domain: transmembrane #status predicted <TM3>
F:291-312/Domain: transmembrane #status predicted <TM4>
F:327-348/Domain: transmembrane #status predicted <TM5>
F:389-410/Domain: transmembrane #status predicted <TM6>
F:411-853/Domain: intracellular #status predicted <INT2>
F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.2%; Score 736.5; DB 1; Length 853;
Best Local Similarity 26.7%; Pred. No. 1.9e-48;
Matches 201; Conservative 130; Mismatches 242; Indels 179; Gaps 21;

QY 27 MPLPAD--KXKQDELIVLVNSGRFQT-WRTTLERYPTLLG----STEKEF---- 74
DB 12 LPPEMEIVRSACSRKRLNVGLAHEVLMR-TLDRIPRTRLGRDCNTHDSLQVCD 70
QY 75 -FNEBDTKEYFFRDPEVRCVNFRTGKLHYPRYECISAYDEDLAFYGLPELIGDCCY 133
DB 71 DYSLEDNEYFDRHGAFTSIINFYRTGRLLHMEEMCALSFSGLEDYWGDEIYLESQQ 130
QY 134 EEEKDRKRENAERLMDNDSENNOE-----SMPSLFRQTMRAFENPHTSTLALVFYV 188
DB 131 ARYHQKKEQNMNELKREAEFTLREHGEFPDNTCAERKKLWDLLEKPNSSVAAKIIAII 190
QY 189 TGFPIAVSVITNVVEVPCGTVPCKELPCGERYSVA-----FFCLDTACVMIFVEYLL 243
DB 191 SIMFVLSTIALSLNTLP-----ELQSLDFGQSTDNPOLAHEAVNCIAFMTEYLL 242
QY 244 RLFAAPSRVRFIRSVMSIIDVVAIMPYIGLVMTNN-----EDVSGAFVTLRVFRVFR 296
DB 243 RFLSSPKWKKEFFKGLNAILDLALIPYVTFILTESNKSVLQPCQNVRRVQIFRIMRLR 302
QY 297 IFRSRHSQGRILGYTKSCASELGLFLSLTMAIIIPATWFEYAEKSSASKFTSIPA 356
DB 303 ILKLARHSTGLSLGFTLRSYNELGLLLEFLAMGIMIFSSLVFAEKDBDTRKSIPIA 362
QY 357 SFWYTIIVMTTGLYGDWVPKTIAGKIFGSLCSLSGLVIALPVVIVSNFSRIYHQNORA 416
DB 363 SFWMATITMTVGYGDYKPTLKGIVGGLCCIAGVYIALPIPIIVNPFSEFYKQKRQ 422
QY 417 DKRRQKKARLARIRVAATGSSNAVILSKRNGLL-----NEALELTGTPEEHMGK 467
DB 423 EKATKRREA-LER-----AKRNGSIVSNMMDKAFARSITEMMDIVVERNGES 467

QY 468 TSLIESQHHL-----LHCLEKTNHEFID--EQMEQNCMESSQNYPS----- 511
DB 468 IAKDKVQDNHLSPNKWKTKRALSETSSSKSFETKQGSPEKARSSSSPQHNVQLLED 527
QY 512 --TRSPSLSHBGLTTCCSRRSKKTTHLPNSNLP-----TRLSMOELSTI 557
DB 528 MYSKAAKTQSQPIINTKEMAPQSKRPEELENSMPSVAPLPARTGVIDMRSMSSIDSF 587
QY 558 HIQSGEOPSLT-----TSRSSLNLRKADDGLRPNC----- 586
DB 588 ISCATPFPEATFHSPLASLSKAGSSTAEVGRGALGAGGRLTETNPPIETRSRGF 647
QY 587 -----KTSQITTAISI-----PTP----- 601
DB 648 FVESPRSSMKTNNPLKLRALKVNFVEGDPTEPLPSIGLYHDPILRNRGAAAVAGLECAS 707
QY 602 ---PALTPE-----GESRPPPASPGPNTNI 623
DB 708 LDKPVLSPSSITYTASARTPPRSPEKHTAI 739

RESULT 9

JH0166

potassium voltage-gated channel - rat

N:Alternate names: potassium channel KV1; potassium channel Rk4; shaker-related potassium

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C:Accession: JH0166; D39113; I55392
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; LunNeuron 4, 929-939, 1990
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectifA:Reference number: JH0166; MUID:90297965; PMID:2361015
A:Accession: JH0166A:Molecule type: mRNA
A:Residues: 1-602 <SWA>

A:Cross-references: UNIPROT:P19024; GB:M27158; NID:g205100; PIDN:AAA41498.1; PID:g205101

R:Roberds, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
A:Reference number: A39113; MUID:91156694; PMID:1705709A:Accession: D39113
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual traA:Molecule type: mRNA
A:Residues: 1-552, 'S', 554-602 <ROB>R:Mori, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
J. Biol. Chem. 268, 26482-26493, 1993A:Title: The transcription of a mammalian voltage-gated potassium channel is regulated by
A:Reference number: I55392; MUID:94075338; PMID:8253777A:Accession: I55392
A:Status: translated from GB/EMBL/DBJA:Molecule type: DNA
A:Residues: 1-15 <RES>A:Cross-references: GB:L23434; NID:g443766; PIDN:AAA42337.1; PID:g443767
A:Experimental source: Sprague-DawleyC:Genetics:
A:Gene: KV1.5C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt.F:242-260/Domain: transmembrane #status predicted <TM1>
F:316-336/Domain: transmembrane #status predicted <TM2>
F:347-368/Domain: transmembrane #status predicted <TM3>
F:387-408/Domain: transmembrane #status predicted <TM4>
F:423-444/Domain: transmembrane #status predicted <TM5>
F:484-505/Domain: transmembrane #status predicted <TM6>
F:10,44,116,181,290/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:81,535,546,569/Binding site: phosphate (Ser) (covalent) #status predictedQuery Match 22.2%; Score 736; DB 2; Length 602;
Best Local Similarity 34.0%; Pred. No. 1.3e-48;

Matches 177; Conservative 90; Mismatches 162; Indels 92; Gaps 11;

QY 30 APADKXKQDELIVLVNSGRFQWRTTLERYPTLLGSTEKEF-FNEBDTKEYFFDRDP 88

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Db      101 APODAGSLHQRVLINISGLAFETQLGAFPTLLGDPAKRLAHFDPLRNEYFPDNR 160
      89 EFERCVLNEVRT-GKLAHYPRYECISAYDDELAFAFGILPEIIGDCCYEYKDRKRENAERL 147
      161 PSFDGILYYQSGGRLRPVNVSLDVFADEIRFYQ-----LGDEAMERFRE----- 206
      148 MDDNDSENNQESMPSLSFRQTMKRAFENPHTSTALVFYVYTGFFIAVSVITNVEYTP- 206
      207 -DEGFIKEEKRLPRNEFORQWLIFFEPBSSGSARAIATVSVLILISITFCLETPBE 265
      207 -----CGTVPGSKE-----LPCGERYSVAFFCLDTACV 234
      266 FRDERELRHPPVPQPPAPAPADGINGSVSGALSGPTVAPLLP--RTLADPPFIVETTCV 323
      235 MITVEYLRLFAPSRRYRFRISVMSIIDVVAIMEYIIGLVMTNEDVSGA----- 285
      324 IWTFFELVRFACPSKAEFSKNIMIIDVAIFPYFITLGTLEAEQPGGGGONGQOAM 383
      286 ----FVTLRVRFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAITFATVMEY 341
      384 SLAILRVIRLVRFRIFKLSRSKSLQLIGTKLQASMBRELGLLIFLFGVILFFSSAVYF 443
      342 AEKSSASKFTSIPASFWYITVMTTGLGYDMVPKTIAGKIFGSGISLGVLYALPVPV 401
      444 AEADNHGSHSPSIDPAFWMAVVTMTTVGCDMRPIVGGKIVGSLCAIAGVLTIALPVPV 503
      402 IVSNFSRIYH-----ONQADKRR-----AQKKARLARIRVAKTSSNAYH 443
      504 IVSNFNYFTHRETDHEGQALKEQNGRRESGLDTGGRVYSCSKASFCKTGSLESSD 563
      444 SKRNGLLNEALELGTPEEHNKGTSLIESQHHLHGLE 484
      564 SIRRG-----SCPLEKCHLKAKSNVDLRSLYALCLD 595

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RESULT 10

JH0193

potassium channel shaker form epsilon - fruit fly (Drosophila melanogaster)

N;Alternate names: potassium channel protein A

C;Species: Drosophila melanogaster

C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004

C;Accession: JH0193; S00508; S01110; S00479; S00482; S02822; S01674

R;Kamb, A.; Tseng-Crank, J.; Tanouye, M.A.

Neuron 1, 421-430, 1988

A;Title: Multiple products of the Drosophila Shaker gene may contribute to potassium cha

A;Reference number: JH0193; MUID:9016523; PMID:3272175

A;Accession: JH0193

A;Molecule type: mRNA

A;Residues: 1-656 <KAM>

A;Cross-references: UNIPROT:P08510

A;Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in the putative G pro

R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.

Nature 331, 137-142, 1988

A;Title: Multiple potassium-channel components are produced by alternative splicing at c

A;Reference number: S00508; MUID:88122563; PMID:2448635

A;Accession: S00508

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-512,514-564,'Q',565-583,'HV',586-656 <SCH>

A;Cross-references: GB:X06742; NID:g288441; PIDN:CAA2917.1; PID:g288442

A;Accession: S01110

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 'MOMT',57,'VAG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-

, 'QL',577-579,'LQ',582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS', 'TNS'

R;Pongs, O.; Kecskemeti, N.; Mueller, R.; Krah-Dentgens, I.; Baumann, A.; Kiltz, H.H.;

EMBO J. 7, 1087-1096, 1988

A;Title: Shaker encodes a family of putative potassium channel proteins in the nervous s

A;Reference number: S00479; MUID:88296413; PMID:2456921

A;Accession: S00479

A;Molecule type: DNA

A;Residues: 1-452,'F',454-462,'V',464-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51

,582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS', 'TNS',640,'QL',643-647,'
A;Cross-references: EMBL:X07131
A;Accession: S00482
A;Molecule type: DNA
A;Residues: 1-348,'V' <PO2>
A;Cross-references: EMBL:X07134; NID:g8606; PIDN:CAA30146.1; PID:g8607
R;Pongs, O.
submitted to the EMBL Data Library, March 1988
A;Reference number: S02822
A;Accession: S02822
A;Molecule type: mRNA
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
,582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS', 'TNS',640,'QL',643-647,
A;Cross-references: EMBL:X07131; NID:g8600; PID:g8601
R;Tempel, B.L.; Papazian, D.M.; Schwarz, T.L.; Jan, Y.N.; Jan, L.Y.
Science 237, 770-775, 1987
A;Title: Sequence of a probable potassium channel component encoded at Shaker locus of D
A;Reference number: S01674; MUID:87292096; PMID:2441471
A;Accession: S01674

A;Molecule type: mRNA
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
,582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS', 'TNS',640,'QL',643-647,
A;Cross-references: EMBL:M17211; NID:g157063; PIDN:AAA28417.1; PID:g157064
A;Note: 360-Met and 464-Ile were also found
C;Comment: This protein is a component of a fast, transient, voltage-dependent, or A-type
C;Genetics:
A;Gene: shaker
A;Cross-references: FlyBase:FBgn0003380
A;Intons: 61/2; 102/3; 159/1; 191/2; 256/3; 297/2; 348/3; 406/1; 449/2; 514/1
C;Superfamily: potassium channel protein drkl
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; potassium channel; trans
F;228-246/Domain: transmembrane #status predicted <TM1>
F;279-300/Domain: transmembrane #status predicted <TM2>
F;311-332/Domain: transmembrane #status predicted <TM3>
F;358-382/Domain: S4-like region #status predicted <S4L>
F;396-417/Domain: transmembrane #status predicted <TM4>
F;432-453/Domain: transmembrane #status predicted <TM5>
F;457-478/Domain: transmembrane #status predicted <TM6>
F;102,259,263/Binding site: carboxylate (Asn) (covalent) #status predicted
F;521/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 22.2%; Score 736; DB 2; Length 656;
Best Local Similarity 31.6%; Pred. No. 1.4e-48;
Matches 181; Conservative 106; Mismatches 171; Indels 114; Gaps 14;

```

QY      40 ELIVLVNAGRRFQWRTTLERYPDTLIGSTKEF-FPNEDTKEYFPDRDPVFRVCLNIFY 98
      97 ERVIVNVGSLRFETQLRTLNQFPDTLLGDPAKRLRYFDPLRNEYFFDRSRPSFDALITYY 156
      99 RT-GKLAHYPRYECISAYDDELAFAFGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQ 157
      157 QGGGRLRRRVNVPDLVFSSEIKFYE-----LGDQAINKFRE-----DEGFIKEE 201
      202 RPLPDNEKQKRWLLFEYPSSQARVAIISVFILISIVICLETLPFFKHVYKVENTT 261
      158 ESNPSLSFQTMKRAFENPHTSTALVFYVYTGFFIAVSVITNVEYTP----- 206
      202 RPLPDNEKQKRWLLFEYPSSQARVAIISVFILISIVICLETLPFFKHVYKVENTT 261
      207 -CGTVPGSKELPCCGERYSVAFFCLDTACVMIFVEYLLRLFAPSRRYRFRISVMSIIDV 265
      262 TNGTKIEBEVP---DITDPFLIETLCIIMFTPELTVRFACPNKLNFCRVMNVII 318
      266 AIMPYIIGLV-----MTNNEVSGAFV-TLRVFRVRIFFKFSRH 303
      319 AIIPIYITLATVVAEEDTLNLPKAPVSPQDKSSNQAMSLAIRVIRLVRFRIFFKLSRH 378
      304 SGGIRIIGTYLTKSCASELGFLLFSLTMAIIFATVMFAEKGSSASKFTSIPASFWYITV 363
      379 SKLQIIGITLKASMBRELGLIIFLLFGVLLPSSAVYFPAEAGSENSFFKSIDAFWMAV 438
      364 TMTTILGYDMVPKTIAGKIFGSGISLGVLYALPVPVIVSNFSRIYHQNGADKRRQK 423
      439 TMTTVGYDMTPVGWGWKIVGSLCAIAGVLTIALPVPVIVSNFNYFHRETQDEMQSQN 498

```


Db 541 SQEILNTKEMAPQSQ--PQELKEMGMSNPSPVAPLPTRTGVIDMRSMSSIDSFISCATDF 598
QY 512 -----TRSP--SISSHPLGLTTT-----CCSRRSKKTTHLPNSN-----LPAT 546
Db 599 PEATRFSSHPLASISGKSGGSTAPEVGMRGALGASGGRIMETNPPEASRSRGFVHSPRS 658
QY 547 RLRS-----MOELSTIHIOGSEQPSLTTSRSSSLNLKADD-GLRPNCKTSQITTAISIPT 600
Db 659 SKMTHNPMKLKALKNFLLEGDPPLL-----PALGLYHDLPLNRGGARAAYAGLECASLDD 714
QY 601 PPALTPPE-----GESRPPASPSPGPNNTNI 623
Db 715 KPVLSPESSSIYTTASARTPPSPKHTAI 743

RESULT 13

66669
potassium channel (Kv1.5) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66669
R;Saaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A;Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit
A;Reference number: S66669; MUID:96032538; PMID:7556635
A;Accession: S66669
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-598 <SAS>
A;Cross-references: UNIPROT:P50638; EMBL:D45025; NID:g1060972; PIDN:BAA08082.1; PID:d100
C;Superfamily: potassium channel protein drkl

Query Match 21.7%; Score 719; DB 2; Length 598;
Best Local Similarity 35.0%; Pred. No. 2.6e-47;
Matches 166; Conservative 85; Mismatches 141; Indels 82; Gaps 9;

QY 42 IVLVNVSGRRTQTWRTLERYPTDILGSTKEF--FNEDEYKFFPDDPEVFCVLYNRYT 100
Db 106 VLINISGLRFTQLGLAQFPNTLLGDPKRLRYFDPLRNEYFFDNRPSFDGILYYQS 165
QY 101 -GKLYPRYECISAYDELAFFGILPEIIGDCCYEYKDKRENAERLMDNDSENNQES 159
Db 166 GGRLRFPVNSLDVFADERFYQ-----LGDEAMERFRE-----DEGFIKDEKRP 210
QY 160 MPSLSFRQTMWRAFENPHTSTLALVFYVYTGFFIYAVSVITNVEYVP----- 206
Db 211 LPRNEFORQVWLIFEYPBESSGSARAIAIVSVLILSIITFCLETLPPEKDERELLRHP 270
QY 207 -----CGTV--PGSKELPCGER--YSVAFCLDTACVMIPTVEYLLRPA 247
Db 271 VPHQPPAPALGANGSAGVAPASGSTVAPLLPRTLADPFIVETTCVIMFTFELLVRFPA 330
QY 248 APSRYRFRISVMSIIDVVAIMPYYIGLVMTNNEVSGA-----FVTLRFV 292
Db 331 CPSKAFFSRMNIIDIVAIFPYFITLGTLEAQPGGGGGQNGQAMSLAILRVIRLV 390
QY 293 RVFRIFKFSRHSQGLRILGYTLKSCASELGFLLSLTMAIIIPATWYAEKSSASAKFT 352
Db 391 RVFRIFKLSRHSKGLQILGKTLQASMRLEGLLIFLFIGVILFSSAVYFAEADNGTFPS 450
QY 353 SIPASFYITVTMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPVIVSNFSRIYHQ 412
Db 451 SIPDAFWAVVMTTIVGYGDMRPIVGGKIVGSLCAIAGVLTIALPVPVIVSNFYFHR 510
QY 413 NQRADKRA-----OKRLARIRVAKTGSSSNAYLHSGKNG 448
Db 511 ETDHEEQALKEEPGSGSGRTSLDAGGQRKASWSKASLCKAGGSLETADSVRG 564

RESULT 14
A49507
potassium channel Kv1.5 - mouse

C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A49507; B49507
R;Attali, B.; Lesage, F.; Ziliani, P.; Guillemaire, E.; Honore, E.; Waldmann, R.; Hugnot, J. Biol. Chem. 268, 24283-24289, 1993
A;Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 delayed rectifier K(+) c
A;Reference number: A49507; MUID:94043264; PMID:8226976
A;Accession: A49507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-602 <ATT>
A;Cross-references: UNIPROT:Q61762; GB:L22218; NID:g435603; PIDN:AAA39365.1; PID:g435604
A;Accession: B49507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 201-602 <AT2>
A;Cross-references: GB:L22218
C;Superfamily: potassium channel protein drkl
C;Keywords: alternative splicing

Query Match 21.7%; Score 719; DB 2; Length 602;
Best Local Similarity 34.3%; Pred. No. 2.6e-47;
Matches 176; Conservative 93; Mismatches 168; Indels 76; Gaps 12;

QY 30 APADKNKRODELIVLVNVSGRRTQTWRTLERYPTDILGSTKEF--FNEDEYKFFPDDP 88
Db 101 APQDSGLHHQRLVNLINISGLRFTQLDPLVQFPNNLLGDPVKRLRYFDPLRNEYFFDNR 160
QY 89 EVFRCVLYNRYT--GKLYPRYECISAYDELAFFGILPEIIGDCCYEYKDKRENAERL 147
Db 161 PSFDGILYYQSGGRLLRPVNSLDVFADERFYQ-----LGDEAMERFRE----- 206
QY 148 MDDNDSNNQESMPSLSFRQTMWRAFENPHTSTLALVFYVYTGFFIYAVSVITNVEYVP- 206
Db 207 -DEGFIKEEKRLPRNEFORQVWLIFEYPBESSGSARAIAIVSVLILSIITFCLETLP 265
QY 207 -----CGT--VPKELPCGERYSVA-----FCLDTACV 234
Db 266 FRVDELLHPVPPOPAPAPAGTNAAGSVLSSGT--TVAPLLPRTLADPFIVETTCV 323
QY 235 MIFVVEYLLRFAAPSRRYRFRISVMSIIDVVAIMPYYIGLVMTNNEVSGA----- 285
Db 324 IWTTELLVRFACPSKAFFSRMNIIDIVAIFPYFITLGTLEAQPGGGGGQNGQAM 383
QY 286 ----FVTLRVFRVRFIFKFSRHSQGLRILGYTLKSCASELGFLLSLTMAIIIPATWYF 341
Db 384 SLALRVIRLVRFVFRIFKLSRHSKGLQILGKTLQASMRLEGLLIFLFIGVILFSSAYF 443
QY 342 AEKGSASAKFTSIPASFYITVTMTTIGYDMVPKTIAGKIFGSIKSLGVLVIALPVPV 401
Db 444 AEADNQSQSLSIDPAFWAVVMTTIVGYGDMRPIVGGKIVGSLCAIAGVLTIALPVPV 503
QY 402 IVSNFSRIYHONQRADKRAQKRLARIRVA-----KTGSSNAYLHSGKNGLL--N 451
Db 504 IVSNFNYFYHRETDHEEQALKEEKGIOQRRESGLDTGGQRKVSCKASFSH-KTGGPLEST 562
QY 452 EALDELGTPEEHMGKTTSLIESQHHLHLCB 484
Db 563 DSIRGSCPLEKCHLKAKSNVDLRRSLVALCLD 595

RESULT 15
A43531
potassium channel Kv1.3 - rat
N;Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel RCK5
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 09-Jul-2004
C;Accession: A43531; JH0168; S06708
R;Douglas, J.; Osborne, P.B.; Cai, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P.
J. Immunol. 144, 4841-4850, 1990
A;Title: Characterization and functional expression of a rat genomic DNA clone encoding
A;Reference number: A43531; MUID:90278098; PMID:2351830
A;Accession: A43531

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:33:59 ; Search time 595.111 Seconds
(without alignments)
547.263 Million cell updates/sec

Title: US-10-062-879-4
Perfect score: 3320
Sequence: 1 MAAGVAAWLPFAPRAAIGWM.....PGPNTNIPSITSNVKSVL 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	3295.5	99.3	655	1 KCD3_HUMAN	Q9UK17 homo sapien
2	3288.5	99.1	655	1 KCD3_RAT	Q62897 rattus norv
3	3278.5	98.8	655	1 KCD3_MOUSE	Q920V1 mus musculu
4	3269.5	98.5	655	1 KCD3_RABIT	Q9TET5 oryctolagus
5	3266.5	98.4	655	2 Q8WN02	Q8WN02 mustela put
6	3126	94.2	658	2 Q9PTD3	Q9PTD3 gallus gall
7	2843.5	85.6	659	2 Q57662	Q57662 xenopus lae
8	2590	78.0	638	2 Q7ZW36	Q7ZW36 brachydantio
9	2530	76.2	630	2 Q8HYZ1	Q8HYZ1 mustela put
10	2524	76.0	630	1 KCD2_RABIT	P59955 oryctolagus
11	2523	76.0	630	1 KCD2_MOUSE	Q920V2 mus musculu
12	2519	75.9	630	1 KCD2_RAT	Q93881 rattus norv
13	2518	75.8	630	1 KCD2_HUMAN	Q9NZV8 homo sapien
14	2517	75.8	632	2 Q8UW33	Q8UW33 gallus gall
15	2141.5	64.5	651	1 KCD1_MOUSE	Q03719 mus musculu
16	2132.5	64.2	647	1 KCD1_HUMAN	Q9N8A2 homo sapien
17	2032.5	61.2	660	2 Q95PC8	Q95PC8 panulirus i
18	2026.5	61.0	660	2 Q95PC7	Q95PC7 panulirus i
19	2023.5	60.9	680	2 Q95PC6	Q95PC6 panulirus i
20	1986.5	59.8	579	2 Q95PC5	Q95PC5 panulirus i
21	1984.5	59.8	585	2 Q95PC4	Q95PC4 panulirus i
22	1981	59.7	546	2 Q26040	Q26040 panulirus i
23	1981	59.7	551	2 Q95PD0	Q95PD0 panulirus i
24	1966	59.2	561	2 Q95PC9	Q95PC9 panulirus i
25	1954.5	58.9	608	2 Q95PC3	Q95PC3 panulirus i
26	1915.5	57.7	490	2 C1KL_DROME	P17971 drosophila
27	1908.5	57.5	490	2 Q7Q1S7	Q7Q1S7 anopheles g
28	1905	57.4	800	2 Q6R4N6	Q6R4N6 ciona intes
29	1859.5	56.0	633	2 Q8IAD3	Q8IAD3 halocynthia
30	1786	53.8	471	2 Q8IAD2	Q8IAD2 halocynthia
31	1770	53.3	609	2 Q95XD1	Q95XD1 caenorhabdi

32	1654.5	49.8	372	2 Q75LS7	Q75LS7 homo sapien
33	1328.5	40.0	478	2 P91784	P91784 polyorchis
34	1103	33.2	236	2 Q619B6	Q619B6 rattus norv
35	837	25.2	409	2 P91783	P91783 polyorchis
36	770	23.2	907	1 KCB2_RAT	Q63099 rattus norv
37	768	23.1	911	2 Q7Z7D0	Q7Z7D0 homo sapien
38	767.5	23.1	908	2 Q18476	Q18476 loligo peal
39	766	23.1	898	2 Q91592	Q91592 xenopus lae
40	766	23.1	911	1 KCB2_HUMAN	Q92953 homo sapien
41	758	22.8	985	1 C1KB_DROME	P17970 drosophila
42	756	22.8	911	1 KCB2_RABIT	Q95111 oryctolagus
43	754.5	22.7	816	2 Q98SV4	Q98SV4 ictalurus p
44	750.5	22.6	876	2 Q91593	Q91593 xenopus lae
45	750	22.6	858	1 KCB1_HUMAN	Q14721 homo sapien

ALIGNMENTS

RESULT 1
KCD3_HUMAN STANDARD; PRT; 655 AA.
AC Q9UK17; O60576; O60577; Q9UH85; Q9UH86; Q9UK16;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
GN Name=KCND3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND
RP FUNCTION.
RC TISSUE=Heart;
RX MEDLINE=99061682; PubMed=9843794;
RA Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.;
RT "Isolation and characterization of the human gene encoding Ito;
RT further diversity by alternative mRNA splicing.";
RL Am. J. Physiol. 275:H1963-H1970(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Brain, and Heart;
RX MEDLINE=99218223; PubMed=10200233;
RA Dilks D., Ling H.-P., Cockett M., Sokol P., Numann R.;
RT "Cloning and expression of the human Kv4.3 potassium channel.";
RL J. Neurophysiol. 81:1974-1977(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Calmels T.P.G., Faivre J.-F., Javre J.-L., Cheval B., Rouanet S.,
RA Bril A.;
RT "Long and short human isoforms of the Kv4.3 channel: cloning,
RT expression, electrophysiology, pharmacology and phosphorylation by
RT protein kinase C.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain cortex;
RX MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;
RA Isbrandt D., Leichter T., Waldschuetz R., Zhu X.-R., Luhmann U.,
RA Michel U., Sauter K., Pongs O.;
RT "Gene structures and expression profiles of three human KCND (Kv4)
RT potassium channels mediating A-type currents I(TO) and I(SA).";
RL Genomics 64:144-154(2000).
RN [5]
RP INTERACTION WITH KCNIP2; KCNE1; KCNE2; SCN1B AND KCNA1.
RX MEDLINE=22233757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9;
RA Deschenes I., Tomaselli G.F.;
RT "Modulation of Kv4.3 current by accessory subunits.";

RL FEBS Lett. 528:183-188(2002).
CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4 (by similarity). Interacts with KCNE1, KCNE2, SCN1B and
CC KCNB1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=KCNB3L, Long;
CC IsoId=Q9UK17-1; Sequence=Displayed;
CC Name=2; Synonyms=KCNB3S, Short;
CC IsoId=Q9UK17-2; Sequence=VSP_008826;
CC -1- TISSUE SPECIFICITY: Highly expressed in heart and brain, in
CC particular in cortex, cerebellum, amygdala and caudate nucleus.
CC Detected at lower levels in liver, skeletal muscle, kidney and
CC pancreas. Isoform 1 predominates in most tissues. Isoform 1 and
CC isoform 2 are detected at similar levels in brain, skeletal muscle
CC and pancreas.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL, AF048712, AAC05121.1, -, -
DR EMBL, AF048713, AAC05122.1, -, -
DR EMBL, AF187963, AAF01044.1, -, -
DR EMBL, AF187964, AAF01045.1, -, -
DR EMBL, AF205856, AAF20924.1, -, -
DR EMBL, AF205857, AAF20925.1, -, -
DR EMBL, AF120491, AAD38898.1, -, -
DR EMBL, AF166011, AAF68177.1, -, -
DR EMBL, AF166009, AAF68177.1, JOINED.
DR EMBL, AF166010, AAF68177.1, JOINED.
DR EMBL, AF166011, AAF68178.1, -, -
DR EMBL, AF166009, AAF68178.1, JOINED.
DR EMBL, AF166010, AAF68178.1, JOINED.
DR HSSP, Q16968, 1A68.
DR Genew, HGNC:6239, KCND3.
DR MIM, 605411, -
DR InterPro, IPR005821, Ion trans.
DR InterPro, IPR001622, K+channel_pore.
DR InterPro, IPR003091, K_channel.
DR InterPro, IPR003131, K_tetra.
DR InterPro, IPR004056, KV43channel.
DR InterPro, IPR003968, Kv_channel.
DR InterPro, IPR005820, M+channel_nlg.
DR InterPro, IPR003975, Shal_channel.
DR Pfam, PF00520, Ion_trans_1.
DR Pfam, PF02214, K_tetra_1.
DR PRINTS, PR00169, KCHANNEL.
DR PRINTS, PR01518, KV43CHANNEL.
DR PRINTS, PR01491, KVCHANNEL.
DR PRINTS, PR01497, SHALCHANNEL.
KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181 Cytoplasmic (Potential).
FT TRANSMEM 182 202 Segment S1 (Potential).
FT TRANSMEM 222 242 Segment S2 (Potential).
FT

FT DOMAIN 243 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Segment S3 (Potential).
FT TRANSMEM 287 307 Segment S4 (Potential).
FT DOMAIN 308 320 Cytoplasmic (Potential).
FT TRANSMEM 321 341 Segment S5 (Potential).
FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).
FT DOMAIN 403 655 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPIC 488 506 Missing (in isoform 2).
FT FTId=VSP_008826.
FT CONFLICT 239 239 V -> G (in Ref. 1).
FT CONFLICT 375 375 P -> L (in Ref. 1).
FT CONFLICT 408 408 R -> G (in Ref. 2).
FT CONFLICT 452 452 E -> G (in Ref. 2).
FT CONFLICT 531 531 T -> Q (in Ref. 2).
FT CONFLICT 564 564 A -> D (in Ref. 2).
FT CONFLICT 646 646 A -> T (in Ref. 1).
FT CONFLICT 654 654 V -> A (in Ref. 3 and 4).
SQ SEQUENCE 655 AA, 73479 MW, ADCE502A97204764 CRC64;
Query Match 99.3%; Score 3295.5; DB 1; Length 655;
Best Local Similarity 96.9%; Pred. No. 7.7e-198;
Matches 635; Conservative 0; Mismatches 1; Indels 19; Gaps 1;
QY 1 MAAVAAALPFAAAAGMMPVANCMPPLADKDKRQDELIVLVNSGRFQWRTTLER 60
DB 1 MAAVAAALPFAAAAGMMPVANCMPPLADKDKRQDELIVLVNSGRFQWRTTLER 60
QY 61 YPDTLGSKEKEFFNEDTKEYFEDRPBEVFCVLFNFTGKLHVPRECTSAAYDELA 120
DB 61 YPDTLGSKEKEFFNEDTKEYFEDRPBEVFCVLFNFTGKLHVPRECTSAAYDELA 120
QY 121 YGILPEIIGDCCYEYKDKRKENAERLMDNDSENNQESMPSLSPQTMWRAFENPHTST 180
DB 121 YGILPEIIGDCCYEYKDKRKENAERLMDNDSENNQESMPSLSPQTMWRAFENPHTST 180
QY 181 LALVFTYTGFPFIASVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFVE 240
DB 181 LALVFTYTGFPFIASVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFVE 240
QY 241 YLLRLFAAPSRYPFRSVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVERFRIFE 300
DB 241 YLLRLFAAPSRYPFRSVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVERFRIFE 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVWFYAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVWFYAEKSSASKFTSIPASFWY 360
QY 361 TIVTMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHQNORADKR 420
DB 361 TIVTMTTLGYGDMVPKTIAGKIFGSLGSLGVIALPVPVIVSNFSRIYHQNORADKR 420
QY 421 AOKKARLARIRVAKTGSSNAYLHASKRGLNLEALGTPEEHNMGKTTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHASKRGLNLEALGTPEEHNMGKTTSLIESQHHL 480
QY 481 HCLEKT-----NHEFIDQMFQNCMESSMWNYPSTRSPSLSSHP 521
DB 481 HCLEKT-----NHEFIDQMFQNCMESSMWNYPSTRSPSLSSHP 521
QY 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTSSSLNKADG 581
DB 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTSSSLNKADG 581
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTSSSLNKADG 600
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIGSEQPSLTSSSLNKADG 600
QY 582 LRPNCKTSQITTAISIPTPPALTPEGSRPPASGPPNTNIPSLTSNVKYSVL 636
DB 582 LRPNCKTSQITTAISIPTPPALTPEGSRPPASGPPNTNIPSLTSNVKYSVL 636
QY 601 LRPNCKTSQITTAISIPTPPALTPEGSRPPASGPPNTNIPSLTSNVKYSVL 655
DB 601 LRPNCKTSQITTAISIPTPPALTPEGSRPPASGPPNTNIPSLTSNVKYSVL 655
RESULT 2
KCD3_RAT
ID KCD3_RAT STANDARD; PRT; 655 AA.

AC Q62897; 008723; P70622; Q63286; Q99P42;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
GN Name=Kcnd3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=96428386; PubMed=8831489;
RA Dixon J.E., Shi W., Wang H.-S., McDonald C., Yu H., Wymore R.S.,
RA Cohen I.S., McKinnon D.;
RT "Role of the Kv4.3 K+ channel in ventricular muscle. A molecular
RT correlate for the transient outward current";
RL Circ. Res. 79:659-668(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=96317227; PubMed=8734615;
RA Scrodio P., Vega-Saenz de Miera E., Rudy B.;
RT "Cloning of a novel component of A-type K+ channels operating at
RT subthreshold potentials with unique expression in heart and brain.";
RL J. Neurophysiol. 75:2174-2179(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hippocampus;
RX MEDLINE=97154683; PubMed=9001401; DOI=10.1016/S0014-5793(96)01388-9;
RA Tsaur M.-L., Chou C.-C., Shih Y.-H., Wang H.-L.;
RT "Cloning, expression and CNS distribution of Kv4.3, an A-type K+
RT channel alpha subunit.";
RL FEBS Lett. 400:215-220(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Smooth muscle, and Vas deferens;
RX MEDLINE=98111009; PubMed=9450548; DOI=10.1016/S0014-5793(97)01483-X;
RA Ohya S., Tanaka M., Oku T., Asai Y., Watanabe M., Giles W.R.,
RA Imaizumi Y.;
RT "Molecular cloning and tissue distribution of an alternatively spliced
RT variant of an A-type K+ channel alpha-subunit, Kv4.3 in the rat.";
RL FEBS Lett. 420:47-53(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=21402960; PubMed=11427525; DOI=10.1074/jbc.M101058200;
RA Song M., Helguera G., Eghbali M., Zhu N., Zarek M.M., Olcese R.,
RA Toro L., Stefani E.;
RT "Remodeling of Kv4.3 potassium channel gene expression under the
RT control of sex hormones.";
RL J. Biol. Chem. 276:31883-31890(2001).
RN [6]
RP SEQUENCE OF 455-606 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97460452; PubMed=9314834;
RA Takimoto K., Li D., Hersman K.M., Li P., Jackson E.K., Levitan E.S.;
RT "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel subunit
RT mRNAs in ventricles of renovascular hypertensive rats.";
RL Circ. Res. 81:533-539(1997).
RN [7]
RP INTERACTION WITH KCNIP1, KCNIP2 AND KCNIP3.
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
RA An W.F., Bowlby M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
RA Hinson J.W., Mattsson K.I., Strassle B.W., Trimmer J.S., Rhodes K.J.;
RT "Modulation of A-type potassium channels by a family of calcium
RT sensors";
RL Nature 403:553-556(2000).
RN [8]
RP SUBCELLULAR LOCATION.
RX MEDLINE=22128857; PubMed=12006572; DOI=10.1074/jbc.M203651200;
RA Takimoto K., Yang E.-K., Conforti L.;

RT "Palmitoylation of KChIP splicing variants is required for efficient
RT cell surface expression of Kv4.3 channels.";
RL J. Biol. Chem. 277:26904-26911(2002).
RN [9]
RP INTERACTION WITH KCNIP4.
RX MEDLINE=21664433; PubMed=11805342; DOI=10.1073/pnas.022509299;
RA Holmqvist M.H., Cao J., Hernandez-Pineda R., Jacobson M.D.,
RA Carroll K.I., Sung M.A., Betty M., Ge P., Gilbride K.J., Brown M.E.,
RA Jurman M.E., Lawson D., Sitos-Santiago I., Xie Y., Covarrubias M.,
RA Rhodes K.J., Di Stefano P.S., An W.F.;
RT "Elimination of fast inactivation in Kv4 A-type potassium channels by
RT an auxiliary subunit domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:1035-1040(2002).
RN [10]
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
RP inactivating A-type potassium channels. May contribute to I(TO)
RP current in heart and I(Sa) current in neurons. Channel properties
RP are modulated by interactions with other alpha subunits and with
RP regulatory subunits.
RN [11]
RP SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.
RN Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
RN KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNAB1 (by
RN similarity).
RN [12]
RP SUBCELLULAR LOCATION: Integral membrane protein. Interaction with
RN palmitoylated KCNIP2 and KCNIP3 enhances cell surface expression.
RN [13]
RP ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=3;
RN Name=1; Synonyms=Kv4.3 long form;
RN IsoId=Q62897-1; Sequence=Displayed;
RN Name=2;
RN IsoId=Q62897-2; Sequence=VSP_008831;
RN Name=3;
RN IsoId=Q62897-3; Sequence=VSP_008832;
RN [14]
RP TISSUE SPECIFICITY: Highly expressed in brain, in particular in
RN the retrosplenial cortex, medial habenula, anterior thalamus,
RN hippocampus, cerebellum and lateral geniculate and superior
RN colliculus. Highly expressed in heart atrium and throughout the
RN ventricle wall, in lung and vas deferens.
RN [15]
RP DOMAIN: The segment S4 is probably the voltage-sensor and is
RN characterized by a series of positively charged amino acids at
RN every third position.
RN [16]
RP SIMILARITY: Belongs to the potassium channel family. D (Shal)
RN subfamily.
RN [17]
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RN [18]
RN EMBL; U42975; AAC52695.1; -;
RN EMBL; U75448; AAB18337.1; -;
RN EMBL; L48619; AAA80459.1; -;
RN EMBL; AF334791; AAK07651.1; -;
RN EMBL; AB003587; BAA24525.1; -;
RN EMBL; U92897; AAB53321.1; -;
RN HSSP; Q16968; 1A68.
RN InterPro: IPR005821; Ion trans.
RN InterPro: IPR001622; K+channel_pore.
RN InterPro: IPR003091; K_channel.
RN InterPro: IPR003131; K_tetra.
RN InterPro: IPR004056; KV43channel.
RN InterPro: IPR003968; Kv_channel.
RN InterPro: IPR005820; M+channel_nlg.
RN InterPro: IPR003975; Shal_channel.
RN Pfam; PF00520; Ion_trans; 1.
RN Pfam; PF02214; K_tetra; 1.
RN PRINTS; PR00169; KCHANNEL.
RN PRINTS; PR01518; KV43CHANNEL.
RN PRINTS; PR01491; KVCHANNEL.
RN PRINTS; PR01497; SHALCHANNEL.
RN Alternative splicing; Ion transport; Ionic channel; Multigene family;

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KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181 Cytoplasmic (Potential).
FT TRANSMEM 182 202 Segment S1 (Potential).
FT TRANSMEM 222 242 Segment S2 (Potential).
FT TRANSMEM 243 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Segment S3 (Potential).
FT TRANSMEM 287 307 Segment S4 (Potential).
FT DOMAIN 308 320 Cytoplasmic (Potential).
FT TRANSMEM 321 341 Segment S5 (Potential).
FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).
FT DOMAIN 403 455 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPPLIC 488 506 Missing (in isoform 2 and isoform 3).
FT VARSPPLIC 608 655 /FTID=VSP_008831.
FT VARSPPLIC 608 655 SQTITATISIPTPALTPBEGSRPPASPGPNTNIPSTISN
VVKVSVL -> QDEQQRGRVVTCKQEEITTCI (in
isoform 3).
FT /FTID=VSP_008832.
FT L -> H (in Ref. 3).
FT CONFLICT 124 124 S -> T (in Ref. 2 and 5).
FT CONFLICT 404 404 S -> T (in Ref. 3).
FT CONFLICT 569 569 P -> A (in Ref. 2).
FT CONFLICT 631 631 V -> A (in Ref. 1 and 4).
FT CONFLICT 654 654
SQ SEQUENCE 655 AA; 73513 MW; 26BC512BDE069C09 CRC64;

Query Match 99.1%; Score 3288.5; DB 1; Length 655;
Best Local Similarity 96.8%; Pred. No. 2.1e-197;
Matches 634; Conservative 1; Mismatches 1; Indels 19; Gaps 1;

QY 1 MAAGVAAMLPBARAAAGMMPVANCMPMLAPADKNKRODEILVANSGRFQWRTTLER 60
DB 1 MAAGVAAMLPBARAAAGMMPVANCMPMLAPADKNKRODEILVANSGRFQWRTTLER 60
QY 61 YPDLLGSTEKEFFENEDTKEYFFEDRDEVEFRCVLNFYRTGKLHYPREYCISAYDELEAF 120-
DB 61 YPDLLGSTEKEFFENEDTKEYFFEDRDEVEFRCVLNFYRTGKLHYPREYCISAYDELEAF 120
QY 121 YGILPEITGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFROTMRAEFNPHST 180
DB 121 YGILPEITGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFROTMRAEFNPHST 180
QY 121 YGILPEITGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFROTMRAEFNPHST 180
DB 121 YGILPEITGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFROTMRAEFNPHST 180
QY 181 LALVEYYVGFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFPCLDTCVMIFVE 240
DB 181 LALVEYYVGFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFPCLDTCVMIFVE 240
QY 181 LALVEYYVGFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFPCLDTCVMIFVE 240
DB 181 LALVEYYVGFIAVSVITNVETVPCGTVPGSKELPCGERYSVAFPCLDTCVMIFVE 240
QY 241 YLRLFAADSRYSRFRSVMISIDVVAIMPYIGLVMTNEDVSGAFYTLRVERFRIFRF 300
DB 241 YLRLFAADSRYSRFRSVMISIDVVAIMPYIGLVMTNEDVSGAFYTLRVERFRIFRF 300
QY 241 YLRLFAADSRYSRFRSVMISIDVVAIMPYIGLVMTNEDVSGAFYTLRVERFRIFRF 300
DB 241 YLRLFAADSRYSRFRSVMISIDVVAIMPYIGLVMTNEDVSGAFYTLRVERFRIFRF 300
QY 301 SRHSGRLRIGYTLKSCASELGFLLSLTMAITTFATVMFAEKSSASKFTSIPASFWY 360
DB 301 SRHSGRLRIGYTLKSCASELGFLLSLTMAITTFATVMFAEKSSASKFTSIPASFWY 360
QY 301 SRHSGRLRIGYTLKSCASELGFLLSLTMAITTFATVMFAEKSSASKFTSIPASFWY 360
DB 301 SRHSGRLRIGYTLKSCASELGFLLSLTMAITTFATVMFAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSCISGLVLAIPVPVIVSNFRIRYHONORADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSCISGLVLAIPVPVIVSNFRIRYHONORADKRR 420
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSCISGLVLAIPVPVIVSNFRIRYHONORADKRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSCISGLVLAIPVPVIVSNFRIRYHONORADKRR 420
QY 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTTSLISQHHLL 480
DB 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTTSLISQHHLL 480
QY 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTTSLISQHHLL 480
DB 421 AOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTTSLISQHHLL 480
QY 481 HCLEKTT-----NHEFIDEQMFQONCMSSMONYPSTRSPSLSSHP 521
DB 481 HCLEKTT-----NHEFIDEQMFQONCMSSMONYPSTRSPSLSSHP 521
QY 481 HCLEKTT-----NHEFIDEQMFQONCMSSMONYPSTRSPSLSSHP 521
DB 481 HCLEKTT-----NHEFIDEQMFQONCMSSMONYPSTRSPSLSSHP 521
QY 522 GLTTTCCSRSSKKTTHLPNSNLPATRLSMQELSTIHIOGSEQPSLTSSSSINLKADG 581
DB 522 GLTTTCCSRSSKKTTHLPNSNLPATRLSMQELSTIHIOGSEQPSLTSSSSINLKADG 581
QY 541 GLTTTCCSRSSKKTTHLPNSNLPATRLSMQELSTIHIOGSEQPSLTSSSSINLKADG 600
DB 541 GLTTTCCSRSSKKTTHLPNSNLPATRLSMQELSTIHIOGSEQPSLTSSSSINLKADG 600
QY 582 LRPNCKTSQITTAISIPTPALTPBEGSRPPASPGPNTNIPSTISNVKVSVL 636
DB 582 LRPNCKTSQITTAISIPTPALTPBEGSRPPASPGPNTNIPSTISNVKVSVL 636
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DB 601 LRPNCKTSQITTAISIPTPALTPBEGSRPPASPGPNTNIPSTISNVKVSVL 655

RESULT 3
KCD3_MOUSE STANDARD; PRT; 655 AA.
ID KCD3_MOUSE
AC Q9Z0V1; Q8CC44; Q9Z0V0;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
GN Name=Kcnd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark R.B., Giles W.R.;
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochoia C., Cobani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guerinclinc S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski B., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai U., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [3]
RP INTERACTION WITH KCNIP3.
RX MEDLINE=21481767; PubMed=11598014; DOI=10.1093/emboj/20.20.5715;
RA Liss B., Franz O., Sewing S., Bruns R., Neuhoff H., Roeper J.;
RT "Tuning pacemaker frequency of individual dopaminergic neurons by
RT Kv4.3L and KChIP3.1 transcription."
RL EMBO J. 20:5715-5724 (2001).
RN [4]
RP INTERACTION WITH KCND2 AND KCNIP2.
RX MEDLINE=21906624; PubMed=11909823;
RA DOI=10.1161/01.RES.0000012664.05949.E0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RA Nerbonne J.M.;
RT "Role of heteromultimers in the generation of myocardial transient
RT outward K+ currents."
RL Circ. Res. 90:586-593 (2002).
```


CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC -1- SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNAB1 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Kv4.3L;
CC IsoId=Q9Z0V1-1; Sequence=Displayed;
CC Name=2; Synonyms=Kv4.3M;
CC IsoId=Q9Z0V1-2; Sequence=VSP_008827;
CC Name=3;
CC IsoId=Q9Z0V1-3; Sequence=VSP_008828, VSP_008829;
CC Note=May be due to intron retention. No experimental
CC confirmation available;
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -----
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CC -----
DR EMBL; AF107781; AAD16973.1; -.
DR EMBL; AF107782; AAD16974.1; -.
DR EMBL; AK033962; BAC28529.1; -.
DR HSSP; Q16968; 1A68.
DR MGD; MGI:1928743; Kcnd3.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K_channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181
FT TRANSMEM 182 202 Cytoplasmic (Potential).
FT TRANSMEM 222 242 Segment S1 (Potential).
FT DOMAIN 243 256 Segment S2 (Potential).
FT TRANSMEM 257 277 Cytoplasmic (Potential).
FT TRANSMEM 287 307 Segment S3 (Potential).
FT DOMAIN 308 320 Segment S4 (Potential).
FT TRANSMEM 321 341 Cytoplasmic (Potential).
FT TRANSMEM 350 380 Segment S5 (Potential).
FT TRANSMEM 382 402 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 403 455 Segment S6 (Potential).
FT DOMAIN 467 555 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPLIC 488 531 GLSYVDPLISVTRSTIKNHEFIDQMFQNCMESSMONY
PST -> VSSSLPPASSLTSQCTHVIIPRESSVFPQ
SKIIVSLPLG (in isoform 3).
/FTId=VSP_008828.
Missing (in isoform 2).
FT VARSPLIC 488 506

FT VARSPLIC 532 655 /FTId=VSP_008827.
FT Missing (in isoform 3).
FT Missing (in isoform 3).
SQ SEQUENCE 655 AA; 73462 MW; 17FCE5AECC2868B33 CRC64;
Query Match 98.8%; Score 3278.5; DB 1; Length 655;
Best local similarity 96.5%; Pred. No. 8.9e-197;
Matches 632; Conservative 1; Mismatches 3; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFAAAAGWMPVANCMPPLADKNKODELIIVNVSGRRPQTRTTLER 60
DB 1 MAAGVAAWLPFAAAAGWMPVANCMPPLADKNKODELIIVNVSGRRPQTRTTLER 60
QY 61 YPDTLLGSTEKEFFNEDTKEYFPDRDPEVRCVLIINFRYTGKLIHPRYECTISAYDELI 120
DB 61 YPDTLLGSTEKEFFNEDTKEYFPDRDPEVRCVLIINFRYTGKLIHPRYECTISAYDELI 120
QY 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNQESMPSISFROTWRAPENPHST 180
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNQESMPSISFROTWRAPENPHST 180
QY 181 LALVFYVVTGFIAVSVITNVETVPCGTVGSKELPCGERYSVAFFCLDTACVMIPTVE 240
DB 181 LALVFYVVTGFIAVSVITNVETVPCGTVGSKELPCGERYSVAFFCLDTACVMIPTVE 240
QY 241 YLLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEVSGAFVTLRVRVRIKF 300
DB 241 YLLRLFAAPSRFRFIRSVMSIIDVAIMPYIIGLVMTNNEVSGAFVTLRVRVRIKF 300
QY 301 SRHSQGLRIIGYTLKSCASELGFLLSLTMAIIPATWVFYAEKSSASAKFTSIPASF 360
DB 301 SRHSQGLRIIGYTLKSCASELGFLLSLTMAIIPATWVFYAEKSSASAKFTSIPASF 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFSGISCSLGVLIAPVPIVSNFSRIYHONORADK 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFSGISCSLGVLIAPVPIVSNFSRIYHONORADK 420
QY 421 TIVMTTLGYGDMVPKTIAGKIFSGISCSLGVLIAPVPIVSNFSRIYHONORADK 420
DB 421 TIVMTTLGYGDMVPKTIAGKIFSGISCSLGVLIAPVPIVSNFSRIYHONORADK 420
QY 421 AOKKARLARIRVAKTGSSNAYLHSGRNLNEALELTGTPPEEHMGKTSLSIESQHLL 480
DB 421 AOKKARLARIRVAKTGSSNAYLHSGRNLNEALELTGTPPEEHMGKTSLSIESQHLL 480
QY 481 HCLEKTTGLSYVDPLLSVRTSTIKNHEFIDQMFQNCMESSMONYSTRSPSSSHS 521
DB 481 HCLEKTTGLSYVDPLLSVRTSTIKNHEFIDQMFQNCMESSMONYSTRSPSSSHS 521
QY 522 GLTTTCCSRRSKKTTHLPNSNLPAIRLRSMQELSTHIOGSEQPSLTGSSSLNKAD 581
DB 522 GLTTTCCSRRSKKTTHLPNSNLPAIRLRSMQELSTHIOGSEQPSLTGSSSLNKAD 581
QY 541 GLTTTCCSRRSKKTTHLPNSNLPAIRLRSMQELSTHIOGSEQPSLTGSSSLNKAD 600
DB 541 GLTTTCCSRRSKKTTHLPNSNLPAIRLRSMQELSTHIOGSEQPSLTGSSSLNKAD 600
QY 582 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGPNTNIPITSNVKVS 636
DB 601 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGPNTNIPITSNVKVS 655
RESULT 4
KCD3_RABIT STANDARD; PRT; 655 AA.
ID KCD3_RABIT
AC Q9TUT5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated
DE potassium channel subunit Kv4.3).
DE Name=KCND3;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=New Zealand white; TISSUE=Corneal endothelium;
RA Rae J.L.;
RT "Ion channels in cornea endothelium.";

RU Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 73-645 FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=22117972; PubMed=12122138;
RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G., Obeso A., Ganforina M.D., Gonzalez C.,
RT "Molecular identification of Kv alpha subunits that contribute to the oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit carotid body."
RT J. Physiol. (Lond.) 542:369-382(2002).
CC -I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.
CC -I- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4. Interacts with KCMB1, KCNE2, SCN1B and KCNAB1 (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=Q9TTF5-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=Q9TTF5-2; Sequence=VSP 008830;
CC -I- TISSUE SPECIFICITY: Detected in carotid body chemoreceptor cells and in frontal cortex.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
CC -I- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF198445; AAF06021.1; -
DR EMBL; AF493549; AAM46843.1; -
DR HSSP; Q16968; 1A68.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1518; KV43CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
DR PRINTS; PRO1497; SHALCHANNEL.
KW Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane; Transport; Voltage-gated channel.
KW DOMAIN 1 181 Cytoplasmic (Potential).
FT TRANSMEM 182 202 Segment S1 (Potential).
FT TRANSMEM 222 242 Segment S2 (Potential).
FT DOMAIN 243 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Segment S3 (Potential).
FT TRANSMEM 287 307 Segment S4 (Potential).
FT DOMAIN 308 320 Cytoplasmic (Potential).
FT TRANSMEM 321 341 Segment S5 (Potential).
FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).

FT DOMAIN 403 655 Cytoplasmic (Potential).
FT SITE 367 372 Selectivity filter (By similarity).
FT VARSPIC 488 506 Missing (in isoform 2).
FT FTId=VSP 008830.
SQ SEQUENCE 655 AA; 73380 MW; C6AE9E85415FAF9 CRC64;
Query Match 98.5%; Score 3269.5; DB 1; Length 655;
Best Local Similarity 96.2%; Pred. No. 3.2e-196;
Matches 630; Conservative 2; Mismatches 4; Indels 19; Gaps 1;
QY 1 MAAGVAAWLPFAARAAGMMPVANCMPPLADKDKKRODELIVLVSGRRQRTWRTLLER 60
DB 1 MAAGVAAWLPFAARAAGMMPVANCMPPLADKSKRDELIVLVSGRRQRTWRTLLER 60
QY 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSPROTMMRAFENPHST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQESMPSLSPROTMMRAFENPHST 180
QY 181 LALVFTYVTFGLVAVSVITNVETVPCGTVPKSGELPCGERYSVAFCLDPAACVMITVE 240
DB 181 LALVFTYVTFGLVAVSVITNVETVPCGTVPKSGELPCGERYSVAFCLDPAACVMITVE 240
QY 241 YLRLFAAPSRYPFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRFRIFKE 300
DB 241 YLRLFAAPSRYPFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRFRIFKE 300
QY 301 SRHSQGLRILGYTLKSCASGLFLSLTMAIIIFATWFFAEKSSASKFTSIPASFWY 360
DB 301 SRHSQGLRILGYTLKSCASGLFLSLTMAIIIFATWFFAEKSSASKFTSIPASFWY 360
QY 361 TIVMTTIGYDMVPKTIAGKIFGSLCSLGVVIALPYVIVNSRIRYHONQADKRR 420
DB 361 TIVMTTIGYDMVPKTIAGKIFGSLCSLGVVIALPYVIVNSRIRYHONQADKRR 420
QY 421 AOKKARLARIRVAKTGSSSNAYLHKSNGLNLNLELGTPEEHNKGTSLIESQHHL 480
DB 421 AOKKARLARIRVAKTGSSSNAYLHKSNGLNLNLELGTPEEHNKGTSLIESQHHL 480
QY 481 HCLEKTT-----NHEFIDQMFQNCMESSMONTPTSTPSLSHP 521
DB 481 HCLEKTTGSLYVDPLLSVTRSTIKNHEFIDQMFQNCMESSMONTPTSTPSLSHP 540
QY 522 GLTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEQPSLTTSRSSLNKADG 581
DB 541 GLTTCCSRRSKKTTHLPNSNLPATRLSMOELSTIHIOGSEQPSLTTSRSSLNKADG 600
QY 582 LRPNCKTSQITTAIISIPTPALTPBESRPPASPGPNTNIPSTSNVAVSVL 636
DB 601 LRPNCKTSQITTAIISIPTPALTPBESRPPASPGPNTNIPSTSNVAVSVL 655
RESULT 5
Q8WN02 PRELIMINARY; PRT; 655 AA.
AC Q8WN02; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Voltage-gated potassium channel Kv4.3 long form.
OS Muscivora putorius furo (ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae; Mustela.
OC NCBI_TaxID=9669;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=21896086; PubMed=11897837;
RA Patel S.P., Campbell D.L., Morales M.J., Straube H.C.;

"Heterogeneous expression of KChIP2 isoforms in the ferret heart.";
RT J. Physiol. 539:649-656(2002).
DR EMBL; AF454388; AAL51038.1; -.
DR HSSP; Q63881; 1SGC.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:000515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR0169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KCHANNEL.
DR PRINTS; PR01497; SHACHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 655 AA; 73375 MW; 3DD3E94819FEF6C1 CRC64;

Query Match 98.4%; Score 3266.5; DB 2; Length 655;
Best Local Similarity 95.9%; Pred. No. 5e-196;
Matches 628; Conservative 4; Mismatches 4; Indels 19; Gaps 1;

QY 1 MAAGVAAWLPFARAAAGMPPVANCMPPLADKNKQDELIVLVNSGRFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAGMPPVANCMPPLADKNKQDELIVLVNSGRFQWRTTLER 60

QY YPDTLLGSTEKEFFFNEDTKEYFFPRDPEVRCVLPNFRYRTGKLIHYPRYECISAYDELA 120
DB YPDTLLGSTEKEFFFNEDTKEYFFPRDPEVRCVLPNFRYRTGKLIHYPRYECISAYDELA 120

QY 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSISFRQTMWRAFENPH 180
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSISFRQTMWRAFENPH 180

QY 181 LALVEYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMI 240
DB 181 LALVEYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMI 240

QY 241 YLRLFAAPSRFRFISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 300
DB 241 YLRLFAAPSRFRFISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 300

QY 301 SRHSOGLRILGYTLKSCASELGFLLFSLTMAIIPATVMFYAEKSSASKFTSIPAS 360
DB 301 SRHSOGLRILGYTLKSCASELGFLLFSLTMAIIPATVMFYAEKSSASKFTSIPAS 360

QY 361 TIVMTTLTGVDMPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONRADKR 420
DB 361 TIVMTTLTGVDMPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONRADKR 420

QY 421 AOKKARLARIYAKTGSNAYLHRSKRNGLNEALLETGPREEHMGKTSLSIESQHHL 480
DB 421 AOKKARLARIYAKTGSNAYLHRSKRNGLLETALBLMGTPREEHVGKSTLSIESQHHL 480

QY 481 HCLEKTY-----NHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 521
DB 481 HCLEKTYGLSYLVDPDPLISVRTSTIKNHEFIDEQMEONCMESSMONTYSTRSPSLSSHP 540

QY 522 GLTTTCCSRKKTTHLPNSNLPAITRLRSMOELSTIHIQSGEOPSLTTSRSSLNKA 581
DB 541 GLTTTCCSRKKTTHLPNSNLPAITRLRSMOELSTIHIQSGEOPSLTTSRSSLNKA 600

QY 582 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPISITSNVKVS 636
DB 601 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGPNTNIPISITSNVKVS 655

RESULT 6
Q9PTD3 PRELIMINARY; PRT; 658 AA.
AC Q9PTD3;

DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Potassium channel Kv4.3.
GN Name=KCND3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed white Leghorn; TISSUE=Lens epithelium;
RA Rae J.L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209722; AAF22832.1; -.
DR HSSP; Q63881; 1SGC.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:000515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003131; K_tetra.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR0169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KCHANNEL.
DR PRINTS; PR01497; SHACHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 658 AA; 73896 MW; 0F8743DAF8B12A8 CRC64;

Query Match 94.2%; Score 3126; DB 2; Length 658;
Best Local Similarity 91.9%; Pred. No. 3.1e-187;
Matches 605; Conservative 19; Mismatches 12; Indels 22; Gaps 4;

QY 1 MAAGVAAWLPFARAAAGMPPVANCMPPLADKNKQDELIVLVNSGRFQWRTTLER 60
DB 1 MAAGVAAWLPFARAAAGMPPVANCMPPLADKNKQDELIVLVNSGRFQWRTTLER 60

QY 61 YPDTLLGSTEKEFFFNEDTKEYFFPRDPEVRCVLPNFRYRTGKLIHYPRYECISAYDELA 120
DB 61 YPDTLLGSTEKEFFFNEDTKEYFFPRDPEVRCVLPNFRYRTGKLIHYPRYECISAYDELA 120

QY 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOE-SMPSISFRQTMWRAFENPH 179
DB 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSISFRQTMWRAFENPH 180

QY 180 TLALVYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMI 239
DB 181 TLALVYYVTGFFIAVSITNVETVPCGTVPGSKELPCGERYSVAFPCLDTACVMI 240

QY 240 EYLRLFAAPSRFRFISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 299
DB 241 EYLRLFAAPSRFRFISVMSIIDVVAIMPYIIGLVMTNEDVSGAFVTLRVFRVRI 300

QY 300 FSRHSOGLRILGYTLKSCASELGFLLFSLTMAIIPATVMFYAEKSSASKFTSIPAS 359
DB 301 FSRHSOGLRILGYTLKSCASELGFLLFSLTMAIIPATVMFYAEKSSASKFTSIPAS 360

QY 360 YTIYMTTLTGVDMPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONRADKR 419
DB 361 YTIYMTTLTGVDMPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHONRADKR 420

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QY 420 RAOKKARLARIRVAKTGSSNAYLHRSKNGLNLEALTEG-TPEEHMGKTSLSIESQH 478
DB 421 RAOKKARLARIRVAKTGSSNAYLHRSKNGLNLEALTEGSTEDEQHTTKGTSLSIESQH 480
QY 479 LHCLKETKT-----NHEFIDQMFQNCMESSMONTYSTRSPSLSS 519
DB 481 LHCLKETKTGLSYLVDPLLSVTRSTIKNHEFIDQLFEQNCMESSMONTYSTRSPSLSS 540
QY 520 HPGLTTCSSRSRKTTHLPNSNLPATRLRSMQELSTIHQGEQPSLTSSSLNKAD 579
DB 541 HHGLTSCSSRRHKKTTHLPNSVSPATRLRSMQELSTIHQGEQPSLTSSSLNKAD 600
QY 580 DGLRPNCKTSQITTAIISIPTPPALTPGESRPPSPGPNNTNI-PSITSNVYKSVL 636
DB 601 DGLRPNCKAAQITTAIISIPTPPALTPGESRPPSPGPNNTNI-PSITSNVYKSVL 658

RESULT 7
ID 057662 PRELIMINARY; PRT; 659 AA.
AC 057662;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Potassium channel xKv4.3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Lautermilch N.J., Spitzer N.C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U89265; AAB94379.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1518; KV43CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
DR PRINTS; PRO1497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 659 AA; 74515 MW; 73F5CF339C6A0F47 CRC64;

Query Match 85.6%; Score 2843.5; DB 2; Length 659;
Best Local Similarity 84.1%; Pred. NO. 1.4e-169;
Matches 556; Conservative 39; Mismatches 39; Indels 27; Gaps 7;

QY 1 MAGVAAWLPFAAAGMGMPVANCMPPLAPADKXKQDELIVLVSGRRFQWRTTLER 60
DB 1 MAGVAAWLPFAAAGMGMPVANCMPPLAPADKXKQDEVIILVSGRRFQWRTTLER 60
QY 61 YPDTLGSTEKEFFNEDTKXYFDRDPEVERCVLNFYRTGLHYPRYECISAYDEELAF 120
DB 61 YPDTLGSTEKEFFNEDTKXYFDRDPEVERCVLNFYRTGLHYPRYECISAYDEELAF 120
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DB 61 YPDNLGRPEKEFFNEETKEYFFDRDPEVERSLNPFYRTGLHYPRYECISAYDEELAF 120
QY 121 YGILPEIIGDCCEEYKORKRENAERLMDNDSENQESMPSLSFRQTMRAFENPHST 180
DB 121 YGILPEIIGDCCEEYKORKRENAERLMDNDSEFNKQDAMPSLNRETMRFAFENPHST 180
QY 181 LALVFYVYTGFFIAVSVINWVEFVPCGTVPQSGKELPCGERYSVAFFCLDTACVMIFVE 240
DB 181 LALVFYVYTGFFIAVSVINWVEFVPCGTVPQSGKELPCGERYSVAFFCLDTACVMIFVE 240
QY 241 YLLRLFAAPSRYPFIRSVM---SIIDVAIMPYYIGLVMTN-NEDVSGAFVTLRVFRVER 296
DB 241 YLLRLFAAPSRYPFIRSVMSVMSIDVVAIMPYYIGLVMTNINEDVSGAFVTLRVFRVER 300
QY 297 IFKFSRSQGLRILGYTLKSCASELGFLLFSLTMAITIFATVMFYAEKSSASKFTSIPA 356
DB 301 IFKFSRSQGLRILGYTLKSCASELGFLLFSLTMAITIFATVMFYAEKSSASKFTSIPA 360
QY 357 SFWYTIVTMTTIGYDMVPKTIAGKIFG-SICSLGVLVIALPVPVIVSNESRIYHONOR 415
DB 361 SFWYTIVTMTTIGYDMVPKTIAGKIFEFHLTSLSGVLVIALPVPVIVSNESRIYHONOR 420
QY 416 ADKRAQKARLARIRVAKTGSSNAYLHRSKNGLNLEALTEGTPPEEHMGKTSLSIESQ 475
DB 421 ADKRAQKARLARIRVAKTGSSNAYLHRSKNGLNLEALTEGTPPEEHMGKTSLSIESQ 480
QY 476 HHHHLHCLKETKTNHEF-IDE-----QMFQNCMESSMONTYSTRSP 515
DB 481 HHHHLHCLKETKTGLSYLVDPLLSVTRSDHEBPCLMNSQMFQNCRENSCKNYPSTATYA 540
QY 516 SLSSHFGITTCSSRSRKTTHLPNSNLPATRLRSMQELSTIHQGEQPSLTSSSLN 575
DB 541 SLSSHFGITTCSSRRNKKTTHLPNSNLPATRLRSMQELSTIHQGEQPSLTSSSLN 600
QY 576 LKADGLRPNCKTSQITTAIISIPTPPALTPGESRPPSPGPNNTNI-PSITSNVYKSV 635
DB 601 LKSEDEMSNCKASQITTAIISIPTPPALTPGEETR-PCSPGPNNTNIH-SNIVKXSA 658
QY 636 L 636
DB 659 L 659

RESULT 8
ID 072W36 PRELIMINARY; PRT; 638 AA.
AC 072W36;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Potassium voltage-gated channel, Shal-related family, member 3.
GN ORFNames=zgc:55306;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.U., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045304; AAH45304.1; -.
DR HSSP; Q63881; 1S6C.
DR ZFIN; ZDB-GENE-030131-5626; zgc:55306.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K_channel_pore.
DR InterPro; IPR004056; KV43channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01518; KV43CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 638 AA; 72053 MW; 038645FB28947F47 CRC64;

Query Match 78.0%; Score 2590; DB 2; Length 638;
Best Local Similarity 77.8%; Pred. No. 9, 7e-154;
Matches 501; Conservative 71; Mismatches 58; Indels 14; Gaps 10;

QY 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIIVLVNSGRRQRTWTLER 60
DB 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIIVLVNSGRRQRTWTLDR 60
QY YPDTLLGSTEKEFFFNEDTKYFPDRDPEVRCVLFNRYRTGKLHYPRYECISAYDEELAF 120
DB YPDTLLGSSSEKEFFFNEDTKYFPDRDPEVRCVLFNRYRTGKLHYPRYECISAYDEELAF 120
QY YGILPEIIGDCCEYEYKDKRENAERLMDNDSENNOESMPSLSFRQTMWRAFENPHTST 180
DB YGILPEIISDCCYEYKDKRENTERLMDLLE-DNKDSKLPNMTFRETWRAFENPHTST 179
QY LALVEYYVTGFFIAVSVITNVEVPCGTVPKSGKELPCGERYSVAFFCLDPAVMTFTVE 240
DB MALVFFYYVTGFFIALSVITNVEVPCGYMPNQRDVPCGERYTEAFECMDTACVMTFTVE 239
QY YLLRLFAAPSRRYRFRSVNSIIDVAALPYIYIGLVMTNNEVSGAFVTLRFRVFRIFKP 300
DB YLLRLFAAPSRRYRFRSVNSIIDVAALPYIYIGLVMTNNEVSGAFVTLRFRVFRIFKP 299
QY SRHSQGLRIIGYTLKSCASELGFILSLTMAIIFATVMFYAEKSSASAKRTSIPASFWY 360
DB SRHSQGLRIIGYTLKSCASELGFILSLTMAIIFATVMFYAEKSSSSSKRTSIPASFWY 359
QY TIVMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVVIVSNFSRIYHONORADKR 420
DB TIVMTTLGVDMPKTIAGKIFGSI CSLSGVLVIALPVVIVSNFSRIYHONORADKR 419

QY 421 AOK--KARLARIYVAKTGSSNAYLHNSKRNGLNLEALLETGTPEE-EHMGKTTSLIESQHH 477
DB 420 AOKVOKARLARLARMRISKSGSTAFHLSKRNGLNQSLLELGLSLEEQQLKKTTSLESGHH 478
QY 478 HLHLCLEKXTNHEFIDEQWFEONCWESSMOWNYPTSTRPSLSHPGLTTTCCSRRSKTTTH 537
DB 479 HLHLCLEKXTNHEFIDEQWFEONCWESSMOWNYPTSTRPSLSHPGLTTTCCSRRSKTTTH 537
QY 538 LPNSNLPAATRLRSMQELSTHIIQSGEQPSLTTRSSSLNKADGRLPNCKTS-QITTAII 596
DB 538 PLNATHHSHTHNLQELSAHIQCGEQQPLNTRSSSLNLSMDESGSLNCKSGGLVTTAII 597
QY 597 SIPTPPA---LTPEGESRPPASPDPNTNIPSTSNVYKVSVL 636
DB 598 SIPTPPSNNSRASPDAPSPNPPEAP-PLLN-PSST-DVVKISAL 638

RESULT 9

Q8HYZ1 PRELIMINARY; PRT; 630 AA.
ID Q8HYZ1;
AC Q8HYZ1;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Voltage-gated potassium channel Kv4.2.
OS Musceta putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Musceta.
OX NCBI_TaxID=9669;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Patel S.P., Straus H.C.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY147192; AAN39878.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 630 AA; 70565 MW; DA4CFD1698A9842 CRC64;

Query Match 76.2%; Score 2530; DB 2; Length 630;
Best Local Similarity 76.1%; Pred. No. 5, 4e-150;
Matches 488; Conservative 68; Mismatches 69; Indels 16; Gaps 6;

QY 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIIVLVNSGRRQRTWTLLE 59
DB 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIIVLVNSGRRQRTWTLLE 60
QY YPDTLLGSTEKEFFFNEDTKYFPDRDPEVRCVLFNRYRTGKLHYPRYECISAYDEELA 119
DB YPDTLLGSSSEKDFYHPEYQYFFDRDPEIFRHLINFNRYRTGKLHYPRHICISAYDEELA 120

Oy		120	FYGLIPELTIIGDCCYEYKORKRENERLMDNDSENNOES-MPSLSFRQTMRAFENPHT	178
Db		121	FFGLIPELTIGDCCYEEYKORRENARLQDDADTDNTGESALPTMTARQRVWRAFENPHT	180
Oy		179	STIALVFYVTGPFIAVSVTNNVETPCGTVPGS-KELPCGERYSVAFPCLDTACVMIF	237
Db		181	STMALVFYVTGPFIAVSIVIANVETVPCGSSPGHIKEPLCGERYAVAFCPLDTACVMIF	240
Oy		238	TVEYLRLRFAPSRRYRFIRSVMSIIDVVAIMPYIIGLVMTNNEVSGAFYTLRVFRVRI	297
Db		241	IVEYLRLRAAPSRKYRFVRSVMSIIDVVAILEYYIIGLVMTDNEDVSGAFYTLRVFRVRI	300
Oy		298	EKFSRHSGGLRIIGVTLKSCASELGFLFSLMAIIIPATVMFYAEKGSSASKFTSI PAS	357
Db		301	FKFSRHSGGLRIIGVTLKSCASELGFLFSLMAIIIFATVMFYAEKGSSASKFTSI PA	360
Oy		358	PWTYIVTMTTLGYGDMVPKTIAGKIPSGISCSGLVLTALPVPIVSNFSRIYHQNRAD	417
Db		361	PWTYIVTMTTLGYGDMVPKTIAGKIPSGISCSGLVLTALPVPIVSNFSRIYHQNRAD	420
Oy		418	KRAAQKKARLARIRVAKTGSSNAYHLSKRNGLINEALEITGTPEEHHMGKTTSLISSQH	477
Db		421	KRAAQKKARLARIRAKTGSAANAYMQSKRNGLLSNQLQ-SSDEDAFVSKSGSSFOTQH	479
Oy		478	HLLHCLKERTNHFEIDQMFEPQNCESSMÖNPVSTRSPSLSHHPGLTTCCRSRKTTTH	537
Db		480	HLLHCLKERTNHFEVDQVFEESSCMEVATGNRRSSHSPSLSSQGCVTSTCCSRHKTKTR	539
Oy		538	LPNSSLPATRLRSMOELSTIHIOGSEOPSLTTSRSSLNKLKADDGLRPNCKTSQITTAIS	597
Db		540	IPNAVSGSHRGSVQELSTIQIRCVERTPLSNSRSSLNAMKEBCVLCNCEOPYVTTAITS	599
Oy		598	IPTPALTPEGESRP--PPASGPNTNIPITSNVKVSVL	636
Db		600	IPTPPTVTEGGDDRPESPESYSG-----NIVRYVAL	630
 RESULT 10 KC2D_RABIT				
ID	KCD2_RABIT	STANDARD:	PRT;	630 AA.
AC	P59995;			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Potassium voltage-gated channel subfamily D member 2 (Voltage-gated potassium channel subunit Kv4.2).			
DE	Name=KCND2;			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RC	STRAIN=New Zealand white; TISSUE=Cornea;			
RL	Rae J.L.;			
RP	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.			
RX	[2]			
CC	SEQUENCE OF 15-614 FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
CC	MEDLINE=22117972; PubMed=12122138;			
CC	Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G.,			
CC	Obeso A., Ganforina M.D., Gonzalez C.;			
CC	"Molecular identification of Kv alpha subunits that contribute to the			
CC	oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit			
CC	carotid body.";			
CC	J. Physiol. (Lond.) 542:369-382(2002).			
CC	-I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly			
CC	inactivating A-type potassium channels. May contribute to I(To)			
CC	current in heart and I(Sa) current in neurons. Channel properties			
CC	are modulated by interactions with other alpha subunits and with			
CC	regulatory subunits.			
CC	-I- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.			
CC	Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and			

```
CC KCN174. Interacts with DPP6, DLG4 and FREQ. Interacts with FLNA  
CC and FLNC (By similarity).  
CC -| SUBCELLULAR LOCATION: Integral membrane protein.  
CC -| TISSUE SPECIFICITY: Detected in brain frontal cortex.  
CC -| DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at  
CC every third position.  
CC -| PTM: Phosphorylated on serine and threonine residues (By  
CC similarity).  
CC -| SIMILARITY: Belongs to the potassium channel family. D (Shal)  
CC subfamily.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb.ch/announce/  
or send an email to licenses@isb-sib.ch).  
-----  
DR EMBL, AF508735; AAM46929.1; -.  
DR EMBL, AF493547; AAM46841.1; -.  
DR InterPro; IPR005821; Ion_trans.  
DR InterPro; IPR001622; K+channel_pore.  
DR InterPro; IPR003131; K_tetra.  
DR InterPro; IPR005820; M_channel_nlg.  
DR Pfam; PF00520; Ion_trans; 1.  
DR Pfam; PF02214; K_tetra; 1.  
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
KW Potassium; Potassium channel; Potassium transport; Transmembrane;  
KM Transport; Voltage-gated channel.  
FT DOMAIN 1 183 Cytoplasmic (Potential).  
FT TRANSMEM 184 204 Segment S1 (Potential).  
FT FT TRANSMEM 225 245 Segment S2 (Potential).  
FT DOMAIN 246 259 Cytoplasmic (Potential).  
FT TRANSMEM 260 280 Segment S3 (Potential).  
FT TRANSMEM 290 310 Segment S4 (Potential).  
FT DOMAIN 311 323 Cytoplasmic (Potential).  
FT TRANSMEM 324 344 Segment S5 (Potential).  
FT TRANSMEM 363 383 Segment H5 (Pore-forming) (Potential).  
FT TRANSMEM 385 405 Segment S6 (Potential).  
FT DOMAIN 406 630 Cytoplasmic (Potential).  
FT SITE 370 375 Selectivity filter (By similarity).  
FT MOD_RES 38 38 Phosphothreonine (By similarity).  
FT MOD_RES 552 552 Phosphoserine (By similarity).  
FT MOD_RES 602 602 Phosphothreonine (By similarity).  
FT MOD_RES 607 607 Phosphothreonine (By similarity).  
FT MOD_RES 616 616 Phosphoserine (By similarity).  
FT CONFLICT 118 118 E -> K (in Ref. 2).  
FT CONFLICT 379 379 K -> R (in Ref. 2).  
SQ SEQUENCE 630 AA; 70613 MW; 5981C87A5E4CA1D1 CRC64;
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Query Match      76.0%; Score 2524; DB 1; Length 630;  
Best Local Similarity 76.0%; Pred. No. 1.3e-149;  
Matches 489; Conservative 69; Mismatches 65; Indels 20; Gaps 7.
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Oy 1 MAAGVAAMLPPARAALIGMPVANCPMLAPADKNKR-ODELIVLNVSGRRFGQTRTTLE 59

Dbl 1 MAAGAVALLPFARRAAAIIGMPVASGPMADPPOERKRTODALIIVLVNSGTROPOTWDTIE 60

Oy 60 RYPDTLTGSTEKEFFFNEDTKERYFPDRDPDEVRCVLNFYRGLKHRYREYCISAYDDLA 119

Dbl 61 RYPDITLGSSSERDFFYHDETQQYFFDRDPDI FRHIILNYFRGLKHYRHECISAYDELTA 120

Oy 120 FYGI LPEI IGDCYE EYKDKREN AERTLDNDSENNOQS-MPSLSRFQTMRPAFENPHPT 178

Dbl 121 FFGLIPETIIIDCCYE YEKDRRRENAERLODADPTNTCESALPTMTARQRWRBAFENPHPT 180

Oy 179 STIALVFYYVTGGFI AVSVITTVAVTCGVTPGS-KELPCGERYSVAFFCLDTACVMIF 237

Dbl 181 STMALVFYYVTGFIA VSIANVVEITVP CGSSPGHKIKELPCGERYAFAAFCLDTACVMIF 240

Oy 238 TWBYLLRLFLAABSRYPRI RSVMSLTDVNAILPIPYIGLVMTNNEDVSQA FVTLARVRVERI 297

Db 241 TVEYLRLAAPSRRYRFRVSVMSIIDVAILPYIIGLWMTDNEEDSGAFVLRVFRERI 300
Qy 298 FKFSRHSGRLRIGYTLKSCASELGLFLSLTMAIITPAVMFAEKSSASKFTSIPAS 357
Db 301 FKFSRHSGRLRIGYTLKSCASELGLFLSLTMAIITPAVMFAEKSSASKFTSIPAA 360
Qy 358 FWYITVMTTLGYGDMVPKTIAGKIFGSCISGLVIALPVPIVSNFSRIYHONRAD 417
Db 361 FWYITVMTTLGYGDMVPKTIAGKIFGSCISGLVIALPVPIVSNFSRIYHONRAD 420
Qy 418 KRAQKKARLARIRVAKTGSSNAYHRSKRNGLNLEALTGTPEEE-HMGKTSLSIESQ 475
Db 421 KRAQKKARLARIRVAKTGSSNAYHRSKRNGLNLEALTGTPEEE-HMGKTSLSIESQ 477
Qy 476 HHHLLHGLEKTNHEFIDQMEQNMESMOMNYPSTRSPSLSHPGTLTCCSRRSKKT 535
Db 478 HHHLLHGLEKTNHEFIDQMEQNMESMOMNYPSTRSPSLSHPGTLTCCSRRSKKT 537
Qy 536 THLPNSNLPATRLSRMOELSTIHIQSEQPSLTSSRSINLKADDELRPNCKTSQITTAI 595
Db 538 FRIPNANVSGSGSVOELSTIQIRCVERTPLNSRSSINAKMEBCVKLNCEQPYVTTAI 597
Qy 596 ISIPTPPALTPGESRP--PPASPCPNTNIPSTSNVYKVSVL 636
Db 598 ISIPTPPALTPGESRP--PPASPCPNTNIPSTSNVYKVSVL 630

RESULT 11
KCD2_MOUSE STANDARD; PRT; 630 AA.
ID KCD2_MOUSE STANDARD; PRT; 630 AA.
AC Q920V2; Q8BSK3; Q8CHB7; Q9JU60;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
potassium channel subunit Kv4.2).
GN Name=Kcnd2; Synonyms=Kiaa1044;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark R.B., Giles W.R.;
RT "Cloning and functional characterization of mouse heart K+ channel
alpha subunits, Kv1.5, Kv4.2 and Kv4.3";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RT Hashimoto K.;
RL "Isolation of full-length cDNA clones from mouse brain cDNA library";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22353125; PubMed=12465718;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RT Ohara O., Koga H.;
RL "Prediction of the coding sequences of mouse homologues of KIAA gene:
I. The complete nucleotide sequences of 100 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries";
RL DNA Res. 9:179-188(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros, and Olfactory bulb;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RL Miki K., Osato N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Garmmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanaei A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Resole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP PHOSPHORYLATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20497051; PubMed=11040264;
RA Varga A.W., Anderson A.E., Adams J.P., Vogel H., Sweatt J.D.;
RT "Input-specific immunolocalization of differentially phosphorylated
Kv4.2 in the mouse brain";
RL Learn. Memory 7:321-332(2000).
RN [6]
RP INTERACTION WITH KCNP3, MTTAGENESIS OF SER-552, AND PHOSPHORYLATION.
RX MEDLINE=22338839; PubMed=12451113;
RA Schrader L.A., Anderson A.E., Mayne A., Pfaffinger P.J., Sweatt J.D.;
RT "PKA modulation of Kv4.2-encoded A-type potassium channels requires
formation of a supramolecular complex";
RL J. Neurosci. 22:10123-10133(2002).
RN [7]
RP INTERACTION WITH KCND3 AND KCNP2.
RX MEDLINE=21906624; PubMed=11909823;
DOI=10.1161/01.RES.0000012664.05949.E0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RT "Role of heteromultimers in the generation of myocardial transient
outward K+ currents";
RL Circ. Res. 90:586-593(2002).
RN [8]
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
inactivating A-type potassium channels. May contribute to I(to)
current in heart and I(Sa) current in neurons. Channel properties
are modulated by interactions with other alpha subunits and with
regulatory subunits.
RN [9]
RP SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3.
Associates with the regulatory subunits KCNP1, KCNP2, KCNP3 and
KCNP4. Interacts with DPP6, DLG4 and FREQ. Interacts with FINA
and FLNC (by similarity).
RN [10]
RP SUBCELLULAR LOCATION: Integral membrane protein.
Tissue specificity: Detected in brain, especially in hippocampus,
medial habenular nucleus, striatum, amygdala, cortex and
cerebellum.
RN [11]
RP DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
every third position.
RN [12]
RP SIMILARITY: Belongs to the potassium channel family. D (Shal)
subfamily.
RN [13]
RP CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 520.
RN [14]
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF107780; AAD16972.1; -.
DR EMBL; AB045326; BAA97986.1; ALT_FRAME.
DR EMBL; AB093280; BAC41464.1; ALT_INIT.
DR EMBL; AK032268; BAC27787.1; -.
DR EMBL; AK032772; BAC28015.1; -.
DR PIR; PT0675; PT0675.
DR HSSP; Q16968; 1A68.
DR MGI; MGI:102663; Kcnd2.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004055; Kv42channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
KM Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 183 Cytoplasmic (Potential).
FT TRANSMEM 184 204 Segment S1 (Potential).
FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 630 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphothreonine.
FT MOD_RES 552 552 Phosphoserine.
FT MOD_RES 602 602 Phosphothreonine.
FT MOD_RES 607 607 Phosphothreonine.
FT MOD_RES 616 616 Phosphoserine.
FT MUTAGEN 552 552 S->A: Abolishes PKA-mediated modulation
of channel activity.
FT CONFLICT 22 22 V -> A (in Ref. 2).
FT CONFLICT 516 516 S -> R (in Ref. 3).
SQ SEQUENCE 630 AA; 70576 MW; 7FB94277429E7683 CRC64;
Query Match 76.0%; Score 2523; DB 1; Length 630;
Best Local Similarity 76.0%; Pred. No. 1.5e-149;
Matches 487; Conservative 68; Mismatches 70; Indels 16; Gaps 6;
QY 1 MAGVAAWLPFAFAAAIGMMPVANCMPPLAPADKNKR-ODELIVLVNSGRFPQWRTTLE 59
DB 1 MAGVAAWLPFAFAAAIGMMPVASCMPMPAPRROERKRTODALIVLVNSGTRFQWQDTLE 60
QY 60 RYDPTLGSIEKEFFENEDTKYFFDRDEVEFRCLNFRYRGKLYHYRECIAYDDELA 119
DB 61 RYDPTLGSSEERDFYHPETOQYFFDRDPDIFRHLNFRYRGKLYHYRECIAYDDELA 120
QY 120 FYGLPEIIDDCYEEYKDKRENAERLMDNDSENQES-MPSLSFQOTMRAFENPH 178
DB 121 FFGLPEIIDDCYEEYKDKRENAERLMDNDSENQES-MPSLSFQOTMRAFENPH 180
QY 179 STLALVFFYVTGFFIAVSVITNVETPGCTVPGS-KELPCGERYSVAFFCLDTACVMIF 237
DB 181 STLALVFFYVTGFFIAVSVIANVETVPGSSPGHIELPCGERYAVAFCLDTACVMIF 240

QY 238 TVEYLRLFAAPSRHYRFRISVMSIIDVAIMPYIGLVMTNNEVSGAFVTLRVFRERI 297
DB 241 TVEYLRLFAAPSRHYRFRISVMSIIDVAIMPYIGLVMTNNEVSGAFVTLRVFRERI 300
QY 298 FKSRSOGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASKFTSIPAS 357
DB 301 FKSRHSGRLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASKFTSIPAS 360
QY 358 FWYTIYMTTLGYDGMVPKTIAGKIRGICSLSGVLVIALPVPVIVSNFSRIYHONRAD 417
DB 361 FWYTIYMTTLGYDGMVPKTIAGKIRGICSLSGVLVIALPVPVIVSNFSRIYHONRAD 420
QY 418 KRAOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 477
DB 421 KRAOKKARLARIRVAKTSSNAYLHRSKRNGLNEALELTGTPEEHMGKTSLSIESQH 479
QY 478 HLHCLKETTNEHFIIDQMEQONCMSSMONTPTSRPSLSHPGLTTCCSRSKTTH 537
DB 480 HLHCLKETTNEHFIIDQMEQONCMSSMONTPTSRPSLSHPGLTTCCSRSKTTH 539
QY 538 LPSNLPATRLRSMQELSTIHIGSEBQPSLTSSSLNLKADGRLPNCKTSQITTAIIS 597
DB 540 IPNAVSGSHRGVQELSTIQRCVERTPLSNRSLSNAKMEECVKLNCEQPYVTIAIIS 599
QY 598 IPTPALTPGESRP--PPASPGPNTNIPITSNVKYSVL 636
DB 600 IPTPVTTPEGDRDPESPEYSGG-----NIVRSAL 630

RESULT 12

KCD2_RAT STANDARD; PRT; 630 AA.
ID KCD2_RAT Q63881; Q00090; Q99249;
AC Q63881; Q00090; Q99249;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
potassium channel subunit Kv4.2) (Shal1) (RK5).
GN Name=Kcnd2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hippocampus;
RX MEDLINE=92000693; PubMed=1840649; DOI=10.1016/0896-6273(91)90299-F;
RA Baldwin T.J., Tsaur M.-L., Lopez G.A., Jan Y.-N., Jan L.Y.;
RT "Characterization of a mammalian cDNA for an inactivating voltage-
sensitive K+ channel.";
RT Neuron 7:471-483(1991).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley; TISSUE=Heart;
RX MEDLINE=91156694; PubMed=1705709;
RA Roberds S.L., Tankun M.M.;
RT "Cloning and tissue-specific expression of five voltage-gated
potassium channel cDNAs expressed in rat heart.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:1798-1802(1991).
RN [3]
RP INTERACTION WITH KCNIP1, KCNIP2 AND KCNIP3.
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
RA An W.F., Bowlby M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
RA Hinson J.W., Mattsson K.I., Strassle B.W., Trimmer J.S., Rhodes K.J.;
RT "Modulation of A-type potassium channels by a family of calcium
sensors.";
RT Nature 403:553-556 (2000).
RN [4]
RP INTERACTION WITH KCNIP1 AND FREO.
RX MEDLINE=21532927; PubMed=11606724; DOI=10.1073/pnas.221168498;
RA Nakamura T.Y., Pountney D.J., Ozaita A., Nandi S., Ueda S., Rudy B.,
RA Coetzee W.A.;

RT "A role for frequency, a Ca²⁺-binding protein, as a regulator of Kv4
RT K⁺-currents.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12808-12813(2001).
RN [5]
RN INTERACTION WITH KCNIP4.
RX MEDLINE=21964093; PubMed=11847232; DOI=10.1074/jbc.M200897200;
RA Morohashi Y., Hatano N., Ohya S., Takikawa R., Watabiki T.,
RA Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.;
RT "Molecular cloning and characterization of CALP/KCNIP4, a novel EF-
RT hand protein interacting with presenilin 2 and voltage-gated potassium
RT channel subunit Kv4.";
RL J. Biol. Chem. 277:14965-14975(2002).
RN [6]
RN MUTAGENESIS OF 627-VAL--LEU-630, AND INTERACTION WITH DLG4.
RX MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;
RA Wong W., Newell E.W., Jungloff D.G.M., Jones O.T., Schlachter L.C.;
RT "Cell surface targeting and clustering interactions between
RT heterologously expressed PSD-95 and the Shal voltage-gated potassium
RT channel 'Kv4.2'";
RL J. Biol. Chem. 277:20423-20430(2002).
RN [7]
RN INTERACTION WITH DPP6.
RX MEDLINE=22464931; PubMed=12575952; DOI=10.1016/S0896-6273(02)01185-6;
RA Nadal M.S., Ozaita A., Amaillo Y., Vega-Saenz de Miera E., Ma Y.,
RA Mo W., Goldberg E.M., Mismis Y., Ikebara Y., Neubert T.A., Rudy B.;
RT "The CD26-related dipeptidyl aminopeptidase-like protein DPPX is a
RT critical component of neuronal A-type K⁺ channels.";
RL Neuron 37:449-461(2003).
CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC -1- SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3.
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC KCNIP4. Interacts with FLNA and FLNC (By similarity). Interacts
CC with DPP6, DLG4 and FREG.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Interaction with
CC DPP6, DLG4 or FREG may increase cell surface expression.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart and throughout the
CC brain, with similar levels in cortex and hypothalamus, and much
CC higher levels in hippocampus, dentate gyrus and the habenular
CC nucleus of the thalamus. Detected at similar levels in heart
CC atrium and ventricle. Detected in aorta, cardiac and smooth
CC muscle.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- PTM: Phosphorylated on serine and threonine residues (By
CC similarity).
CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 477.
CC -----
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CC -----
DR EMBL; S64320; AAB19939.1; -;
DR EMBL; M59980; AAA40929.1; ALT_FRAME.
DR PIR; JU0271; JU0271.
DR PDB; 1S6C; X-ray; B=1-30.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K_channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR004055; KV42channel.
DR InterPro; IPR003968; Kv_channel.

DR	InterPro; IPR005820; M+channel_nlg.		
DR	InterPro; IPR003975; Shal_channel.		
DR	Pfam; PF00520; Ion_trans_1.		
DR	Pfam; PF02214; K_tetra_1.		
DR	PRINTS; PRO0169; KCHANNEL.		
DR	PRINTS; PRO1517; KV42CHANNEL.		
DR	PRINTS; PRO1491; KVCHANNEL.		
DR	PRINTS; PRO1497; SHALCHANNEL.		
KW	3D-structure; Ion transport; Ionic channel; Multigene family;		
KW	Phosphorylation; Potassium; Potassium channel; Potassium transport;		
KW	Transmembrane; Transport; Voltage-gated channel.		
FT	DOMAIN	1	183
FT	TRANSMEM	184	204
FT	TRANSMEM	225	245
FT	DOMAIN	246	259
FT	TRANSMEM	260	280
FT	TRANSMEM	290	310
FT	DOMAIN	311	323
FT	TRANSMEM	324	344
FT	TRANSMEM	363	383
FT	TRANSMEM	385	405
FT	DOMAIN	406	630
FT	SITE	370	375
FT	MOD_RES	38	38
FT	MOD_RES	552	552
FT	MOD_RES	602	602
FT	MOD_RES	607	607
FT	MOD_RES	616	616
FT	MOD_RES	627	630
FT	MUTAGEN		
SQ	SEQUENCE	630 AA; 70548 MW; 1 FDE57E8A5113BABF CRC64;	

Query Matchn	75.9%	Score 2519	DB 1	Length 630
Best Local Similarity	75.8%	Pred. No. 2.6e-149		
Matches 486	Conservative 69	Mismatches 70	Indels 16	Gaps 6
Qy	1	MAAGVAAWLPFARAALIGMPPVANCMPMLAPADKXNR-QDELIIVLVNSGRRFQWRTTLE	59	
Db	1	MAAGVAAWLPFARAALIGMPPVASCMPMPADPRQGRKXTQDALIVLVNSGRRFQWRTTLE	60	
Qy	60	RYPDTLLGSTKEKFFFNEDTKERYFFDRDPEVFRVCVINFYRTGKLHYPRXCISAYDELA	119	
Db	61	RYPDTLLGSSSERDPFFYHPETQYQYFPDRDPDIFRHILNFYRTGKLHYPRHCISAYDELA	120	
Qy	120	FYGLPEILIGDCCYEYKDKRENAERLMDNDSENNOES-MPSLSFROTMRAFENPHT	178	
Db	121	FFGLIPEIIGDCCYEYKDRRRENAERLQDDADTDNTGESALPTMTARQVRWRAFENPHT	180	
Qy	179	STLALVFYVYVGFIAVSIVTNTVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF	237	
Db	181	STMALVFYVYVGFIAVSIVANVETVPCGSSPGHikelPCGERYAVAFCLDTACVMIF	240	
Qy	238	TVEYLRLFAAPBRYRFRISVMSIIDVVALMPYIIGLWMTNNEVDVSGAVTLRVERVRI	297	
Db	241	TVEYLRLFAAPBRYRFRISVMSIIDVVALIPYIIGLWMTNNEVDVSGAVTLRVERVRI	300	
Qy	298	EKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWVFYAEKSSASAKFTSIPAS	357	
Db	301	EKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWVFYAEKSSASAKFTSIPAA	360	
Qy	358	FWYTIYMTTLGYGDMVPKTIAGKIFGSIISLGSUVIALPVPVIVSNFSRIYHONORAD	417	
Db	361	FWYTIYMTTLGYGDMVPKTIAGKIFGSIISLGSUVIALPVPVIVSNFSRIYHONORAD	420	
Qy	418	KRAQOKARLARIRVAKTGSSNAYLHRSKRGGLNLEALDELGTGPREEHNGKTTSLIESQHH	477	
Db	421	KRAQOKARLARIRVAKTGSSNAYWQSKRNGLLSNOLQ-SEDEPAFVSKSGSSPFTQHH	479	
Qy	478	HLHLCEKTTNHFIDEQMFQONCESSMONEYPSTRSPSLSGHPGLTTTCCSRRSKTTTH	537	
Db	480	HLHLCEKTTNHFVDEQVFEEESCMEVATVNRPSHSPLSSQOGVSTCCSRRHKKSFRR	539	
Qy	538	LPSNSLPATRLRSMQELSTIHIGQSEQPSLTSRSSLNLKADDDGLRPNCKTSQITTAIIS	597	


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Db      540 IPNANVSGSHRGVQELSTIQICRVERPPLSNRSRLNAAKECVKLNCQOPYVTTAIS 599
QY      598 IFPPPALTPGESRP--PPASPGPNTNIPSTSNVVKVSVL 636
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      600 IFPPVPTPEGDDRPESPESYSGG-----NIVRVSL 630

RESULT 13
KCD2_HUMAN STANDARD; PRT; 630 AA.
AC      Q9NZV8; O95012; O95021; Q9UBV7; Q9UN98; Q9UNH9;
DT      29-MAR-2004 (Rel. 43, Created)
DT      29-MAR-2004 (Rel. 43, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
DE      potassium channel subunit Kv4.2).
DE      Name=KCND2; Synonyms=KIAA1044;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=99061682; PubMed=9843794;
RA      Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.;
RT      "Isolation and characterization of the human gene encoding Ito:
RT      further diversity by alternative mRNA splicing."
RL      Am. J. Physiol. 275:H1963-H1970(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=99397452; PubMed=10470851;
RA      Kikuno R., Nagase T., Ishikawa K.-I., Hiroseawa M., Miyajima N.,
RA      Tanaka A., Kotani H., Nomura N., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. XIV.
RT      The complete sequences of 100 new cDNA clones from brain which code
RT      for large proteins in vitro."
RL      DNA Res. 6:197-205(1999).
RN      [3]
RP      SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.
RX      MEDLINE=20017432; PubMed=10551270;
RA      Zhu X.-R., Wulf A., Schwarz M., Isbrandt D., Pongs O.;
RT      "Characterization of human Kv4.2 mediating a rapidly-inactivating
RT      transient voltage-sensitive K+ current."
RL      Recept. Channels 6:387-400(1999).
RN      [4]
RP      SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC      TISSUE=Brain cortex;
RX      MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;
RA      Isbrandt D., Leichter T., Waldschuetz R., Zhu X.-R., Luhmann U.,
RA      Michel U., Sauter K., Pongs O.;
RT      "Gene structures and expression profiles of three human KCND (Kv4)
RT      potassium channels mediating A-type currents I(TO) and I(SA).";
RL      Genomics 64:144-154(2000).
RN      [5]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22616434; PubMed=12690205; DOI=10.1126/science.1083423;
RA      Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayashi K.,
RA      Herbrick J.-A., Carson A.R., Parker-Katiraei L., Skaug J., Khaja R.,
RA      Zhang J., Hudak A.K., Li M., Haddad M., Duggan G.B., Fernandez B.A.,
RA      Kanematsu E., Gentles S., Christopoulos C.C., Choufani S.,
RA      Kwasnicka D., Zheng X.H., Lai Z., Nuskern D., Zhang Q., Gu Z., Lu F.,
RA      Zeebman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C.,
RA      Weksberg R., Zackai E.H., Grebe T.A., Cox S.R., Kirkpatrick S.J.,
RA      Rahman N., Friedman J.M., Heng H.H.Q., Pelicci P.G., Lo-Coco F.,
RA      Belloni E., Shaffer L.G., Pober B., Morton C.C., Gusella J.F.,
RA      Bruns G.A.P., Korf B.R., Quade B.J., Ligon A.H., Ferguson H.,
RA      Higgin A.W., Leach N.T., Herrick S.R., Lemyre E., Farra C.G.,
RA      Kim H.-G., Summers A.M., Griep K.W., Roberts W., Szatmari P.,
RA      Winsor E.J.T., Grzeschik K.-H., Teebi A., Minassian B.A., Kere J.,
RA      Armengol L., Pujana M.A., Estivill X., Wilson M.D., Koop B.F.,
RA      Tosi S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B.,

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RA      Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner H.,
RA      Doehner K., Rommens J.M., Vincent J.B., Venter J.C., Li P.W.,
RA      Mural R.J., Adams M.D., Tsui L.-C.;
RT      "Human chromosome 7: DNA sequence and biology."
RL      Science 300:767-772(2003).
RN      [6]
RP      MUTAGENESIS OF 601-PRO--PRO-604, SUBCELLULAR LOCATION, AND INTERACTION
RP      WITH FLNA AND FLNC.
RX      MEDLINE=20556633; PubMed=11102480;
RA      Petrecca K., Miller D.M., Shrier A.;
RT      "Localization and enhanced current density of the Kv4.2 potassium
RT      channel by interaction with the actin-binding protein filamin."
RL      J. Neurosci. 20:8736-8744(2000).
CC      -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC      inactivating A-type potassium channels. May contribute to I(TO)
CC      current in heart and I(Sa) current in neurons. Channel properties
CC      are modulated by interactions with other alpha subunits and with
CC      regulatory subunits.
CC      -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
CC      Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
CC      KCNIP4. Interacts with DPP6, DLG4 and FREQ (By similarity).
CC      Interacts with FLNA and FLNC.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Detected in
CC      dendrites in cultured hippocampal neurons.
CC      -1- TISSUE SPECIFICITY: Highly expressed throughout the brain.
CC      Expression is very low or absent in other tissues.
CC      -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC      characterized by a series of positively charged amino acids at
CC      every third position.
CC      -1- PTM: Phosphorylated on serine and threonine residues (By
CC      similarity).
CC      -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC      subfamily.
CC      -----
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CC      -----
DR      EMBL; AF121104; AAD22053.1; -.
DR      EMBL; AB028967; BA82996.2; ALT_INIT.
DR      EMBL; AJ010969; CAB56841.1; -.
DR      EMBL; AF166008; AAF65618.1; -.
DR      EMBL; AF166007; AAF65618.1; JOINED.
DR      EMBL; AC004888; AAC83405.1; -.
DR      EMBL; AC004946; -; NOT ANNOTATED_CDS.
DR      EMBL; AF142568; AAD52159.1; -.
DR      HSSP; Q16968; 1A68.
DR      H-InvDB; HGNC:6238; KCND2.
DR      MIM; 605410; -.
DR      InterPro; IPR005821; Ion trans.
DR      InterPro; IPR001622; K+channel_pore.
DR      InterPro; IPR003091; K channel.
DR      InterPro; IPR003131; K_tetra.
DR      InterPro; IPR004055; KV42channel.
DR      InterPro; IPR003968; Kv channel.
DR      InterPro; IPR005820; M+channel_nlg.
DR      InterPro; IPR003975; Shal channel.
DR      Pfam; PF00520; Ion_trans_1.
DR      Pfam; PF02214; K_tetra; 1.
DR      PRINTS; PR00169; KCHANNEL.
DR      PRINTS; PR01517; KV42CHANNEL.
DR      PRINTS; PR01491; KVCHANNEL.
DR      PRINTS; PR01497; SHALCHANNEL.
DR      PRINTS; PR01497; SHALCHANNEL.
DR      Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW      Potassium; Potassium channel; Potassium transport; Transmembrane;
KW      Transport; Voltage-gated channel.
FT      DOMAIN 1 183 Cytoplasmic (Potential).
FT      TRANSMEM 184 204 Segment S1 (Potential).

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FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 630 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphothreonine (By similarity).
FT MOD_RES 552 552 Phosphoserine (By similarity).
FT MOD_RES 602 602 Phosphothreonine (By similarity).
FT MOD_RES 607 607 Phosphothreonine (By similarity).
FT MOD_RES 616 616 Phosphoserine (By similarity).
FT MUTAGEN 601 604 PRPP->ATMA: Abolishes interaction with FLNC.
FT CONFLICT 450 450 N -> S (in Ref. 1).
FT CONFLICT 464 464 Q -> P (in Ref. 1).
FT CONFLICT 550 550 Q -> R (in Ref. 1).
FT CONFLICT 553 553 I -> V (in Ref. 1).
SQ SEQUENCE 630 AA; 70536 MW; 0C11E62FFA220421 CRC64;

Query Match 75.8%; Score 2518; DB 1; Length 630;
Best Local Similarity 75.8%; Pred. No. 3e-149;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAGVAAWLPFAAAAIIGMPVANCMPPLADKNKR-QDELIVLVNSGRRFQWTTLTLE 59
DB 1 MAGVAAWLPFAAAAIIGMPVASCMPAPRQERKRTQDALIVLVNSGRRFQWTDLTLE 60
QY 60 RYPDTLLGSTKKEFFFNEDTKYEFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 119
DB 61 RYPDTLLGSSSERDFYHPETQYFFDRDPDIFRHILNFRYRTGKLHYPRHICISAYDELA 120
QY 120 FYGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178
DB 121 FFGILPEIIGDCYEEYKDRRENAERLQDDADDTDTAGESALPMTARQVMRAFENPHT 180
QY 179 STLAIFYYYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
DB 181 STMALIFYYYVTGFFIAVSIVANVETVPCGSSPGHIXELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAADSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 297
DB 241 TVEYLRLFAADSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 300
QY 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPAS 357
DB 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPAA 360
QY 358 FMYTIVMTTIGYGDMPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONORAD 417
DB 361 FMYTIVMTTIGYGDMPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRRACKKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGPBEEHMGKTSLIESQHH 477
DB 421 KRRACKKARLARIRVAKTSSNAYLHSKRNGLLSNOLQ-SSDEQAFVSKSSGSSFEYTOHH 479
QY 478 HLLHCLEKTNNHEFIDEQMFQONCMSSMONTPTSRPSLSHGLTTCSSRSRKTTH 537
DB 480 HLLHCLEKTNNHEFIDEQMFQONCMSSMONTPTSRPSLSHGLTTCSSRSRKTTH 539
QY 538 LPSNLDPATRLRSMOELSTIHIGSEQPSLTSSSLNLKADDLRPNCKTSQITTAIIS 597
DB 540 IPNAVSGSHQSIQELSTIQIRCVERTPLSNSRSSSLNAKMECVKLNCEQPYVTTAIIIS 599
QY 598 IPTPALTPGESRP--PPASGPNTNIPSTISNVKSVL 636
DB 600 IPTPVYTPTEGDHPESPEYSG-----NIVRSAL 630
RESULT 14

Q8UW33 ID Q8UW33 PRELIMINARY; PRT; 632 AA.
AC Q8UW33;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Shal-1 like voltage-gated potassium channel.
GN Name=kva.2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakai Y., Sokolowski B.H.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075160; AAL56633.1; -.
DR HSSP; Q63881; 1S6C.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF02214; K tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV42CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 632 AA; 70982 MW; 147C92979F2297D9 CRC64;

Query Match 75.8%; Score 2517; DB 2; Length 632;
Best Local Similarity 76.2%; Pred. No. 3.5e-149;
Matches 489; Conservative 62; Mismatches 75; Indels 16; Gaps 6;

QY 1 MAGVAAWLPFAAAAIIGMPVANCMPPLADKNKR-QDELIVLVNSGRRFQWTTLTLE 59
DB 1 MAGVAAWLPFAAAAIIGMPVATGMPAPRQERKRSQDSLIVLVNSGIQFQWTDLTLE 60
QY 60 RYPDTLLGSTKKEFFFNEDTKYEFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELA 119
DB 61 RYPDTLLGSSSERDFYHPETQYFFDRDPDIFRHILNFRYRTGKLHYPRHICISAYDELA 120
QY 120 FYGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQES-SMPSLSFRQTMRAFENPHT 178
DB 121 FFGILPEIIGDCYEEYKDRRENAERLQDDADQDHTAESLSMTARQVMRAFENPHT 180
QY 179 STLAIFYYYVTGFFIAVSITNVETVPCGTVPGS-KELPCGERYSVAFCLDTACVMIF 237
DB 181 STLAIFYYYVTGFFIAVSIVANVETVPCGVSPGRIKELPCGERYAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAADSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 297
DB 241 TVEYLRLFAADSRRYRFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVERI 300
QY 298 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPAS 357
DB 301 FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFAEKSSASKFTSIPAA 360
QY 358 FMYTIVMTTIGYGDMPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONORAD 417
DB 361 FMYTIVMTTIGYGDMPKTIAGKIFGSI CSLGVLVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRRACKKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGPBEE-HMGKTSLIESQHH 476
DB 421 KRRACKKARLARIRVAKTSSNAYLHSKRNGLLSNOLQSSSDEQAFVSKSSGSSFEYTOHH 480
QY 478 HLLHCLEKTNNHEFIDEQMFQONCMSSMONTPTSRPSLSHGLTTCSSRSRKTTH 536
DB 480 HLLHCLEKTNNHEFIDEQMFQONCMSSMONTPTSRPSLSHGLTTCSSRSRKTTH 536

Db 481 HHLHLCKETNTNEFVDEQLYEESSCMEVSTVNRPPSHSPSSQQGVGTCCSRHKKT 540

Qy 537 HLPNSNLPATRLRSWQELSTHIQGSSEPSLTSSSLNKLKADGLRPNCKTSQITTAII 596

Db 541 RLPNTALTSRHSVQELSTIQRVETPLNSRSLNAKVECVLNCDEQYVTTAII 600

Qy 597 SIPTPALPPEGESRP--PPASPGPNTNIPITSNVKSVYL 636

Db 601 SIPTPPTPEGGDDRPESPEVSGG-----NIVRVSL 632

RESULT 15

KCD1_MOUSE

ID_KCD1_MOUSE STANDARD; PRT; 651 AA.

AC Q03719; Q8CC68; 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE potassium voltage-gated channel subfamily D member 1 (Voltage-gated

GN Name=Kcnd1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RC TISSUE=Brain;

RX MEDLINE=91239573; PubMed=2034678;

RA Pak M.D., Baker K., Covarrubias M., Butler A., Ratcliffe A.,

RA Salkoff L.

RT "msh1, a subfamily of A-type K+ channel cloned from mammalian

RT brain.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:4386-4390(1991).

RL [2]

RP SEQUENCE OF 145-647 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Spididymis;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,

RA Nagahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirczane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arahawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [3]

RP INTERACTION WITH KCNIP1.

RX MEDLINE=21316019; PubMed=11423117; DOI=10.1016/S0014-5793(01)02560-1;

RA Nakamura T.Y., Nandi S., Pountney D.J., Artman M., Rudy B.,

RA Coetzee W.A.;

RT "Different effects of the Ca(2+)-binding protein, KChIP1, on two Kv4

RT subfamily members, Kv4.1 and Kv4.2.";

RL FEBS Lett. 499:205-209(2001).

CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly

CC inactivating A-type potassium channels. May contribute to I(To)

CC current in the heart and I(Sa) current in neurons. Channel

CC properties are modulated by subunit assembly.

CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND2 and/or KCND3.

CC KCNIP4 (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is

CC characterized by a series of positively charged amino acids at

CC every third position.

CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)

CC subfamily.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M64226; AAA39745.1; -.

DR EMBL; AK033805; BAC28480.1; -.

DR PIR; A39372; A39372.

DR HSSP; Q16968; 1A68.

DR MGI; MGI:96671; Kcnd1.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K+-channel_pore.

DR InterPro; IPR003091; K channel.

DR InterPro; IPR003131; K tetra.

DR InterPro; IPR004054; KV41channel.

DR InterPro; IPR003968; Kv_channel.

DR InterPro; IPR005820; M+-channel_nlg.

DR InterPro; IPR003975; Shal channel.

DR Pfam; PF00520; Ion_trans_1.

DR Pfam; PF02214; K_tetra_1.

DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PR01516; KV41CHANNEL.

DR PRINTS; PR01491; KVCHANNEL.

DR PRINTS; PR01497; SHALCHANNEL.

KW Ion transport; Ionic channel; Multigene family; Potassium;

KW Potassium channel; Potassium transport; Transmembrane; Transport;

KW Voltage-gated channel.

FT DOMAIN 1 184 Cytoplasmic (Potential).

FT TRANSMEM 185 205 Segment S1 (Potential).

FT TRANSMEM 227 247 Segment S2 (Potential).

FT DOMAIN 248 261 Cytoplasmic (Potential).

FT TRANSMEM 262 282 Segment S3 (Potential).

FT TRANSMEM 292 312 Segment S4 (Potential).

FT DOMAIN 313 325 Cytoplasmic (Potential).

FT TRANSMEM 326 346 Segment S5 (Potential).

FT TRANSMEM 365 385 Segment H5 (pore-forming) (Potential).

FT TRANSMEM 387 407 Segment S6 (Potential).

FT DOMAIN 408 651 Cytoplasmic (Potential).

FT SITE 372 377 Selectivity filter (By similarity).

FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).

SO SEQUENCE 651 AA; 71697 MW; 801DECC3C56C721F CRC64;

Query Match 64.5%; Score 2141.5; DB 1; Length 651;

Best Local Similarity 65.7%; Pred. No. 11e-125;

Matches 434; Conservative 76; Mismatches 116; Indels 35; Gaps 13;

Qy 1 MAGVAAWLPFARAAGIGWMPVANCPMLAPADKNKRODELIVLVNSGRRFQWRTTTLR 60

Db 1 MAGVATWLPFARAAGVGLPLAQOPLPAPPEVYKASRGDEVLVVNVSGRRFETWKTTLDR 60

Qy 61 YPDTLLGSEKEFFENEDTKEYFFDRPPEVFRCLTNFYRTGKHVPRYECISAYDDELAF 120

Db 61 YPDTLLGSESEKEFFYDAESGEYFFDRPDMFRVLTNFYRTGRLHCRQECIQAFDEELAF 120

QY 121 YGILPEIIGDCCYEYKORRENAERLMDNDSENNQSMPSL----SFRQTMWRAENP 176
 Db 121 YGLVPELVGDCCEYEYRDRKKEAERLAEDERAEQAGEG-PALPAGSSLRQRLWRAENP 179
 QY 177 HTSTLAVFYVYTGFFIAVSVITNVEVPCGTVP--GSKELPCGERYSVAFCLDTACV 234
 Db 180 HTSTLAVFYVYTGFFIAVSVIANVETIIPCRGTPRWPSKEQSCDRPPTAFPCMDTACV 239
 QY 235 MIFTVEYLLRLFAAPSRVRFIRSVMIIIDVVAIMPYITGLVMTNEDVSGAFVTLRVFV 294
 Db 240 LIFTGEYLLRLFAAPSRRCFLRSVMSLIDVVAILPYITGLFVPKNDVSGAFVTLRVFV 299
 QY 295 FRIFKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSSASKFTSI 354
 Db 300 FRIFKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGTSKINFTSI 359
 QY 355 PASFWYTIIVMTTLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHQNQ 414
 Db 360 PAFAWYTIIVMTTLGYGDMVPSTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHQNQ 419
 QY 415 RADKRRRAQKKARLARIRIVAKTGSSNAYLHSKRNGLLNEALELGTPEEEMH-GKTSLE 473
 Db 420 RADKRRRAQKKARLARIRILAKSGTTNAFLQYKONG---GLEDSGSGDGQMLCVRSRSAFE 475
 QY 474 SQHHHLHLEKXTNHEFIDEQMFECNCESSMQNYPSTRPSLSHP----GLTTCCS 529
 Db 476 QQHHHLHLEKXTNHEFIDEQMFECNCESSMQNYPSTRPSLSHP----GLTTCCS 534
 QY 530 RR-SKKTTHLPNSNLPAIRLRSMQELSTIHIOGSEQPSLTSRSSLNKADDLRPNCKT 588
 Db 535 RRVNRRAIRLANSTASVSR-GSMQELDT--LAGLRSPAPQTRSSLNAKPHDSLNLNCDS 591
 QY 589 SQITTAIISIPFPALTPGESRPPASP-----PNTNI-----PSITSNVVYKVS 635
 Db 592 RQFVAALISIPFPANTPD-ESQPSPPSGGSGGTPTNTLRNSSLGTPCLLPETVRISS 650
 QY 636 L 636
 Db 651 L 651

Search completed: April 6, 2005, 07:13:42
 Job time : 597.111 secs

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